

1073

AGCATCTGCT TTGACAACAT CTTCTATTGC CTGATAAGAA AACTGGTCTG GCAAGATTTT	4500
TAAATACTTA GCTACATGCT TATCGTAGTT AACATAGCCT CTAACCGAAA ACTGACCAAA	4560
AAAGGAAGCT TGGCGTTCAT TAAAACGAGC CAATAATTCA ATCATTTTCAT TGTCTGCTGT	4620
CGACAATTCT TCTTTACTTG CCAACTTCTG AACCAGGTCC TTCATAGCTA CGTTTGGGAA	4680
CTGTTGCAGT AAGCGAGTCG CTGCATATTG ACTAGCCTGA TCCCCAGATT GATGTTTCAG	4740
AAAACCTAGTC AACTGGTCTC CATTAAAATA CTGCTGGAAG GCTGCTGGAT CATAGCCATT	4800
TTTACTGAAC CACTGAGGTG AGATAACATA CACAACCTGT TTATTCTCCA GCTGTGGTAA	4860
CATCTGTTGC ATTCCAAAAT ATTGGTTAAG CGATGCAGCT CCCCCCTGTC CTAAGAGATA	4920
AGGACGGTAG GAACGATTGT ATTTCTCAGC TAATACCGCA GGATGAGCAC CGTCAAAACG	4980
AAGCCATTCA CTAGAGCCAA AGAAGGGAAC AAAACGCACA TTTGGATCAG ATAGTGCTCT	5040
GACTTTTGA CTTCGCTCCT TAAACTATC GATAGTAGTA GCCACTGCTG AACGCTTTTC	5100
AGCTCCTAGA TTATGATGCA TCTCAGTAGG ATAAAAGAAA ATGAGCAGAA AAACCAACAA	5160
ACCAGCGATC AAGACCGGTC CGAAGATCAT CCATAAGCGT TTAAGCATTT TGTAGCTCCA	5220
CAATACCAGC TATGATTTTA TTAGCTGTAT TCCAGTCGTC ACGACCAAAC TCTGTTACAG	5280
GGACACGAAT GTCAAAACGG TTCTCAATCT CCACAATCAA CTCAACCGTT CCCATACTAT	5340
CCAAGACACC TGCATCAAAA AGATCTTCAT CCATCATGTC AGAAACATCT TCCATAAACA	5400
ACTCATCAAT AATTTCATA ACTTCTGATT TGATATCCAT ATTTTATTTT CTTTATTTT	5460
TTAAACCATA GATTATTCOA GAATCCAGAA AAGATTAAGA ATGACAACAT GACAACATGG	5520
AAAGTGACAA CCATGCCAAG CAACTGAATC CAGCGATTCT CAGGTAGGGC AGCCTTCCCT	5580
GCTTTTTCCT GTTCCTTATT GAGCGTTTTT TTCTTGCGAA CCCAGGCATC ATTGATGACC	5640
AAGCCTAGTC CATGAAAGAG TCCATAGGCG ATATAGTACC AGGTACACAC ATGCCAAAAT	5700
CCCATAATCA GCATATTTAC AATGTAGGCC ATGCTTGAGG TTACATTACG ATTTTAAAG	5760
ACTTCTTTC TGGTTAACAC CATCACCATT CGCATAAAGA CAAAGTCACG GAACCAGAAG	5820
GACAGACTCA TATGCCAGCG ATTCCAAAAC TCCTTTAAAT CCCTTGATAA AAAGGGCTTG	5880
TTAAAGTTGA TAGGGCTACG GATTCCTATC AAGTTTGAGA TGGCCAAAGC AAACATAGAA	5940
TAACCTGCAA AGTCAAAGAA GAGTTCAGA CCAAAAGTAT ACATAACTGC CAAGGCATAG	6000
AGATTAAAGA AGCCACCTGA CTGCAAGGCT AAATCTTCA GAGGAGGTAG TAAGGTCTCT	6060
CCTAAAACAT GAGCTAGGAT AAACCTATAC AAAAAGCCCC ACATGATATA GCGGACAGAT	6120
TCATCCAGCA TATCCATCAA CTCATCTCGC TCAGGAATAG CCTGATAATT TTCATTAAAT	6180

1074

CGCTTAAAGC GATCGATTGG ACCACTCGAG AAAGTTGGCA TGAAGAGAAG GAAACGGAGG	6240
AATTCCCAGA GGGTAAAATC CTTAATCACT CCATCTCTCA GCTCGATGAC AATTCCAACC	6300
GAACGAAAGG TCAGGTAAGA AATTCCAAG AACCCAAGCA AAGACTGCGT TCCATTGATA	6360
GCTGGTTGCA CCTTGACAAA GATAATCGGA AGTAGGGACA GAAAACTAAC TAAGTAGAAG	6420
ACCCACTTGC CATCCTTGCT TTTTCGATAA TGCTTGTAGA AAAGCAGGAG CAATATTTCC	6480
CAGCAAAGGT AAATACCCAA GGCAGCTAGT TGATTGGTCT TTCCACCCAC CAACATGGTG	6540
ACAATAAAGA AGAGACTTAC CAACACTTCA TACCAGGCAA AGCGTTTCTT GAAAAAGAGA	6600
CCTATAAAGA TGGGCAAGGT TGCAGCAATC ACATAAACAA AATACTGAGG ATTGCCATAT	6660
GGCTCTAAAT GAGGAAGCTG TTGAAAAAC TCCATCATCT CTTATTCACC TCGTTAATCA	6720
ATCCTTTGAT GTCAATCTTT CCATTGGAG TTAGTGGCAA ACTGTCTCGG TAAAGGAATT	6780
TAGATGGCAT CATATAGGAC ATCATGATGT CTGTCAGGTC TTCTTGATG GCCTTGGTAA	6840
TATCGATATC TCGCTCAAAC TGCTCACGAA CACCGTCTTT TAAGATGACA TAAGCCAATA	6900
GATTTGTAC CTTGTGGTCC TTGTTATAGC GCGGTACTGC GACAGCAGAT TCGATAAAGC	6960
GAGACTTGT GAGGTTTGA GAGACATCTT CTAACCTCAAT GCGGTAACCG TTAAACTTAA	7020
TCTGGAAGTC CATGCCGCCG CCGTAGAGAA GCAAGCCCTC ATCTGTCATG GTTCCCACAT	7080
CGCCTGTGTG ATAGGCTGGC AGATCTTCAA ACTCAAAGAA GGCTTCTGCT GTTTTTTCAG	7140
GATTGTTTAT ATAACCTTTT GAAACAGCTG GCCCAGAAAC AATGATTCTT CCCTGCTCAC	7200
CATTGGCAG TTTATTTCTT TCCTCGTCAA TGATAAAGGT TGGAGAATCA GCCTTGGTAT	7260
AGCCGATTGG TAGGCGTTTG AGAGTCGCTA ACATCTCGTC TGTCACGGCA ACTGCTGACA	7320
GAGCTACTGT CGCTTCTGTT GGGCCGTAAG CATTGATGAT ACGGGCATTG GGGAAACGCT	7380
CGCGCAGTTT TTGAGCTGTT TTGACCGTCA ATTCTTCACC ATCAAAGTAG AAATGCGTGA	7440
TTCCAGGCAT TTTCTCACTG TTGAAGTATT CAGACAACAT GGCCATATCT GCAAAGGATG	7500
GTGTTGATGT CCAGATAGCG ATTGGCAATG AAAAGATAGC CGCAAAGAGT TGCTTAAAGT	7560
CCTGAGTGAT GACTGAAGGA AGAGTGAAAA GCGTACCACC AAGTGCCAAG GTCGGTGCCC	7620
AATACATGAC AGACAAGTCA AAAGAATAAG GTGGCTGTGC CAGCATTGTC GGACGACTCG	7680
GTGTCGAAA TTCCTTATCC GTAATCATCC AGTTTGTAAG GCTGAGGAGA TTATCATGTG	7740
AAATCTGCAC TCCCTTAGGC TTACCAGTCG TACCAGAAGT AAAGATAATG TAGTAATTAT	7800
CATCTCCCTT GACTGGATGC GTGATTTCAT AGTTATTCCC TTGGGCAAAG GCTTCTTGAA	7860
CCTGAGCTAG ATTTATCATT GGTGTAGAAA CCGCTCCAA GGGAAAGGCT GAAATGGCAA	7920
TAATCAAGCT TGGCTCTGCT ACTTCTAAAA TAGCTGAAAC TCGCTCCAAG GCCGAATGGC	7980

1075

TATCAATTGG AATGTAGGCA TGACCTGACT TAGTCAGCGC TACAAAGGTT GCCAACATTT	8040
CATATTCTTG GCCACCAAAA ACAACCACAG GAGACTTCTC AGGCAAGCCT AGTTGGTCAA	8100
TGACTGCAGC CAACTATCC GAATCAGCCT TTAAATCGCC ATAAGTGTGT TCCTGCCCCA	8160
AAACATTATA GACAGGATAG CTAGGCTGTG TCTGAGCAAA ATGCTCAATG GTTTCATCA	8220
TATCTGCTAT TGGTTTATTT GACACAATAG GGATTCTCCT TCAAGTTAAA ATTCATTATA	8280
GATAAAGCTT CCTTGACCCT GACCAAGATA GCTAAAGAAG TAAAGCAGCC CTAGAAAGAT	8340
AAGAAAATAC AAGGCTGTCC GACCAAGAAA GAGGTACAAT TCTTTTCTCT GTTTCATCAA	8400
GAAAAACCAT TCATTTCTGT AATTTTTCGC TAAATAAGA GTGATTCTTA CTAGCTTATT	8460
TTTCTACCAT TGTACCACTT TATATAGTAT CTTTTCATTT GTTTACCGTA TGTTCCTAAT	8520
AGATTTCAAG TTATTTTAAAG GATTATACAG TTTTCTATG TATATTTTCA AATAGAGTGA	8580
TCCTGCTTCA AAATCCATT TCAGGAGACA ATGAAGTAAA TCTTCCATA ATAAACACA	8640
CAATATCAAG TTTTTCATC ACCTGATACT ATGCGCTTTT CTGATTTTAA AAGACTTTTT	8700
AACCACTCTC TCATTTAAAA TAATCTCGTC TGATATAAAT TAAATAGCT TCTATCATCA	8760
GACAAATGGC TGATAGCCAA AAATGATGC TAATACCAAA ACTCTCAGTA ATATAGCTCA	8820
TTAGCAAAAC AAATACTGAA AATGCTAATG TAGAAATCAC TTCAAGAACG GAATAGACAT	8880
TAACTAAATG ATTTTCTCT ACTGTTTCTT GAAGAAATAC ACTTTCAGGA ACTTCTTTTA	8940
GTTCGATAA CATACTAACT AAAGCTGAAA ATAATAAAAA CATCTGTGCG TTGGGAAAAT	9000
ATAGAATAGT CAGTGTCACT ATTTCCATAG CTACAAGAGG AAAAGAATA CTTTCCCCC	9060
AAATCATTCA TACCTCTCTC AACTAGATGT AACTTACAAA ACCCCTGACC TCATGAGCCA	9120
CTTCTTCTCT CCTCATGAGG TCAGTTTAC TTTCTGCTGT TCCAGTATCG TTTTCTCTCG	9180
CTAGATTTCC TCAAAGGGC AGACTCCTCC CTTGGTGCCT CACACGATTT TTTTCTCTCG	9240
ACTGTTCTTT AATGCATCAT TAACGACGCT TTTCTTCTAG GTGGTTCATA AGGAACAGGA	9300
AGATTCAGGT TGACTTTTCT AATCCTAGAA TAAAGTGCTG AAAACAATTC GGAATAGGCA	9360
TAGAGACTAG ACAATTTGAG GAGCTGCTTG CGTCCTGTTT GAACACATTT TCCCACCACG	9420
TGAAGAAAAA GATGGCGGAA GCGTTTGATT GTTAAAGTTT GGAAGTCACC TCCAGCTAGA	9480
TGTTTGAGAA AAAGATAGAG ATTGTAGGCG ATACAGCTCA TCATCATACG AACTTCGTTT	9540
TTGATTAAGG TTGAATATC CGTTTATCG CCAAAAAATC CTCCTTCAT CTCCTTGATG	9600
AAATCTCTCG CTTGACCACG TCCACGATAA AGCTGAAACT GGTCTTGGCT GTTCCACTCG	9660
TCATATTTGT AACGAGAGAA ATAACATCGT AGAACAAGTA TCCTTCTTTT C	9711

1076

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3025 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

CCCCTTTGTC AAAACTGTAA AATTAACGAC TCAACAATTC ATCTTTACAC CAATCTCAAT	60
GGAAAACAAA AACAAATTGA CCTCTGTCAA AACTGCTATA AGATTATCAA AACAGATCCT	120
AACAATAGCC TCTTCAAAGG TATGACGGAT CTGAACAATC GTGACTTCGA TCCCTTTGGT	180
GATTTCTTCA ATGATCTAAA CAATTTCAGA CCTTCTAGCA ATACTCCTCC TATTCCTCCA	240
ACCCAATCAG GTGGAGGTTA CGGTGGAAAC GCGGGTTATG GTTCCCAAAA TCGTGGATCT	300
GCTCAAATC CGCCACCTAG CCAAGAAAAA GGCCTGCTGG AAGAATTGG TATTAATGTA	360
ACTGAAATTG CCCGTCGTGG AGACATTGAC CCCGTTATTG GCGCGACGA TGAGATTATC	420
CGTGTCATCG AGATTCTCAA TCGTAGAACC AAGAATAATC CTGTCCTTAT CGGTGAACCT	480
GGTGTCGGA AAACGGCCGT TGTGGAAGGT CTAGCTCAGA AAATTGTCGA TGGCGATGTG	540
CCACATAAAC TCCAAGGTAA ACAAGTCATC CGTCTGGATG TGGTTAGCTT AGTTCAAGGA	600
ACGGGGATTC GAGGACAATT TGAAGAACGC ATGCAAAAAC TCATGGAAGA AATTCGCAAA	660
CGTGAAGACA TCATCTCTT TATCGATGAA ATCCATGAAA TTGTTGGTGC TGGTTCTGCG	720
AGTGATGGTA ATATGGACGC AGGAAATATC CTCAAGCCAG CCCTTGCTCG TGGAGAATCG	780
CAACTAGTCG GTGCTACTAC CCTCAATGAA TACCGTATCA TTGAAAAGGA TGCTGCCCTC	840
GAGCGTCGTA TGCAGCCTGT TAAAGTCGAT GAACCAACGG TGGACGAAAC AATCACTATT	900
CTCAAAGGGA TTCAAAGAA ATACGAAGAT TACCACCACG TTCAATATAC AGATGCTGCG	960
ATTGAAGCAG CTGCAACTCT TTCCAATCGC TACATCCAAG ATCGCTTCTT GCCTGACAAG	1020
GCCATTGACC TCCTAGATGA AGCTGGTTCT AAGATGAACT TGACCTTGAA TTTTGTGGAT	1080
CCTAAAGTAA TTGATCAGCG CTTGATTGAG GCTGAAAATC TCAAGTCTCA AGCTACACGA	1140
GAAGAAGATT TTGAGAAGGC GGCCTACTTC CGCGACCAGA TTGCCAAGTA TAAGGAAATG	1200
CAAAAGAAAA AGATCACAGA CCAGGATACT CCTAGCATCA GCGAGAAAAC TATTGAGCAC	1260
ATTATCGAGC AGAAAACCAA TATCCCTGTT GGTGATTGTA AAGAGAAAGA ACAATCTCAA	1320
CTCATCCATC TAGCCGAAGA TCTCAAGTCT CATGTTATTG GTCAAGATGA TGCAGTCGAT	1380
AAGATTGCCA AGGCTATTCT CCGTAATCGT GTCGGACTTG GTACCCCTAA CCGCCCAATC	1440

1077

GGAAGCTTCC TCTTCGTTGG GCCAACTGGT GTCGGTAAGA CAGAACTTTC CAAACAACTG	1500
GCTATCGAAC TTTTGGTTC TGCTGATAGT ATGATTGCTT TGGATATGAG TGAATACATG	1560
AAAAACATA GTGTGGCTAA GTTGGTCGGC GCTCCTCCAG GTTATGTTGG CTATGATGAG	1620
GCTGGTCAAT TAACTGAAAA AGTTCGCCAC AATCCATATT CTCTCATCCT TCTCGATGAA	1680
GTGGAAAAAG CTCACCCAGA TGTATGTCAC ATGTTTCTTC AAGTCTTGGA CGATGGTCGT	1740
TGACAGACG GGCAAGGACG CACCGTTAGC TTCAAGGATG CCATCATTAT CATGACCTCA	1800
AATGCAGGTA CAGGAAAGAC CGAAGCTAGC GTTGGATTG GTGCTGCTAG AGAAGGACGT	1860
ACCAATTCTG TCCTCGGTGA ACTCGGTAAC TTCTTTAGCC CAGAGTTTAT GAACCGTTTT	1920
GATGGCATT TCGAATTAA GGCTCTCAGC AAGGATAACC TCCTTCAGAT TGTCGAGCTC	1980
ATGCTAGCAG ATGTTAACA GCGCCTCTCT AGCAACAACA TTCGTTTGA TGTAAGTATG	2040
AAGGTCAAGG AAAAGTTGGT TGACCTAGGT TATGATCCAA AAATGGGAGC ACGCCCACTT	2100
CGTCGACTA TTCAAGACTA TATTGAGGAC ACAATCACTG ACTACTACCT TGAAAATCCA	2160
AGCGAAAAAG ATCTCAAAGC AGTTATGACT AGCAAGGGAA ACATTCAGAT TAAATCTGCC	2220
AAAAAAGCTG AAGTTAAAG TTCTGAAAAA GAAAAATAA TCCTATAAAA AAGGAGTAGA	2280
AAATGAAATT TTTCTGCTTC TTTTCTTACT AAAATAACTG TAATTTCTTG ACAGCTTGCC	2340
CTTTGTCCAT TATGATATAT AGTAGACTGA ATCTGAAATA GTACGAAACA ATTGCTAAAA	2400
CATTATAGA AATTAATTTT ACTTTCCCAA TCGATTGTG CTCATCTTAT TTCAATCTGC	2460
TATAGTCAAT TGAAACAAGA ACAAGACAAA AGAGCCTCAT AAAAGGTATT GCAACTTGGT	2520
AATACCTTTT TGAGGTGCTT TTTGATATGA GCCCATGTTT TCTCAATAGG ATTGTACTCA	2580
GGTGAGTAGG GAGGAAGAGG TAAAAGTTTA TACCCAACT CTTACACAA GAGTTCTAAC	2640
TTACCCATTC TATGGAATCT TGCATTATCC ATAATAATA CCGATGGTGT GGTTAATGTT	2700
GGTAAGAGAA ACTTCTGAAA CCAAGCTTCA AAAAAGTCGC TCGTCATCGT CTCTTCGTAA	2760
GTCATTGGAG CGATTAACTC ACCATTCAAT TGTAGACCT GCAACCAAAG AAATTCTCTG	2820
ATATCTTCTT CCAGATACTT TGCCTCTTCT TAACTGACCT TTTAATGAGC GACCATATTC	2880
TCGATAAAAA TAAGTATCGA ATCCTGTTTC GTCAATCTAA ACAGGTGCTA GTGCTTTAA	2940
ACTATTAAAA TTCTTAAGAA ATAAGGCTAC TTTTCTGGG TCTTGTTTAT AGTAGGTGTA	3000
GTTCCTTTTT TTTTCGAGTG TAGCC	3025

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4104 base pairs

1078

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

TTTAAGGTTT TAAAAAAGT TTTCGAAAGG TTTCTTCTTT ATTTTSTAAG GGAGAGATAA	60
CGTTGATATC TAAATCGTGG TCAAAGCCGG CAATTTTCC TTTAGATGTG TATTGGTGAA	120
TATCATAATC TAAATCAGTT TTAGGACTGC TCTCCAAAA TCCTGAGTCT GAGCCGTAGA	180
CGGAATCCAA ACAGAGGTAA ACTTGCCTGT ATCAATACTG TGTCTTCCA TGAAGTAGAC	240
ACCAACGTAG ATGCCGATGT TTTTAGCACC CAGTGATGCT AGTTTGTGCTC GAAAGTTTC	300
GACACCTTCG TTCATATTAG ACATGGTTTT GTCTTCCACG TCAAGCCAAT AGTAACTAGG	360
GCTGTAAGGA GAGGCAGCAT TGTAAGAAC TTCGGCAGCC TTTTCCATTT CTGGGACACT	420
TTTTCCAGCT ACATAAGCGT AGACAGCAAC TGGGACATTC CGCTTTTGAA GTTCAGTGAT	480
ATGACTCTTA TAGGCCTTGT CTATTCCATT GATAAATGAA GCATCATTTT CTTTGTCTGT	540
TTGAGCACCA CTGTGAACAC GAACAATAGC ACCTGAAATA TTTTGTGAGA GGGCATCGTA	600
GTTGATTTCC TCAGGACGCT GCCAGCCAGA GAGGTCAATA ATCGGTTTGT CTAAGTGTTC	660
CAAAGCCTGT GCTTCAATCT GTGCTATATT GGATTTTGT TTAACGATT GGCTGTCATT	720
AAGTGGGCGA TTGATGATTA AAATGAACAT CATAATCCCA AAAAACTAA ATAAATAAG	780
TGGATGAATT TGTTTCTCA TATCTTATAA TTCTACCTA AAAATCAAAA AAAATCAAAA	840
AAATGGGTTA AGGAAGAGAC TTTAGAGCAT TTTTTCATTC AAGAGTGCGG AATGATTGA	900
AATATGGTAT AATAAAGGG AATTTCTACA GAAAAGAGAA GATTATGTCA AATTTGCCA	960
TTATTTTAGC AGCGGTAA GGGACTCGCA TGAAATCTGA TTTGCCAAAA GTTTGCACA	1020
AGGTTGCGGG TATTTCTATG TTGGAACATG TTTTCCGTAG TGTGGGAGCT ATCCAACCTG	1080
AAAAGACAGT AACAGTTGTA GGACACAAGG CAGAATTGGT TGAGGAGGTC TTGGCTGGAC	1140
AGACAGAAAT TGTGACTCAA TCTGAACAGT TGGGAAGTGG TCATGCAGTT ATGATGACAG	1200
AGCCTATCTT AGAAGGTTTG TCAGGACACA CCTTGGTCAT TGCAGGAGAT ACTCCTTTAA	1260
TCACTGGTGA AAGCTTGAAA AACTTGATTG ATTTCCATAT CAATCATAAA AATGTGGCCA	1320
CTATCTTGAC TGCTGAAACG GATAATCCTT TTGGTTATGG ACGAATTGTT CGTAATGACA	1380
ATGCTGAGGT TCTTCGTATT GTTGAGCAGA AGGATGCTAC AGATTTTGAA AAGCAAATCA	1440
AGGAAATCAA CACTGGAACA TACGTCTTTG ACAACGAGCG TTTGTTTGAG GCTTTGAAAA	1500
ATATCAATAC CAATAACGCT CAAGCGAAT ACTATATTAC AGACGTCATT GGTATTTTCC	1560

1079

GTGAAACTGG TGAAAAAGTT GCGCCTTATA CTTTGAAAGA TTTTGATGAA AGTCTTGGGG	1620
TAAATGACCG TGTGGCGCTT GCGACAGCTG AGTCAGTTAT GCGTCGTCGC ATCAATCATA	1680
AACACATGGT CAACGGTGTT AGCTTTGTCA ATCCAGAAGC AACTTATATC GATATTGATG	1740
TTGAGATTGC TTCGGAAGTT CAAATCGAAG CCAATGTTAC CTTGAAAGGG CAAACGAAAA	1800
TTGGTGCTGA GACTGTTTTG ACAAACGGTA CTTATGTAGT GGACAGCACT ATCGGAGCAG	1860
GAGCGGTCAT TACCAATTCT ATGATTGAGG AAAGTAGTGT TGCAGACGGT GTGATAGTCG	1920
GTCCCTATGC TCACATTCGT CCAAAATCAA GTCTGGGTGC CCAAGTTCAT ATTGGTAACT	1980
TTGTTGAGGT GAAAGGATCT TCAATCGGTG AGAATACCAA GGCTGGTCAT TTGACTTATA	2040
TCGGAACTG TGAAGTGGGA AGCAACGTTA ATTTCCGTGC TGGAACTATT ACAGTCAACT	2100
ATGACGGCAA AAACAAATAC AAGACAGTCA TTGGAAACAA TGTCTTTGTT GGTTCAAATT	2160
CAACCATTAT TGCACAGTA GAACTTGGTG ACAATTCCTT CGTTGGTGCT GGTTCAACTA	2220
TTACTAAAGA CGTGCCAGCA GATGCTATTG CTATTGGTCG CGGTCGTCAG ATCAATAAAG	2280
ACGAATATGC AACACGTCTT CCTCATCATC CTAAGAACCA GTAGGAGCCT ATCATGGAGT	2340
TTGAAGAAAA AACGCTTAGC CGAAAAGAAA TCTATCAAGG ACCAATATTT AAAGTGGTCC	2400
AAGATCAGGT TGAATTACCA GAAGGCAAGG GAACTGCCCC ACGGGATTGT ATTTCCACA	2460
ATGGGGCTGT CTGTGTTTTA GCAGTAACGG ATGAACAAAA ACTTATCTTG GTCAAGCAGT	2520
ACCGCAAAGC TATCGAGGCT GTCTCTTACG AAATTCAGC CGGAAAATTG GAAGTAGGAG	2580
AAAACACAGC CCCTGTGGCA GCTGCCCTTC GTGAATTAGA GGAAGAAACA GCCTATACAG	2640
GGAAATTAGA ACTCTGTAC GATTTTATT CAGCTATTGG CTTTGTAAAT GAGAAGTTAA	2700
AACTATATTT AGCAAGCGAT TTGACAAAAG TGAAAAATCC GCGTCCGCAG GATGAGGATG	2760
AAACCTTGGA AGTCCTTGAA GTGAGCTTAG AAGAAGCGAA AGAATTAATC CAATCAGGTC	2820
ATATCTGTGA TGCCAAGACA ATTATGGCTG TTCAGTATTG GGAGTTGCAG AAAAAATAGA	2880
GGAGGTCACT ATGGGTAAAT CTTTATTAAC GGATGAAATG ATTGAAAGAG CTAATAGAGG	2940
CGAAAAAATT TCAGGTCCTC CTTTGCTAGA TGATAATGAG GAACTAAGA TTTTACCAAC	3000
CTCTTCTTCC CGTTTGGTT ATGCCAATCC TAAGGATCAT GGTTTTAGCC AGGAAACCTT	3060
GAAGATTCAG GTCGAACCAT CTATTCATAA AAGCCGTCGT ATTGAAAATA CCAAGAGAAA	3120
TGTCTTCAAT TCTAAGTTGA ATAAATCTT ATTTGCGGTC ATCTTTCTCT TGATTTTGCT	3180
TGTTTTAGCA ATGAAACTTT TGTAATAGAA AAGGAATTGA AATGAAAATA GGAATTATTG	3240
CTGCTATGCC AGAAGAACTG GCTTATCTGG TCCAGCATTT AGATAATGCC CAGGAGCAAG	3300

1080

TTGTTTTGG GAATACCTAT CATAACAGGAA CCATTGCTTC TCATGAAGTC GTTCTTGTA	3360
AAAGTGAAT TGGAAGGTC ATGTCTGCTA TGAGTGTGGC GATTTTGGCT GATCATTTCC	3420
AGGTGGATGC CCTTATTAAT ACGGGTTCAG CTGGGGCAGT AGCAGAAGGT ATCGCTGTTG	3480
GGGATGTCGT GATTGCTGAC AAATTAGCCT ATCATGACGT GGATGTCACA GCTTTTGGCT	3540
ATGCTTATGG ACAAATGGCG CAACAACCGC TTTATTTCGA ATCAGACAAA ACCTTTGTTG	3600
CTCAAATCCA AAAGAGTTTA TCTCAATTGG ACCAAAACG GCATCTTGGT TTGATTGCTA	3660
CAGGAGATAG TTTTGTGCA GGAAATGACA AGATAGAAGC GATTAAGTCC CATTTCCAG	3720
AAGTTTTAGC CGTGGAGATG GAGGGGGCAG CTATTGCTCA AGCAGCGCAT GCCCTCAATC	3780
TCCCAGTCTT AGTCATCCGA GCTATGAGTG ACAATGCCAA CCATGAAGCA AACATCTTTT	3840
TTGATGAGTT TATTATCGAA GCTGGACGTC GCTCTGCCA AGTCTTGTG ACCTTTTGA	3900
AGGCTTTAGA TTAAGCGAA ATTTGACAGT TTTTCTAGCT TATGATAAGA TTAAAGTAAA	3960
GAAAAGCTAG AAAACGTTT AGAGGATATT ATGAGTATTG AAATGACCGT CAGTGAGATT	4020
GCAGAGGTCT TAGGATTATC TCGCCAAGCA ATCAATAACC GTGTCAAAGA ATTACCAGAA	4080
GAAGACACAG ATAAAAATGA CAAG	4104

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8876 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CACGGATAGG CTCGGCTTTC ATCAGTCCTC AGGCTGATT ACTAATAGCA ACTTTCCTCG	60
ACAAAGTCCA CAGCGATACG TnTGGGTATC AATCCTACGC TTACGCTGAT ACCTTTGCTG	120
GCAGGATTGG CAACGATAGA GCTTGATTGG CTGGAGTTA CTATTGGGCA AGGATGGTAC	180
AAACCGTAAT CCATCCACTG CTTTCAACAG TTCCTTAAAA TCCCGATCCT TGTGTTGATA	240
GCCTTTCCCT TGAAAATAGA GGTGATAATG ACAGAGTTCA TGTCGGACAA TTTTCCTAAA	300
AACGTCCAAC CCCAGTTCCT GATAAACCTT GGGATTAAAA TCCAAATGCC CATCTTTGGG	360
GAAAAATCGC CCACCTGTCG AACGTAGACG CCTATTCCAC TGGACATGAT GGATAAAAGG	420
TCTGCCGAAG TCTTCTAGTG AAACCTGCTT GACGTAATCA GTCAGTTTCA TTTGGAGCTA	480
GGAGAGACAG ATTAACTTT TCACGTTTCA TATCAATTTT CTTAACCCAA ACGCTCACCA	540
AATCTCCAAC TGCCACCACT TGACTAGGGT GTTTGATAAA CTTGCGACTC ATATGGGAAA	600

1081

TATGGATGAG ACCGTCCTCA TGAATTCCGA TATCAACAAA AGCACCGAAA TCAACAACGT	660
TACGCACCAC TCCTTCTAGC TTTTGTCCAA CCACTAAGTC CTTGATATCT AGGACATCTT	720
GGCGAaCACA GGTGCGTCAA AGGAATCACG GAAATCTCGA CCTGGTTTGA GAAGATCTGC	780
AATGATATCT TTAAGAGTTT CTGGACCAAG GTCTAACTCT TGCGCCATTT CCTTGACTGA	840
AAGCGACTTG AGTTTGCTTT GGGCTTCTTC GTTTAGGTCT TTAATATCTA AACGTTTGAA	900
GAGTTCCTTA ACTGCAGTGT AATTCTCTGG GTGAACTCCT GTATTATCAA GGATATTGCT	960
ACTTTCAGGG ATACGAAGGA AACCAGCAGC CTGCTCAAAG GCCTTGGCTC CCAGACGAGG	1020
AACCTTCTTG ATTTGGGCGC GTGAAGTGAT TTTTCCTTCT TCCTCGCGGT ATTTGACAAT	1080
ATTTTCAGAG ATAGTTTGT TGAGTCCAGC TACGTGTGAA AGAAGAGCTG GGCTAGCTGT	1140
ATTGACATTG ACACCAACTT GGTAAACCAC TGTATCGACA ACAAAGTCCA GACTCTCAGA	1200
TAGTTTCTTC TGACTGACAT CGTGTGGTA TTGACCGACA CCAATTGACT TAGGATCGAT	1260
TTTGACCAAT TCCGCAAGAG GATCTTGCAA ACGACGGGCG ATAGAAATGG CAGAGCGTTT	1320
TTCAACGGTC AAGTCTGGAA ACTCCTGACG AGCAAGTTCG CTGGCAGAAT AGACAGAAGC	1380
ACCACTTTCA TTAACGATAA CATAGCTGAC TTCAGGGAAA TCTTTCAGAA CTTCGGCTAC	1440
AAAAGCTTCA CTTTCACGAC TGGCCGTTCC ATTTCCAATG GCAATAATCT CTACACCGTA	1500
TTGACCAATT AAATCTGCTA AATCTTCTT GGCTTCTTCG ATTTGACGAG CTGATGCTGG	1560
TTTAACAGGA TAAATAACCT GAGTTGTCAG CATTTTCTCT GTTGCATCCA CGACAGCTAG	1620
CTTGGCACCT GTACGAAAGG CTGGGTCAA TCCAAGAACC ACGCGCCCTT TCAGTGAGAC	1680
AACCAAGAGG AGATTGCGCA GATTGTCAGA AAAAAGTTGG ATAGCTCCTT CTTGAGCTTT	1740
CTCAGTTAAT TCTGTCCGAA TACGACGCTC GATAGCAGGC AAGACCTTTT TCTTAACGGA	1800
TTGCTGAACA ACTTCATCA TATAAGCATT TTTACCTTG AAACGAGTAG CAAAGAAGGC	1860
AAGAATACGG TCCGTGCGAT GTTCAAAACC GATCTTCAAG ACACCAAGTT TCTCCCCACG	1920
ATTGAGAGCC AAGGTACGAT AGCCTTGCAT AGTTCCAAT GTCTCTGAAA AATCATAATA	1980
AATCTGAAAA ACCTGCTTTT CATCAAGACT TTCATCCTTG GCTTGAGAAG TAAGTTTAGA	2040
GTGTCTCAGC ACTTCCTGAT AAGTCATAGA ACGCAAGGTC ACATCTTCCG ATAAGGCTTC	2100
GACCAAAATA TCAACTGCAC CGGTCAAGGC TTCCTTGCCA GTCGCAAATC CTTACAGAC	2160
GAACTTTCA GCTTCTTCT CTAAGTCAAC TATATTCTGC AAAATCAAGC GAGCAAGAGG	2220
AAAGAGTCCA GCTTCACGGG CAATGGTTGC CTTGGTACGA CGCTTTCTCT TATAAGGAAG	2280
ATAGAGTTCT TCAACGCTG CTAATTTTTC GGCAACTAAG ATAGCTTCTT CCAATTCCTT	2340

GGTCAACTTA CCTTGCTCTT GAATCTTAGC TAAGACAGCT TCCTTACGGT CATTGAGATT	2400
TGTCAGACTT TTATCCAAAT CAATAATAGC CTTAATCGCC ACCTCATCCA GACTACCACT	2460
CATGTCCTTG CGATAACGCG CGATAAAGGG AATAGTCGCC CCTTCAGCTG TCAAACCTAG	2520
AACGGTATCA ATTTGCTTTA ACGTCACTCC CAAATCCTGA GAGATTTTTT CATATTTTTT	2580
ATCCATAAAT CTATTATACC ACAAGCTAAA CGTTTCAAAT TAACTCGTAG AACATTTAAA	2640
AAATATGTAG GAAATAGATT TATATGCTAC AGCGCAATAA CTTGCACTTA AAGAGCATTG	2700
CCACCTTTTT TTAACCAAGC CATGATATCA AAAGTATTTA ATGGATCAGA CATAATAGCC	2760
AGTTCTGGAA GATGTTCTTG ACCTGGAATA ACACATTGAC TTTTCAAATT TTTATATGGA	2820
CGATTGACTA AAATTAATTT ATTAGAATAA GGAAGATTAT CCATCTTATT TAAAATTTCT	2880
TCACTAGCTG AATCTTTATT ATCAAATTTA AAATAAAGAT TATCCAATT TATGCGTTTT	2940
TTTCTTTTTT CCCACTTAGT TCGTGCTTCT TCAATACTAG AATAATGTAG AAAATGAATA	3000
TCTATATCTC CTAAGTGCCC CAAAGGATAA ACTTCATGAG TCCAGCTCGG TGAAATAAGT	3060
TCCTCTTCGA AAACAAGTTC TTGTTCCATA TAATAACGAA AATGCTTTGT AAGTTTATAA	3120
TAATCATCAG GAAGAATAAA TAAACCAACA AAAGGTGTTT TATATTGAAA ACCAAGCTGT	3180
TTATAAATTA ATCTCCAAC ACAATTATTA CTTATAATCG TAAATCTAA TCTATCAAGC	3240
TCAAGAAAAG GGAAAATTC TTTCTCTGCA GCTATTAACT TATGATAAAC AATATCAGAA	3300
TCTAAATATT CACCGTCATT TTTTAACCAA GCACTAAAAA TTGCCAATTC TTGAATATAT	3360
TGTTTTTTTCG CTCTTTCTAT ATCATAGTTT TCTAAGACGG CGCAATCTTT GATTCTATTT	3420
TCATAATTTT CTAATATGAT TTTGTAGGAG TCTTTTAGAG GTTTAGCATC TATAACAGGT	3480
TTATAGATAT ATGTCGGGAA ATTAATATAG GTTGCAGTTT TAGAGTGAAT ATAAAGTCTC	3540
CAAATAAGGT TGTTTATATC AAATTGATTT ATTTTTCGTA AAAGCTTACT ATTGAATAAT	3600
TTTCCAAATA ATGAGCGATA TTGTTTCTTA ATTGATGAT CTGTATCATC CATCTTTTGT	3660
AAAACTTGAA CATTCGTAA ATTTTCTGTC AACCAATTAT CCCCCAAA AGGATAAAAG	3720
TAAAATACTC CATCAACCA ATCAGCAAAA TGACCAAGAA CAACATCAGA ATCGGATAAT	3780
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AACGTAATAT AATCTCCTGT AATCATATCA GACAACTCAG CAAAAGAATT CTCATCTATA	3900
ATCTTAATAT TAAATGATAG ATTCACTGTG TGGCTAATGG AAGCTATCTC CTCTGTAGAT	3960
TGATTTACAA TAATACTTC TATATCTTTT AATGTTTGTC TCTCCACTAT TGACAAAGAC	4020
TCTAATAAAC TATTTTATC TCCTTGATGT AACAAAACAA CACTAATTGA GTAAGTCAGT	4080
TTGACTACCT CCCATAATTT TCTGATAATG ATTTTCTTTT TATTTAATTA TAGCACAATT	4140

1083

ATGATATATA TCAGGTAATA TCAAGCTATA TTATCTCTTA GCTACTCAAT TTGAAATTTT	4200
AACTTTTCCC TTTTCCGCAA AATAATAGTA TAATAGAGGT AGAATCTAGA ATCGAGGTAC	4260
ACCTATGGCT GTCAAATTTA CAAAACGAGA CGACTTGGAC AAGATGTTTG AAGAGTTTGC	4320
TAAACTCCCT GATTTGAAAC AAGTTACTTT CCCTGATGAC AAAGAGAAAA AAGTCAAAGC	4380
AGAAAAGAAA AACTAGATGA CTGCTTTTCA ACAACTCCCA TCTAGTGTAC TTCAAAGTGG	4440
AGCCATTTTT CTCTCCATTA TCATTGAAGC CCTTCCCTTC GTTCTGATAG GAAGCATTGT	4500
CTCAGGGCTG ATTGAAGTTT ATATCACACC TGACAAGGTT TATCATTTTC TCCCTCGAAA	4560
TCGTTGGGGG AGAATCTTTT TTGGGACCTT TGTGGGTATA CTTTCCCTT CTTGTGAATG	4620
TGGAATCGTC CCCATCATCA ATCGTTTCTT GGAAGAAAAG GTTCCAAGTT ACACGGCCGT	4680
TCCTTTTCTT GTGACAGCAC CTGTTATCAA TCCCATTGTT CTTTTGCGA CCTATTCTGC	4740
CTTTGGCAAC TCCTCCATG TCGCCCTATT ACGAGCTCTG GGTCCATTC TTGTGGCTGT	4800
AATACTAGGA ATTTTCTAG GATTTTCTG GCAAGAACCG ATTCAGAAAG AAAATCGTCT	4860
GGCTTGTCAT GAGCATGATT TTTCTTACTT GAGTTCTGCA AAAAAAGTTT TTCAAGTCTT	4920
TGTGCAGGCC ATTGATGAAT TTTTGTATAC GGGGCGTTAT TTGGTATTTG GCTGCCTCTT	4980
TGCTTCTATA ATACAGGTCT ACGTTCCGAC TCGGATTCTG ACCTCTATCA GTGCGACCCC	5040
TCTTTTGGCC ATCCTGCTCT TGATGATTTT AGCCTTCTT CTTTCGCTCT GTAGTGAGGC	5100
GGATGCCTTT ATAGGTGCTT CTCTTCTCTC GAGTTTCGGT TTGGCACCAG TTCTGGCCTT	5160
TCTCGTCATT GGTCCAATGC TGGATATCAA AAATATTCTC ATGATGAAAA ATTACTTGAA	5220
AGCACGATTT ATCAGTCACT TCATAACAAT TGTAAGTCTT GTCGTCTTAG TCTATTCTCT	5280
CTTGATTGGA GTTATCCTAT GATTCGATTT TTAGTTT TAGTCTGCTATT TGAAGTACT	5340
ATTTACCTCC ATCTGTGCGG CAAACTAAAC CAGTACATCA ACATGCACTA TTCCTATCTG	5400
GCCTATATCT CCATGGTGCT TTCTTTTATC TTGGCTATCG TTCAATTGTA TATCTGGATG	5460
AAGCAAGTCA AAACCCACAG TCATCTGAAC AGCCGATTAG CCAAGATAAC GAGTATTTCT	5520
CTTCTGGCTA TTCCACTTGT CATCGGCTTA ACTTTCCCAA CTGTTAGCTT GGATTCTCAG	5580
ACTGTTTCTG CTAAAGGTTA TCATTTCCCC CTATCGGAAG GAACGGATCT AGCCATTGAG	5640
ACAAGCGAAG GGACGACAAG CCAATATTTG AAACCAGATA CCAGTCTTCTA TTTTCAAAA	5700
TCAGCCTATG AAAAGGAAAT GCGAACGGCG GCGGATAAAT ACTTATCCCA AGATAGTATT	5760
CAGATCACTA ATGAAAATA TATGGAAGTC ATGGAGGCTA TCTACGACTA TCCAGATGAG	5820
TTTGAGGGCA AGACAATCCA GTTTACAGGC TTTGTCTATA ACGACCCAG TCATGCCAAT	5880

1084

AGTCAATTTC TGTTCGATT CGGCATTATC CACTGTATCG CAGATTCTGG TGTCTATGGA 5940

TTGCTGACCA AGGGCAATAC CCGGCAGTAT GAAAACAACA CTTGGATAAC AGCCAAAGGA 6000

AAACTGGTCA ATCACTACCA TAAAGAACTC AAACAAAACC TTCCAACCTT GGAAATCGAC 6060

AGCTTTACCA AAGTCGATAA ACCAGAAAAT CCCTATGTAT ATAGAGCTTT TTAAGAAAAT 6120

CAAGATAAAA ACGAACAAGT TCTCTTCTGA ATAACAGAAA AAGAGCCTGT TCGTTTTTTG 6180

TTATATGAAA ATTAGTGACT TGTAGATTTT CATCTTATAC CATTCCCAGC AATACAAGTA 6240

GCTCATAGAA AATAAGCGAG CCACTCATTC ATTAGACTAG CGATTTCTTT AGGTGCTTGA 6300

GTATAAAGCT CATGGCCAAA GTTTTCTAAA AAAATAGTAT CAAAATAGTC TGGCAATTCT 6360

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TCTCCCACTT CTCTCTTAAA AGCTTGATTT TTTCTCCGTA GCGGAGTATC GCTTCTATAT 6480

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GAACATCTAA GTCCGAAACA ATTTGAGATT TGATATAATT TTAGTTTTCC TCTAACTCTG 6660

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CATCTCGAAG ATGCTTTTCA TATGGATTTA GAAAATAGAC CTGCGAATCT AGTTCTTGAA 6900

GAAAATCCTT GCTATGATAG GCATTGCTTC CCAAACCGCC AATAAAATAT TTTTTCATTC 6960

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CACTAATATT AGACATTGTA AGCCTTTTCT TAATCATTTT CTGTTCTTTT TCTGTAAAAT 7260

CTTTTAATTC CATTCGATTA GTCCTCTAT TTTCTCTAAG TTAAATTATG TACTAATACA 7320

GATGAAACTA CAAAGAATAA ACTTTAAGAA ATCTTCTCAC TGATAAGATT TTAGCATTAG 7380

ACTTCCTGCG AAACAAAATA TGGTATAGTA GTTCTATGAA TTATGAAGCA AGTAAACAAC 7440

TAACTGATGC ACGATTTAAA CGTCTTGTTG GTGTTGAGCG CACGACTTTT GAAGAGATAT 7500

TAGCTGTATT AAAACAGCT TATCAACTTA AACACGCAA AGGTGGACGA AAACCTAAAT 7560

TAAGCCTAGA AGACCTTCTT ATGGCCACTC TTCAATATGT GCGAGAATAC CGCACTTATG 7620

AAGAAATTGC GGCTGATTTT GGTATTCACG AAAGCAACTT AATCCGTCGG AGCCAATGGG 7680

1085

TTTAAGTAAC TCTTGTTCAA AGTGGTGTTA CGATTTC AAG AACTCCTCTC AGTTCTGAGG	7740
ACACGGTAAT GATTGATAGC CATTCCTCATC AATATCGTAT CTTTGGACAT AGCCAATAAA	7800
TGTTTCATTT TTGCGTGGTT TCTGGCTATT AACGATTGAA ATAACCCACC AACTTATCAA	7860
AAATAGAAAT AAAATCCTA AGATTACTGT CATATCATAA CACTATTAAA GTTTAACCCA	7920
CTTATCATTA TCCATGATAA AAGGCTTAGC CAGTCCCTCG CCTGTATAAT CCGCATACTT	7980
GGTGCCCAA TACTTGTAGC AATCTTCCTT ACTAGCAAAT TTAATCGCTT GGTAGGGCTC	8040
TTTGAAAGTC AATTCTCTA CAAATAAGAA ACCGTCATCA GCAGGTACTA AGACCCCAAC	8100
GTGGCCTACA AACAGATACT CGCCATCCAA ATTGTCGTGC AAGACTACAG ACAGCATTCG	8160
AGCTTTTCA TTGAATTGAA ATTGTGAGAA GAATGCTTCC ATCTTTTCAG CGTGAACCTT	8220
GACATCTGTA GTTGACTCAG TTGGAATCT CGAAAATAGA ATATCAAAT CTTCCTTATC	8280
TTGTGAATCA AAGACCTTTC CTTTATCAAT CGCATCATTA TCTAGGAAAA GCAACTGGTC	8340
ATTCTTTTCA AGCTTTGAA TGGTGACTGA ATTTTTCAAA AGACAATAAC TATTGATACG	8400
GCAGTTGGTC CCAACAAAAT CGCCCTTCTT TTGATTCCAG AGATGACTGA TTTTCTCAAC	8460
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GGTATTATAG TCATTAACGA GATTAAAAA TGCATCAACA CTATTGGAT CCAAGTGAGC	8580
TGATAAGAGA GATTTGACCT CTTCTGTACT TACCTGGTTG TTTAGGTTGG TGTATGAAGC	8640
TTTCCATGGA ACTTTCGCTG AACTGCTTTG CCTTTGATTC GTCCCTCAG AAGTAGCATG	8700
TTGTTGTGTA CAAGCAGCCA AGCCTAAAA CAAGGCTGAA CAGATTCCTA ATGTGGCTAA	8760
TTTCTTGAT TTCTTCATTT CTTTCTCCTA AATGTCTTGG ATTAAAGTTT CTTAACTAT	8820
TGCTTTACAG ATATTGATTA CTTTCTCATT TAATGTGTTT ATCGTCTTTC CTCCGG	8876

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

CGCAAACCTT CGCGGTCGGA AGGTAGTTTT ATGACACGAT TTGAGATACG AGATGATTTC	60
TATCTCGATG GAAATCATT TAAGATTTTA TCTGGTGCCA TTCATTATTT TAGGGTTCCT	120
CCAGAGGATT GGTATCATTC GCTCTATAAC TTGAAGGCTC TTGGTTTAA TACGGTAGAG	180

1086	
ACTTATGTTG CTTGGAATTT ACACGAGCCT TGTGAAGGTG AGTTTCATTT TGAAGGTGAT	240
CTGGATTTAG AGAAATTTCT CCAAATAGCG CAGGATTTGG GTCTCTACGC AATTGTGCGT	300
CCGTCTCCAT TTATCTGTGC GGAATGGGAA TTCGGTGGCT TACCAGCTTG GCTCTTGACC	360
AAGAACATGC GAATTCGCTC ATCCGACCCA GCATATATCG AGGCAGTTGG TCGCTACTAT	420
GATCAGTTAT TGCCAAGACT GGTGCCTCGT TTGTTGGACA ATGGTGGCAA TATTCTCATG	480
ATGCAGGTTG AAAATGAGTA TGGTTCTTAC GGAGAAGATA AGGCTTACCT GAGAGCGATT	540
CGACAGCTAA TGGAAGAGTG TGGCGTAACC TGTCCCTCTT TTACATCAGA TGGTCCATGG	600
CGAGCTACTC TGAAAGCTGG AACCTTAATT GAAGAGGACC TCTTTGTAAC AGGAACTTT	660
GGTTCTAAGG CACCTTACAA CTTTTCGCAG ATGCAGGAAT TCTTTGATGA ACATGGTAAG	720
AAATGGCCAC TCATGTGTAT GGAGTTCTGG GATGGTTGGT TCAATCGCTG GAAAGAACCG	780
ATTATCACAC GGGATCCTAA GGAATTGGCA GATGCAGTTC GAGAGGTTTT GGAACAAGGC	840
TCTATCAATC TTTACATGTT CCACGGTGGT ACAAACCTTG GTTTCATGAA TGGTTGCTCA	900
GCTCGAGGAA CTTTGGACCT GCCACAAGTT ACGTCTTATG ATTACGATGC CCTTCTGGAT	960
GAAGAAGGAA ATCCAACGTC TAAATATCTT GCAGTCAAGA AGATGATGGC AACACATTTT	1020
TCAGAGTATC CGCAGTTGGA ACCACTCTAC AAAGAGAGTA TGGAGTTGGA TGCTATTCCA	1080
CTAGTTGAAA AAGTTTCTTT GTTTGAAACC TTAGATAGCT TGTCAAGTCC TGTAGAAAGT	1140
CTCTATCCTC AAAAGATGGA GGAGCTGGGA CAAAGTTATG GCTACCTACT TTATCGAACA	1200
GAAACAACT GGGATGCAGA AGAAGAAAGA CTTCTGTATCA TTGATGGTCG AGATAGGGCC	1260
CAGCTGTATG TCGATGGTCA GTGGGTAAA ACTCAATATC AGACAGAGAT TGGGGAAGAT	1320
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GGGCGTGTCA ACTATGGGCA TAAGTTCTTA GCGGATACGC AACGTAAGGG AATTCGGACA	1440
GGGCTCTGTA AGGATCTGCA TTTCTTACTA AACTGGAAAC ACTATCCACT CCCACTAGAC	1500
AATCCTGAGA AAATTGATTT TTCAAAAGGA TGGACTCAAG GACAACCAGC CTTTACGCT	1560
TATGACTTTA CAGTCGAAGA GCCAAAAGAT ACTTACCTAG ACTTGTCTGA GTTGGTAAG	1620
GGGGTTGCCT TTGTCAATGG GCAGAATCTA GGACGTTTTT GGAACGTTGG CCCAACTCTC	1680
TCACTTTATA TCCCTCATAG CTATCTCAAG GAAGGTGCCA ACCGCATCAT TATCTTTGAA	1740
ACAGAAGGTC AATATAAAGA AGAGATTCAT TTAACGCGTA AACCTACACT AAAACATATA	1800
AAGGGGAAA ACTTATGACA ATTGTAGGAT GCCGTATTGA TGGACGTTTG ATCCACGGAC	1860
AAGTAGCCAA TCTTTGGGCT GGAAACTAA ATGTTTCACG CATTTATGGTT GTAGACGACG	1920
AAGTTGTCAA CAACGATATT GAAAAGAGTG GTTTGAAACT TGCACACCA CCAGGTGTGA	1980

1087

AATTGAGTAT TTGCCCAGTT GAGAAAGCTG CAGCCAATAT TCTTGGTGGC AAATACGATA	2040
GCCAACGTCT CTTTATCGTG GCTCGTAAAC CAGACCGCTT CCTTGGTTTG GTAGAAGCAG	2100
GTGTACCACT TGAAACCCTT AATGTTGGGA ATATGTCTCA AACACCAGAA ACTCGTTCTA	2160
TTACACGPTC TATCAACGTA GTAGACAAGG ATGTGGAAGA CTCCACAAA CTGGCAGAAA	2220
AAGGTGTTAA ACTTACTGCT CAGATGGTTC CAAATGATCC AATTCAGAC TTTTGTAGCT	2280
TATTAATAA GGAATAAAT TTTTAGGAGG TCATTGTTAT GATACAATGG TGGCAAAATT	2340
TACTTCTCAC TTTGTACTCA GCTTATCAAA TCTGTGATGA GTTGACGATC GTTTCATCTG	2400
CAGGTTCCTC TGTATTTGCT GGTTCATTA CTGGTTTAAT CATGGGAGAT GTGACTACTG	2460
GTTTACTTAT CGGTGGTAAC TTGCAACTGT TCGTCTTGG GGTGGGTACC TTCGGTGGTG	2520
CTTCTCGTAT CGACGCAACT TCTGGTGGG TTCTTGGCAG ACCTTCTCTG TTTACAAGG	2580
AATTGATGCA CCGCTTGCCA TTAACAAT CGCTGTACCA GTAGCAGCTC TCTTGACTTA	2640
CTTCGACGTT CTTGGTCGTA TGAATACTAC CTCTTCGCT CACCGTGTGG ATGCTGCAAT	2700
CGAACGCTT GACTATAAAG GTATTGAACG CAACTACTTG CTTGGTGGCA TTCGTGGGC	2760
TCTATCTCGT GCCCTTCCAG TCTCTTTGC CTTGCTTTT GGTGGTGCCT TTGTACAATC	2820
AGTAGTAGAC TTCGTTGAAG CCTACAAATG GGTGCAGAT GGCTTGACAC TTGAGGACG	2880
TATGCTTCCA GGTCTGGAT TTGCAATCTT GCTTCGTTAC CTCCAGTTA AACGTAACCT	2940
TCACTACCTT GCTATGGGAT TTGGTTTGAC AGCTATGTTG ACTGTTCTTT ACTCATATGT	3000
AACAGGTCTT GGTGGCGCTG TTGCTGGTAT CGTAGGTACT CTTCTGCTG AAGTTGCTGA	3060
AAAAATTGGT TTCGTGAACA ACTTCAAAGG TTTGTCTATG ATTGGTATTT CTATCGTAGG	3120
TATTTTCCTT GCAGTGCTTC ACTTCAAAA TAGCCAAAA GTAGCTGTAG CAGCACCTTC	3180
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AAGATTTTAA TCAAATCAAC AAACGTAGCT TGTTTACTTT CCAATTAGGT TGGAACACG	3300
AACGTATGCA AGCTTCTGGT TACCTTTACA TGATCTTGCC TCAGTTGCGT AAAATGTATG	3360
GTGATGGAAC TCCTGAATTG AAAGAAATGA TGAAAGTTCA TACTCAATTC TTCAATACTT	3420
CACCATCTT CCATACCATT ATCGCTGGTT TTGACCTGC CATGGAAGAA AAAGATGGTG	3480
TAGGTTCAAA AGACGCCGTT AACGGTATCA AGACAGGTTT GATGGGACCA TTCGCTCCTC	3540
TTGGGGATAC AATCTTTGGT TCACTTGATC CTGCTATCAT GGGGTGAGT GCAGCAACTA	3600
TGGCTATCGC TGGCCAACT TGGGGATCT TCCTTTGGAT TGCAAGTGCA GTAGCGTATG	3660
ACATCTCCG TTGGAACAG TTGGAATTTG CTTACAAAGA AGGGGTTAAC CTTATCAACA	3720

1088

ACATGCAAAG TACCTTGACA GCTTTGATTG ACGCTGCATC TGTACTTGGT GTCTTCATGA	3780
TGGGTGCTCT TGTAGCAACA GTGATTAAC TTTGAAATTC TTACAAGTTG CCAATCGGTG	3840
AAAAGATGAT TGATTTCCAA GACATCTTGA ACCAAATCTT CCCACGTTTG CTTCCAGCAA	3900
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TCGGTATTAT TATCGTACTT GCTTTGGCTC TTTCTGCCCT TGGTCACTTT GCACTTGGAA	4020
TGTAATTCCT TATGACTAAA TCATTAATTT TGGTGAGCCA TGGTCGCTTC TGTGAGGAGC	4080
TTAGAGGTAG CACAGAAATG ATTATGGGCC CACAAGACAA CATTTACACA GTAGCTCTTC	4140
TTCCAGAAGA TGGCCAGAA GAATTTACTG CTAAATTTGA AGCTGTTATT GAAGGATTGG	4200
ATGATTTCCCT AGTCTTTGCG GATCTTCTCG GTGGGACACC TTGTAATGTG GTGAGTCGCT	4260
TGATCATGGA AGGTCGTGAT ATTGACCTTT ACGCAGGGAT GAATCTTCCA ATGGTGATTG	4320
AATTTATCAA TGCAGCCTT ACAGGCGCAG ATGCGGACTA CAAGAGCCGT GCTGCAGAAA	4380
GCATTGTGAA AGTTAATGAC CTGTTAGCGG GCTTCGATGA TGACGAAGAT GAATAATACT	4440
CTTCGAAAAT CTCTTCAAAC TACGTCAACG TCGCCTTGCC GTAGGTATAT GTTACTGACT	4500
TCGTCAGTCT TATCCGGCAA CCTCAAAACG GTGTTTGTAG CTGACTTCGT CAGTCTTATC	4560
CGGCAACCTC AAAGCAGTGC TTTGAGCAGC CTGCGGCTAG TTTCTACAG ATTTTAGTTG	4620
GAACGCGATT CAATTCATGT GACAACGTGA AAATCGTTAG AGCATTTTAT ATAGAATATA	4680
CATGGGAATG TAGCTTACTC CCATTCCCAT ATTTAATAGA AAAAGAGGAA CTCAATGCTA	4740
CATTATACAA AAGAAGACTT GCTCGAATTG GGTGCAGAAA TCACTACGCG TGAAATCTAC	4800
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GCAGCCTTCC TACAAGAAAT CGCTGATAAA CATGACTATA TTAAGGTTAT CTTGACAGGT	4920
GCTGGGACTT CTGCTTATGT GGGAGATACC TTGCTACCTT ATTTTAAGGA AGTCTATGAC	4980
GAACGCAAAT GGAATTTCAA TGCTATTGCG ACAACAGATA TCGTTGCCAA TCCAGCAACC	5040
TATTTGAAAA AAGATGTGGC AACTGTCCTT GTGTCTTTTG CTCGTAGTGG GAATTCGCCT	5100
GAAAGTTTGG CGACTGTGA TTTGGCCAAA TCCTTGGTGG ATGAGCTTTA TCAAGTGACG	5160
ATTACTTGTG CAGCAGATGG TAAATGGCT CTTCAAGCTC ACGGTGATGA TCGTAATCTC	5220
TTGCTCTTGC AACCAGCTGT CTCTAATGAT GCTGGATTTG CCATGACTTC TAGCTTTACG	5280
TCTATGATGT TGACAACTCT CTGGTCTTT GATCCTACAG AATTGCTGT TAAGTCTGAA	5340
CGTTTGAAG TTGTATCTAG TCTTGCCCGT AAAGTTTGTG ACAAGGCAGA AGATGTCAAA	5400
GAGCTCGTTG ATTTAGACTT TAACCGTGT ATCTATCTAG GCGCTGGTCC TTTCTTTGGA	5460
CTTGCTCATG AAGCTCAGCT CAAGATTTTG GAATTAACCTG CTGGTCAAGT TGCGACCATG	5520

1089

TATGAAAGCC CAGTTGGCTT CCGTCACGGT CCAAAATCTC TTATCAACGA CAATACAGTT	5580
GTTTTGGTCT TTGGTACAAC GACAGACTAC ACTCGTAACT ACGACTTGGA CTTGGTTCGT	5640
GAAGTTGCTG GTGACCAGAT TGCTCGTCGT GTTGTGCTTT TGAGTGATCA AGCTTTTGGT	5700
CTTGAAAATG TCAAAGAAGT GGCCCTTGGT TGTGGCGGTG TCTTGAATGA TATTTACCGT	5760
GTCTTCCCTT ACATCGTTTA TGCCCAACTC TTTGCTTTAT TGACTTCACT CAAGGTAGAA	5820
AATAAACAG ATACACCGTC TCCTACAGGT ACAGTAAACC GTGTAGTACA AGGTGTCATA	5880
ATTACGAAT ATCAAAAGTA AGACAGTGTT TATGAATTCT TGACAAGAGG ATTTGTAAAT	5940
TATCAGATAA ACCATAGATT GTCAGTACGC TTTCTATGGT TTGTTTGCTT GAGAGAAATA	6000
GTAAGAGGAG AACAGAATGA AAGCATACAC AGAGCGTGTA TTTGGAATG TTGAGGGTGA	6060
GGATGCTCTG GCCTATCGAT TTGAGACAGA CGGTGGCTAC CAACTTGAGG TTATGACTTA	6120
TGGTGCGACT ATCTTGCCTT ATGTCGCACC TGACAAGGCT GGAAATTTTG CCAATGTTAT	6180
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AGGTCTGTGA GCGGGTCGTA TTGCAGGTGC GACCTTTGAG CTCAATGGTA AGACCTATGA	6300
CCTTGAGGTT AATAATGCTA GCAACTGTAA TCACAGTGGT TCAACTGGTT GGGATTCCAG	6360
CTTGTGTTGAA GTTGAAGAAG TAAGCGATCA TGGCTTGACT CTCTACACAG AGCGTACAGA	6420
TGGGACAGGA GGGTTCCTTG GAAATCTCAA GATTTGGATC AGTTATCACT TGAAGAAAC	6480
TGGTGCCTAT GAAATCAGCT ACAAGGTAAC GACCGATCAG GATACGCTGG TCAATCCAAC	6540
CAACCACAGC TATTTCAACT TGTCTGGTGA TTTCACGCAG ACGATTGACC GTCATGCTTT	6600
CCAACTAAAC ACAGAGGGCA TTTACTCAAT CGCTCCTGAC GGTGTTCCCTG CCAAACTCC	6660
AGAAGCCAAC CGTGATGTGG TCAAACACGT CTACAATGGT ACCTTGTTGA AGGATATCTT	6720
TGCAGAAGAA GATGAGCAAA TCCAGCTGGC ATCAGGTTTG GATCATCCAT TTGCCCTTCC	6780
TGCAGGCCAT GACAATGCTG GATTCCTTTA TGACCAAAAT TCAGGTCGCT TCCTGCTTTT	6840
CAAGACAGAA GTCCTTGCTT TTGTGGTCTA CACAGCAAAC TTTGTGGATG AAAGTGTCAT	6900
CATAGGAGGT CAGCCAATGC TACAGCACA TGGGATTGCT CTTGAAGCGC AAGCTTTACC	6960
AGATGCCATT CACAGTGACC TTAAAGGCCA AGTCATTCTT AAAGCTGGTC AAACCTTCAC	7020
CAGTAAGACA CGTTATGAAC TTGTTGTGAA GTAAAAGAGT CATTGCGCCT ACTTTTGGGA	7080
GCTAGGAATA GGTACGCAGA GACAAATAGT AGGAAAATAT GATATAACTA AGCGTTGAAA	7140
GCTATCTGTT AATATAATAT TCAAATACA ATAAGGAGTA AGAAAGAAAC GAAGAAAATT	7200
GTATTTGCTA GTCCCTTGGC TTTGACCTTG GCTGGAGCAG TTTTGACAAA TGATGTTTTT	7260

1090

GCGAACGACA GACTTGTGGC AACACAAACT ACTGATGGTA AAAATGAAA TGTATTGACC	7320
TCAGAGGTGC TAAACCTTC TAGTGGCAAT GTTTTGGTTG GAATCAAAGG AGAATTTGTG	7380
GCTCCTCATC AACAACTCTAT TTTGGATGCC ATCAATGCTA TCTGTAAAGA AGCGGCTGAC	7440
GAAGGTTTGG TAGATAAGTA TGTCCCTATC AAATGATCAA CTGACCTAGA AAAGGCAGCT	7500
TTTGCCAGAG CTACAGAAGC ATCTATAACC ATGGATCATA CCCGTCTTTC TAGCAAAGAT	7560
CTTTGGAGTG CCTTTCCAAC TTCTAATAGT ATAATGGGAG AAAATTTGGC ATGGAATCAT	7620
GACGGTTTTC TAAAGCTAT TGAACAATGG CGTGCTGAAA AAGCAGATTA TGTGGAGAAA	7680
AAAAAGTGG TTCAGACAAC GGGAAATCTG GTCACATGA GTCGCTAATT AACCCATAAT	7740
TTACACACAT GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA	7800
TTGCTCAAAC TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG	7860
CTGTTCAAGT TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGTACGG	7920
TTGTAGAAAA ACCACTGAAA GATTTTAGAG CGTCTACGTC TGATCAGTCT GGTGGGTGG	7980
AATCTAATGG TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA	8040
CAGATGGTAA ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAA	8100
TTTCTGGTAG CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTACAGGC TGGGGAACAG	8160
ATGGTAGCAG ATGGTCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG	8220
AAAATGGCAC TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG	8280
TCGGACCACA CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC	8340
CAGATGGTTA CCGTGTAAT GGTAAATGGT AATGGGTAAA CTAGGCTCAG GCCATAGGTA	8400
AAGCATTCAT CTTACTTAGC AAAAAGAATG AACGATAAGA AAGAGTTGA TGGCGAACAT	8460
TGGCCTCTTT TGATTATATA AGATTGGATT CTTGTGCGCT CAATTCAGA CTTTCTATT	8520
GTAAGCTAAT ATTTTATAGC CCATTAAAAG CATAAGCGGT AATCTAATTT AAAAAATGCT	8580
GTAATTAGTC TGAAGTCCAC ACTTACTTGT TGAGATGTTA TCTCTGTTTT TTATCGTTA	8640
AATTTACTGT ATTTTTTATA GTATGCAGAA TATTTTAAAG TATATTTCAA TAGAAATTTT	8700
TATCGATTTA TTGTATAATG ATAAGTAATT GTTGAAAAGT ACTCAGAAAA TTCCATACTA	8760
TATTATTTTT ATGTTTATAC TTTTATGCTA TAAAATATAG ATTGATATAA AGAATATAGA	8820
AAAAGCGAGG TTAATATGAG CCGAAAAAGC ATTGGTGAGA AACGCCATAG TTTCTCGATG	8880
AGAAAGTTGT CAGTGGGATT GGTATCAGTT ACTGTATCTA GTTCTTTTTT GATGAGTCAA	8940
GGGATTCAAT CCGTATCGGC CGATAATATG GAAAGTCCAA TTCATTATAA GTATATGACC	9000
GAGGGTAAAT TGACAGACGA GGAAAAATCC TTGCTGGTAG AGGCCCTTCC ACAACTGGCT	9060

1091

GAAGAATCAG ATGATACTTA TTA	CTTGGTT TATAGATCTC AACAGT	TTTTT ACCGAATACA	9120
GGTTTTAACC CAACTGTTGG TACT	TTTCCTT TTTACTGCAG GATTGAGCTT	GTTAGTTTTA	9180
TTGGTTTCTA AAAGGGAAAA TGGAAAGAAA	CGACTTGTTT ATTTTCTGCT GTTGACTAGC		9240
ATGGGAGTTC AATGTTGCC GGCCAGTGCT	TTTGGGTTGA CCAGCCAGAT TTTATCTGCC		9300
TATAATAGTC AGCTTTCTAT CGGAGTCGGG	GAACATTTAC CAGAGCCTCT GAAAATCGAA		9360
GGTTATCAAT ATATTGGTTA TATCAAACT	AAGAAACAGG ATAATACAGA GCTTTCAAGG		9420
ACAGTTGATG GGAAATACTC TGCTCAAAGA	GATAGTCAAC CAAACTCTAC AAAAATCA		9480
GATGTAGTTC ATTCAGCTGA TTTAGAATGG	AACCAAGGAC AGGGGAAGGT TAGTTTACAA		9540
GGTGAAGCAT CAGGGGATGA TGGACTTTCA	GAAAAATCTT CTATAGCAGC AGACAATCTA		9600
TCTTCTAATG ATTCATTCGC AAGTCAAGTT	GAGCAGAATC CGGATCACAA AGGAGAATCT		9660
GTAGTTTCGAC CAACAGTGCC AGAACAAGGA	AATCCTGTGT CTGCTACAAC GGTGCAGAGT		9720
GCGGAAGAGG AAGTATTGGC GACGACAAAT	GATCGACCAG AGTATAAACT TCCATTGGAA		9780
ACCAAAGGCA CGCAAGAACC CGGTCATGAG	GGTGAAGCCG CAGTCCGTGA AGACTTACCA		9840
GTCTACACTA AGCCACTAGA AACCAAGGT	ACACAAGGAC CCGGACATGA AGGTGAAGCT		9900
GCAGTTTCGCG AGGAAGAACC AGCTTACACA	GAACCGTTAG CAACGAAAGG CACGCAAGAG		9960
CCAGGTTCATG AGGGCAAAGC TACAGTCCGC	GAAGAGACTC TAGAGTACAC GGAACCGGTA		10020
GCGACAAAAG GCACACAAGA ACCCGAACAT	GAGGGCGAAG CCGCAGTAGA AGAAGAACTT		10080
CCGGCTTTAG AGGTCACTAC ACGAAATAGA	ACGGAAATCC AGAATATTCC TTATACAACA		10140
GAAGAAATTC AGGATCCAAC ACTTCTGAAA	AATCGTCGTA AGATTGAACG ACAAGGGCAA		10200
GCAGGGACAC GTACAATTCA ATATGAAGAC	TACATCGTAA ATGGTAATGT CGTAGAACT		10260
AAAGAAGTGT CACGAACTGA AGTAGCTCCG	GTCAACGAAG TCGTTAAAGT AGGAACACTT		10320
GTGAAAGTTA AACCTACAGT AGAAATTACA	AACTTAACAA AAGTTGAGAA CAAAAATCT		10380
ATAACTGTAA GTTATAACTT AATAGACACT	ACCTCAGCAT ATGTTTCTGC AAAAACGCAA		10440
GTTTTCATG GAGACAAGCT AGTTAAAGAG	GTGGATATAG AAAATCCTGC CAAAGAGCAA		10500
GTAATATCAG GTTTAGATTA CTACACACCG	TATACAGTTA AAACACACCT AACTTATAAT		10560
TTGGGTGAAA ATAATGAGGA AAATACTGAA	ACATCAACTC AAGATTTCCA ATTAGAGTAT		10620
AAGAAAATAG AGATTAAAGA TATTGATTCA	GTAGAATTAT ACGGTAAAGA AAATGATCGT		10680
TATCGTAGAT ATTTAAGTCT AAGTAAGCG	CCGACTGATA CGGCTAAATA CTTTGTAATA		10740
GTGAAATCAG ATCGCTTCAA AGAAATGTAC	CTACCTGTAA AATCTATTAC AGAAAATACG		10800

1092
GATGGAACGT ATAAAGTGAC GGTAGCCGTT GATCAACTTG TCGAAGAAGG TACAGACGGT 10860
TACAAAGATG ATTACACATT TACTGTAGCT AAATCTAAAG CAGAGCAACC AGGAGTTTAC 10920
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GCTTCAGATA TGACCCGAGA TGAGGTGAGC TTAGGCGATA AGCAGACAAG TTATCTCACA 11040
GGTGCATTTA CAGGGAGCTT GATCGGTTCT GATGGAACAA AATCGTATGC CATTTATGAT 11100
TTGAAGAAAC CATTATTTGA TACATTAAAT GGTGCTACAG TTAGAGATTT GGATATTAAA 11160
ACTGTTTCTG CTGATAGTAA AGAAAATGTC GCAGCGCTGG CGAAGGCAGC GAATAGCGCG 11220
AATATTAATA ATGTTGCAGT AGAAGGAAAA ATCTCAGGTG CGAAATCTGT TGCGGGATTA 11280
GTAGCGAGCG CAACAAATAC AGTGATAGAA AACAGCTCGT TTACAGGGAA ACTTATCGCA 11340
AATCACCAGG ACAGTAATAA AAATGATACT GGAGGAATAG TAGGTAATAT AACAGGAAAT 11400
AGTTCGAGAG TTAATAAACT TAGGGTAGAT GCCTTAATCT CTACTAATGC ACGCAATAAT 11460
AACCAAACAG CTGGAGGGAT AGTAGGTAGA TTAGAAAATG GTGCATTGAT ATCTAATTCG 11520
GTTGCTACTG GAGAAATACG AAATGGTCAA GGATATTCTA GAGTCGGAGG AATAGTAGGA 11580
TCTACGTGGC AAAACGGTCG AGTAAATAAT GTTGTGAGTA ACGTAGATGT TGGAGATGGT 11640
TATGTTATCA CCGGTGATCA ATACGCAGCA GCAGATGTGA AAAATGCAAG TACATCAGTT 11700
GATAATAGAA AAGCAGACAG ATTCGCTACA AAATTATCAA AAGACCAAAT AGACGCGAAA 11760
GTTGCTGATT ATGGAATCAC AGTAACTCTT GATGATACTG GGCAAGATTT AAAACGTAAT 11820
CTAAGAGAAG TTGATTATAC AAGACTAAAT AAAGCAGAAG CTGAAAGAAA AGTAGCTTAT 11880
AGCAACATAG AAAAAGTAT GCCATTCTAC AATAAAGACC TAGTAGTTCA CTATGGTAAC 11940
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GATGATGAAG TAGTAACGGA TATTAATAAT AAGAAAAATT CAATAAATAA AGTTATGTTA 12060
CATTTCAAAG ATAATACAGT AGAATACCTA GATGTAACAT TCAAAGAAAA CTTCATAAAC 12120
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AACTCAGAAG CTAATAAAAA AGTACTAGGA GCAGCGAATG ATGCAGCCTT AGATAACCTA 12300
TACTTAGATA GACAATTTGA AGAAGTTAAA GCTAATATAG CAGAACACCT AAGAAAAGTA 12360
TTAGCGATGG ATAAATCAAT CAATACTACA GGAGACGGTG TAGTTGAATA CGTAAGTGAG 12420
AAAATCAAAA ATAACAAAGA AGCATTATG CTAGGTCTTA CTTATATGAA CCGTTGGTAC 12480
GATATTAATT ATGGTAAAT GAATACAAAA GATTATCTA CGTACAAGTT TGACTTTAAC 12540
GGAAATAATG AGACTTCAAC GTTGGATACT ATTGTCGCAT TAGGAAATAG TGGACTAGAT 12600

1093

AACCTGAGAG CTTCAAATAC TGTAGGTTTA TATGCGAATA AACTTGCATC GGTAAGGGA	12660
GAAGATTCAG TCTTTGACTT CGTAGAAGCG TATAGAAAAC TGTTCCTACC AAACAAAACA	12720
AATAACGAGT GGTTTAAAGA AAATACAAAG GCATATATAG TCGAAATGAA GTCTGATATT	12780
GCAGAAGTAC GAGAAAAACA AGAATCACCA ACAGCCGATA GAAAATATTC ATTAGGAGTT	12840
TACGATAGAA TATCAGCACC AAGTTGGGG CATAAGAGTA TGTATTACC ACTACTAAT	12900
TTACCTGAAG AATCTGTGTA TATTTTCATCG AATATGTCTA CACTTGCATT CGGTTTCGTAT	12960
GAAAGATATC GTGATAGTGT GGATGGAGTT ATTCTTTTCTAG GAGATGCTTT ACGAACTTAT	13020
GTAAGAAATA GAGTTGATAT AGCAGCGAAA AGGCATAGAG ACCATTATGA TATTTGGTAC	13080
AATCTTCTTG ACAGTGCTTC AAAAGAAAA CTTTTCCGTT CTGTGATAGT TTATGATGGA	13140
TTCAATGTAA AAGATGAGAC AGGAAGAACT TATTGGGCAA GGTAAACGGA TAAAAACATC	13200
GGCTCTATTA AAGAATTCTT CGGACCTGTT GGGAAATGGT ATGAGTATAA TAGTAGTGCA	13260
GGAGCGTATG CGyAtGGAAG TTAAACGCAC TTTGTGTTAG ATAGATTATT AGATGCTTAT	13320
GGAACGTCGG TTTATACTCA TGAAATGGTT CATAATTCTG ATTCTGCAAT CTACTTTGAA	13380
GGAAATGGTA GACGTGAAGG ATTGGGAGCG GAGTTATACG CACTTGGTTT ACTGCAATCT	13440
GTAGATAGTG TAAATTCTCA TATTTTAGCT TTAAATACGT TATATAAGC AGAAAAAGAT	13500
GATTTGAATA GATTGCATAC ATATAATCCG GTGGAACGTT TCGATTGGA TGAGGCGCTT	13560
CAAAGTTATA TGCATGGATC ATATGATGTA ATGTATACAC TTGATGCGAT GGAAGCAAAA	13620
GCGATATTAG CTCAAAATAA TGATGTTAAG AAAAAATGGT TTAGAAAAAT AGAAAAATTAT	13680
TACGTTCTGT ATACTAGACA TAATAAGAT ACACATGCAG GAAATAAGT CCGTCCATTA	13740
ACAGATGAAG AAGTAGCTAA CTTAACATCG TTAAACTCAT TAATCGACAA CGACATCATA	13800
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ATGTTCTCTC CTGTATACGC AGCGCTAAGC AATTCGAAAG GTGCTCCTGG AGATATTATG	13920
TTTAGAAAAA TAGCTTATGA ATTACTTGCG GAAAAGGTT ATCACAAAGG ATTCCTACCT	13980
TATGTTTCTA ATCAGTACGG AGCAGAAGCA TTTGCCAGCG GAAGCAAAAC ATTCTCATCA	14040
TGGCATGGAA GAGATGTTGC TTTAGTGACA GATGATTAG TATTTAAGAA AGTATTCAAT	14100
GGTGAGTACT CATCATGGGC TGATTTCAAA AAAGCAATGT TTAAACAACG TATAGATAAA	14160
CAAGATAATC TGAAACCAAT AACAATTCAA TACGAATTAG GTAATCCTAA TAGTACAAAA	14220
GAAGTAACTA TAACAACGGC TGCACAAATG CAACAATTAA TTAATGAAGC GGCTGCGAAA	14280
GATATTACTA ATATAGATCG TGCAACGAGT CATACCCAG CAAGTTGGGT GCATTTATTA	14340

1094

AAACAAAAA TCTATAATGC ATATCTTCGC ACTACAGATG ACTTTAGAAA TTCTATATAT	14400
AAATAAGATT GTAGAGTTTC ATTGTTGACT AGTGTTTCTT GTAAGGATGA GGAGTCAGAT	14460
GACAAATCGA CTCCTTTTTC TTATGGATCG ATGTAGAGAT TTGATTGAAT GCAGATTGCA	14520
GGAATCATCT TCAACTCATC AACGACCAAT GGTGACAAGG TGGATTTCAA TCCCACAGAA	14580
AATGTTGATT TGAGAAATAA CTTTGCTAGT CTAGTAAAAT AAATACAAAA CAATCCTAGA	14640
AGATTTTTTC TGGGATTGTT TTTTGCTGAG TGGGATGCTT CAAGTTGTCT GGCTTGACTT	14700
TCTTGAGGGA AGTTATATAA TAGTTGTAAT AATTAG	14736

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11770 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

ACAGGAAAGC ACGATAGCAA TCTCTTTGGA AGATTTAAAA AATATTCCTC AAAGTTTCGC	60
TGTGCTTAC GGTGATACGA AAGTATCTTC GATTCTCTCT GTCTTGCGTG CTAATTTAGT	120
AAATCATTTG ATTACAGACA AAAATACAAT TTTAAAAGTT TTGGAACAAG ATGGGGATTT	180
GACTTTTAGA GAGATTCTAG GTGAGTGAAA ATGATAGACT GATTCAAGTT ATCGTTTTTC	240
TTTTTAGTTG ATTGCACATT TGTGCTTATA TAAACAAAA TAGTTTATCT GTTGTTTTTG	300
GATTGACAAC TTTATTATGT AGTTGTATTC TATAGTTACA AAAGAAAAT TTTAAATTTT	360
AAATGAAAA AGCTTTTTAC ATAGTGAAAT GAGGAGGAAT TTATGGAAAT GATTGTTCCA	420
GATCAAATTA TCATGGGTTT AATTTTATAT GCTGGTGATG CGAAACAACA TATTTATAAA	480
GCGTTAGATT ACATAAAAAA TGGTACATGT GAACGGTGTG AAGAAGAAAT ACAGTTAGCT	540
GATGCAGCCT TATTAGAAGC TCATAATCTA CAAACAAAAT TTTTGGCACA GGAAGCGTCT	600
GGTACAAAGA CAGAAATTAC AGCTCTCTTT GTTCATTAC AAGATCATCT CATGACCACT	660
ATGACGGAGA TTAATTTAAT CAAAGAAAT ATTAGTTTGA GAAAAGAACT TCATAAAAAA	720
TAATACTAGA GTATTATCAT TGTATTAAAC ATAGAGGAGG AAAACATAAT GGTGAAGATT	780
GGTTTGTTTT GTGCAGCAGG TTTTCTACT GGTATGCTTG TAAATAATAT GAAAATTGCA	840
GCGCAATCTA GTGGAGTTGA GGCAGAAATA GAGGCGTTTT CTCAGTCTAA ATTAGCGGAT	900
TATGCGCCAA ATATAGATGT TGCACTATTG GGTCCACAAG TTGCTTATAC ATTAGATAAA	960
TCAAAAGAAA TTTGTGATAA GTGTGATGTT CCGATAGCTG TTATTCCGAT GATGGACTAT	1020

1095

GGTATGTTAG ATGGGAAAAA AGTATTAGAT TTGGCCCTAT CTTTGATTAG TGGGTAAGAA	1080
AAGGAGATTT ATTATGTCAA AGATGGATGT TCAGAAAATC ATTGCACCGA TGATGAAGTT	1140
TGTGAATATG CGTGGCATTAG TAGCTCTAAA AGATGGGATG TTAGCAATTT TGCCATTGAC	1200
AGTAGTTGGT AGTTTGTCT TGATTATGGG ACAATTGCCG TTCGAAGGAT TAAATAAGAG	1260
CATTGCTAGT GTTTTGGAG CTAATTGGAC AGAGCCGTTT ATGCAAGTAT ATTCAGGAAC	1320
TTTTGCTATT ATGGGTCTAA TTTCTTGT TTCAATTGCC TATTCTTATG CTAAGAATAG	1380
CGGAGTAGAG GCTTTACCAG CTGGAGTTCT ATCTGTATCT GCATTCCTTA TTTTGCTAAG	1440
ATCATCTTAT ATCCCTAAAC AAGGTGAGGC GATTGGGGAC GCTATTAGTA AAGTTTGTT	1500
TGGAGGCCAA GGAATTATCG GTGCTATCAT TATAGGTTTG GTAGTAGGAA GTATTTATAC	1560
CTTCTTTATA AAGAGAAAAA TTGTTATTAA GATGCCAGAA CAAGTCCAC AAGCTATTGC	1620
CAAACAGTT GAAGCAATGA TTCCAGCATT TGTAATTTTC TTATCTTCTA TGATTGTATA	1680
TATTTTAGCG AAGTCATTGA CTAATGGCG AACATTCATA GAAATGATTT ATCTCGCTAT	1740
TCAAGTCCG TTGCAAGGTT TAACTGGATC TTTGTATGGT GCTATTGGAA TTGCATTCTT	1800
TATATCATTT TTGTGGTGGT TTGGTGTTCA TGGGCAATCG GTAGTAAATG GAGTAGTGAC	1860
AGCTCTGCTT TTATCTAATC TTGATGCTAA TAAAGCTATG TTAGCCTCTG CTAATCTATC	1920
ATTAGAAAAA GGTGCACATA TTGTTACTCA ACAATTTTGA GATTCATTTT TAATCTATC	1980
AGGTTCAGGG ATTACGTTTG GTCTTGTAGT TGCCATGCTT TTTGCAGCAA AATCAAAACA	2040
ATACCAAGCC TTAGGAAAAG TTGCAGCTTT TCCAGCAATA TTTAACGTAA ATGAGCCAGT	2100
TGTATTTGGA TTTCCGATTG TCATGAATCC AGTTATGTTT GTACCTTTCA TTCTTGTTCC	2160
TGTAATTGCA GCTGTGATAG TATATGGAGC TATTGCAACA GGTTCATGC AGCCATTCTC	2220
AGGGGTAACA TTGCCTTGGA GTACACCAGC TATTTTATCA GGATTTTGG TGGGTGGATG	2280
GCAAGGAGTT ATTACTCAGC TGGTGATATT AGCGATGTCT ACATTGGTTT ATTTTCCATT	2340
CTTTAAAGTA CAGGATCGTT TAGCTTACCA AAATGAAATC AAACAATCTT AGAGGTATTT	2400
GTGTGTACT GTTAACTCA CACATTTGTG CTAAAAATTA GAGAGTTAAA ATTTTCTAG	2460
TTAAAAGCTT GAAAATTCT ATAAAATCG GTATTATATT TTCGAAAGAA ATAAAATAT	2520
TTTCGAAAGA AAGGTGCTTA CGATGGTAAA TACAGAAGTA GCAAGAACAA CAATCAAGAC	2580
AGAATATTTT GGCAGCCTTA CTGAAAGGAT GAACAAATAT CGAGAAGATG TTTTAAATAA	2640
AAAACCTTAT ATTGATGCTG AGAGAGCAGT TCTAGCAACA CGCGCTATG AACGATACAA	2700
GGAACAACCT AATGTCCTAA AACGTGCATA TATGCTGAAA GAAATTTGG AAAATATGAC	2760

1096				
TATCTATATT	GAAGAAGAAT	CTATGATTGC	GGGAAATCAA GCTTCTTCCA ATAAAGATGC	2820
TCCTATTTTT	CCGGAATATA	CGCTAGAATT	TGTTCTCAAT GAGTTGGATC TTTTGTAAAA	2880
GCGTGATGGA	GATGTTTTCT	ATATTACAGA	AGAAACAAAA GAACAACCTA GAAGTATTGC	2940
TCCGTTTTGG	GAAAATAATA	ATTACGTGC	TAGAGCTGGT GCCTTATTAC CTGAAGAAGT	3000
GTCTGTTTAT	ATGGAAACAG	GATTCCTCGG	TATGGAAGGT AAGATGAATT CTGGAGATGC	3060
TCACTTAGCA	GTAACTATC	AGAACTTTT	GCAATTTGGT TTAAGAGGTT TTGAAGAGCG	3120
GGCTCGTAAA	GCAAAAGTAG	CTCTAGATTT	AACAGATCCA GCAAGTATTG ATAAATATCA	3180
TTTTTACGAC	TCTATATTTA	TCGTAATCGA	TGCTATTAAA GTATATGCAA AGCGCTTTGT	3240
TGCTCTTGCT	AAAAGTTTAG	CCGAAAATGC	AAATCCTAAA CGTAAGAAAG AATTACTTGA	3300
GATTGCAGAT	ATTGCTCTA	GAGTCCCATA	TGAACCGGCA ACTACTTTTG CAGAAGCTAT	3360
TCAATCAGTT	TGGTTTATTC	AATGTATTTT	ACAAATTGAA TCTAATGGCC ACTCTCTTTC	3420
ATATGGCCGT	TTTGATCAAT	ATATGTATCC	ATATATGAAG GCTGATTTAG AAAGTGGTAA	3480
AGAAACAGAA	GATAGCATTG	TTGAACGTCT	GACAAATCTT TGGATTAGA CAATTACAAT	3540
TAATAAGGTT	CGCAGTCAAT	CACATACATT	TTCTTCAGCA GGAAGTCCTT TATATCAAAA	3600
TGTTACAATT	GGTGGACAGA	CTCGAGATAA	GAAGGATGCT GTTAACCCAT TATCTTATTT	3660
GGTATTAAAA	TCAGTTGCAC	AAACCCATCT	ACCGCAACCT AATCTAACTG TACGTTACCA	3720
TGCAGGTTTA	GATGCTCGTT	TCATGAATGA	GTGTATTGAA GTGATGAAAC TTGGTTTTGG	3780
TATGCCTGCA	TTTAATAATG	ATGAGATTAT	TATTCCTTCT TTTATTGCAA AAGGAGTATT	3840
GGAAGATGAT	GCTTATGATT	ACAGTGCCAT	TGGATGTGTT GAAACGGCAG TTCCAGGGAA	3900
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GATGAATGAT	GGAATTGATC	CGGCTTCGGG	TAAACGGTTT GCACCAAGCT TTGGTCGTTT	4020
TAAGGATATG	AAGAACTTTT	CTGAATTAGA	AAATGCTTGG GATAAAACAC TAAGATATTT	4080
GACACGAATG	AGTGTATTG	TTGAAAATTC	TATTGATTTA TCATTGGAAC GAGAAGTTCC	4140
TGATATTCTA	TGTTCAAGAT	TGACTGATGA	TTGTATTGGT CGTGAAAAAC ACCTTAAAGA	4200
AGGTGGAGCA	GTATATGATT	ATATATCAGG	ATTGCAAGTT GGAATTGCAA ATTTGTCCGA	4260
TTCATTAGCT	GCAATTAAAA	AATTGGTGTT	TGAGGAAGAA CGTATAAGCC CAAGTCAGCT	4320
TTGGCATGCA	CTGGAACAG	ATTATGCCGG	AGAAGAAGGT AAGGTCATTC AAGAAATGTT	4380
GATTCATGAT	GCACCTAAGT	ATGGTAATGA	TGATGATTAT GCTGACAAAT TGGTTACTGC	4440
TGCTTATGAC	ATTTATGTTG	ATGAAATTGC	TAAATATCCT AATACACGTT ATGGAAGAGG	4500
GCCTATTGGA	GGAATTCGTT	ATTCAGGAAC	ATCTTCTATC TCAGCCAACG TAGGGCAGGG	4560

1097

ACGTGGAACA TTAGCAACTC CAGATGGACG CAACGCGGGT ACACCGTTAG CAGAGGGTTG	4620
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ATTACCAACA GATGAAATCG TAGGTGGGGT TCTCTTAAAT CAGAAAGTAA ATCCTCAAAC	4740
GTTAGCCAAA GAAGAAGATA AATTAAACT AATTGCTTTG TTACGAACAT TCTTTAATCG	4800
TTTACATGGG TACCATATTC AATACAATGT TGTTCGTCAGA GAGACGCTGA TTGACGCTCA	4860
GAAACATCCT GAAAAACACA GAGACTTAAT TGTTCGTGTT GCAGGATACT CTGCATTCTT	4920
CAATGTTCTT TCTAAGGCAA CCCAAGATGA CATTATAGGA CGTACTGAGC ATACTTTGTA	4980
AAATAAAGAG GTTCTTTTTA TGAATTTAT GCTTGACACA TTAAATTTAG ATGAGATTAA	5040
AAAGTGCTCT GAAATTTTGC CGCTAGCTGG GGTAACCTCA AATCCCACTA TTGCAAAAAG	5100
AGAGGGTTCT ATTAATTTTT TTGAACGAAT CAAAGATGTA AGAGAATTGA TTGGCTCTAC	5160
ACCCCTTATT CATGTTTCAGG TGATTTCTCA AGATTTTGAA GGCATCTTAA AGGATGCTCA	5220
TAAAATTCTGA AGACAAGCAG GAGATGATAT ATTTATCAAA GTACCTGTTA CTCCAGCTGG	5280
ATTACGTGCA ATAAAGGCGC TAAAAAAGA GGGCTACCAT ATCACTGCAA CAGCTATTTA	5340
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TAATAGAATG GAAATCTGA ACATTGATTC AAATCTGTC ATTCGTCAAT TAGCTCTTGC	5460
TATTGATAGA CAGAACTCTC CTAGTAAGAT TTTAGCTGCA TCCTTTAAAA ATGTAGCACA	5520
AGTAAATAAT GCTTTAGCTG CAGGTGCGCA TGCTGTTACA GCAGGAGCGG ATGTTTTTGA	5580
ATCAGCTTTC GCCATGCCAT CTATCCAAA GCGGGTTGAT GATTTTTCTG ACGATTGGTT	5640
TGTTATTCAA AATAGTCGTT CCATTTAGAT AGAGAGGAAA TACATATGAG AATTTTGCT	5700
AGTCCTTCTA GATATATTCA GGGGAAAAT GCCTTGTTTG AAAATGCCAA ATCAATTTTG	5760
GATTTGGGAA ATTGCCCTAT TCTATTATGC GATCAGTTGG TTTATGATAT TGTGGAAAA	5820
CGATTTGAAG ATTACCTACA TAGGTATGGT TTCCATATTG TTCTGGCGCT ATTTAATGGT	5880
GAAGCTTCTG ACAATGAAAT CAATCGAGTT GTTGCCCTGG CTGAGAAAGA AAATGTGAT	5940
AGTATTATCG GTCTTGGTGG GGGAAAGACG ATTGATAGCG CAAAAGCTAT TGCAGATTG	6000
ATTGAAAAGC CTGTTATTAT TGCTCCAACA ATTGCATCGA CCGACGCACC TGTATCTGCT	6060
TTATCTGTTA TTTATACAGA TGAAGGTGCA TTTGATCATT ATCTATTTTA TTCTAAAAAT	6120
CCAGATTTAG TTTTGGTTGA TACAAAAGTT ATTCACAAG CCCCTAAGCG TTTATTAGCG	6180
TCTGGTATTG CAGATGGTTT AGCAACTGG GTTGAGGCGC GTGCGTTAT GCAGGCAAAT	6240
GGAAAACTA TGTTGGGACA ACAGCAAACA TTGGCTGGAG TTGCAATTGC GAAGAAATGT	6300

1098

GAAGAAACGC TGTTCGAGA TGGTTTACAG GCTATGGCAG CTGTGAAGC TAAAGTGGTG	6360
ACACCAGCAT TAGAAAATAT TGTGAAGCT AATACTTTAT TGAGTGGTCT AGGTTTTGAA	6420
AGTGGAGGAT TAGCTGCGGC GCATGCAATT CATAATGGTT TTAAGTCATT GACAGGTGAC	6480
ATTTCATCATT TAACACATGG TGAAAAAGTA GCTTATGGAA CTTTAGTACA ACTATTATTG	6540
GAAAATAGAC CTAAGAAGA ACTTGATAAG TATATTGAGT TTTACAAAAA AATTGGTATG	6600
CCAACAATC TAAAAGAAAT GCATTTGGAT CAAGTTGGAT ATGATGATTT AATAAAAGTT	6660
GGTAAACAAG CAACTATGGA GGTGAGACA ATTCATCAGA TGCCGTTTAA GATTTGCGCT	6720
TCAGATGTTG CTCAAGCTAT TATCGCTGTA GATGCCTATG TAAATTCAA ATAAACAATA	6780
AGGACTACTG TTTTCCAAAT GGTAGTCTTT TATTGATCCC TGTATTGAAT TCTATAGAAG	6840
ATTGAAATAG GATGAGAACA AATCGATTGG GAAAGTAAAA TTAATTTCTA TAAATGTTTT	6900
AGCAATTGTT TCGTACTATT TCAGATTCAG TCTACTATAT GTTCTTCATA AATCAAAAAG	6960
CGACATAGGT TGTCGGCTAT TTATTGTGAA TACATTAATT AGCATTCCAG TTTTATCTTC	7020
GGTCTAAAAA AAGTATTTTG TGCTATACGA GATAAGCTTC TTGACTTACT CCTTGATTTA	7080
CTGCATAACA ATGGGATAAA AAGTGGGAGA TAGAGCAATT CATAGTCATC AAAATTAATG	7140
AGATACAGTA TACAGTTTTT CCTTTAAACA CATTTCAAAT TCCCTCAAAA ATGGTATAAT	7200
AGTAACATCA CAAAATTGGA GAGAGACCAT GAGTTTTTAC AATCATAAAG AAATTGAGCC	7260
TAAGTGGCAG GGCTACTGGG CAGAACATCA TACATTTAAG ACAGGAACAG ATACATCAAA	7320
ACCTAAGTTT TATGCGCTTG ATATGTTCCC TTATCCGTCT GGAGCTGGTC TGCACGTAGG	7380
ACACCCAGAA GGTATACTG CAACCGATAT CCTCAGTCGT TACAAACGTG CGCAAGGCTA	7440
CAATGTCCTT CACCCAATGG GTTGGGATGC TTTTGGTTTG CCTGCAGAGC AATACGCTAT	7500
GGTACTGGT AATGACCCAG CAGAATTAC AGCGGAAAAC ATTGCCAACT TCAAACGTCA	7560
AATTAATGCG CTTGGATTTT CTATGACTG GGATCGTGA GTCAACACAA CAGATCCAAA	7620
CTACTACAAG TGGACTCAAT GGATTTTCAC CAAGCTTTAC GAAAAGGCT TGGCCTATCA	7680
AGCTGAAGTG CCAGTAACT GGTTGAGGA ATTGGGAACT GCCATTGCCA ATGAAGAAGT	7740
GCTTCCTGAC GGAAGTCTG AGCGTGGAG CTATCCAGTT GTCCGCAAAC CAATGCGCCA	7800
ATGGATGCTC AAAATCACGG CTTACGCAGA GCGCTTGCTC AATGACTTAG ATGAAGTAGA	7860
TTGGTCAGAG TCTATCAAG ATATGCAACG CAACTGGATT GGTAAATCAA CTGGTGCCAA	7920
TGTAACTTTC AAAGTAAAAG GAACAGACAA GGAATTTACA GTCTTTACTA CTCGTCCGGA	7980
CACACTTTTC GGTGCGACTT TCACTGTCTT GGCTCCTGAA CATGAATTAG TAGACGCTAT	8040
CACAAGTTCA GAGCAAGCAG AAGCTGTAGC AGACTATAAA CACCAAGCCA GCCTTAAGTC	8100

1099

TGACTTGGCT CGTACAGACC TTGCTAAAGA AAAACAGGG GTTGGACTG GTGCTTATGC	8160
CATCAACCCCT GTCAATGGTA AGGAAATGCC AATCTGGATT GCAGACTATG TCCTTGCTAG	8220
TTATGGAACA GGTGCGGTTA TGGCTGTGCC TGCCACGAC CAACGTGACT GGGAATTTGC	8280
CAAACAATT GACCTTCCAA TCGTCGAAGT ACTTGAAGGT GGAAATGTCTG AAGAAGCTGC	8340
CTACACAGAG GATGGCCTGC ATGTCAATTC AGACTTCCTA GATGGATTGA ACAAAGAAGA	8400
CGCTATTGCC AAGATTGTGG CTTGGTTGGA AGAAAAAGGC TGTGGTCAGG AGAAGGTTAC	8460
CTACCGTCTC CGCGACTGGC TCTTTAGCCG TCAACGTTAC TGGGGTGAGC CAATTCCAAT	8520
CATTCATTGG GAAGATGGAA CTTCAACAGC TGTTCTGAA ACTGAATTGC CGCTTGCTCTT	8580
GCCTGTAAAC AAGGATATCC GTCCTTCAGG TACTGGTGAA AGTCCACTAG CTAACCTGAC	8640
AGATTGGCTT GAAGTGACTC GTGAAGATGG TGTCAAAGGT CGTCGTGAAA CCAACACTAT	8700
GCCACAATGG GCTGGTTCAA GCTGGTACTA CCTCCGCTAT ATTGACCCGC ACAATACTGA	8760
GAAATTGGCT GATGAGGACC TCCTCAAACA ATGGTTGCCA GTAGATATCT ACGTGGGTGG	8820
TGCGGAACAT GCTGTACTTC ACTTGCTTTA TGCTCGTTTC TGGCATAAAT TCCTCTATGA	8880
CCTCGGTGTT GTTCCGACTA AGGAACCATT CAAAAACTC TTTAACCAAG GGATGATTTT	8940
GGGAACAAGC TACCGTGACC ACCGTGGTGC TCTTGTGGCA ACCGACAAGG TTGAAAAACG	9000
TGATGGTTCC TTCTTCCATG TAGAAACAGG GGAAGAGTTG GAGCAAGCGC CAGCCAAGAT	9060
GTCTAAATCG CTCAAGAACG TTGTTAACCC AGACGATGTG GTGGAACAAT ACGGTGCCGA	9120
TACCCCTCGT GTTTATGAAA TGTTTATGGG ACCACTCGAT GCTTCGATTG CTTGGTCAGA	9180
AGAAGGTTTG GAAGGAAGCC GTAAGTTCCT TGACCGAGTT TACCGTTTGA TTACAAGTAA	9240
AGAAATCCTT GCGGAAAACA ATGGTGCTCT TGACAAGGTT TACAACGAAA CAGTCAAAGC	9300
TGTTACTGAG CAAATGAGT CTCTCAAAT CAACACAGCT ATTGCCCAAC TTATGGTCTT	9360
TGTCAATGCT GCTAACAAGG AAGATAAGCT TTATGTTGAC TATGCCAAAG GCTTTATTCA	9420
ATTGATTGCA CCATTTGCAC CTCACTTGGC AGAAGAACTC TGGCAAACAG TCGCAGAAAC	9480
AGGTGAGTCA ATCTCTTATG TAGCTTGGCC AACTTGGGAC GAAAGCAAAT TGGTTGAAGA	9540
TGAAATTGAA ATTGTCGTCC AAATCAAAG AAAAGTTCGT GCCAAACTCA TGGTTGCTAA	9600
AGATCTATCA CGTGAAGAAT TACAAGAAAT CGCTTTAGCT GATGAAAAAG TCAAAGCAGA	9660
AATTGACGGT AAGGAAATCG TGAAAGTAAT TGCGGTACCG AATAAACTCG TTAATATCGT	9720
CGTTAAATAA CGAGTTTATT AGCTCTATCT GCCACCTTCA ATAGTCCACT GGACTATTGA	9780
AsCCAACTAA ATTAGTTAAC ATTGTTGTGA AATAAGATAG GAGTCCTTCA GAGTAGAATC	9840

1100

TGGAGGATTT TTTGAATCTT CTTATGAAAG TATGATATAC TATGGGCAAC TATAAAGTTT	9900
AAAAAGTGAA ATAAGGAGAA TAAGATGCCA GTAAATGAAT ATGGTCAAAT GATTGGGGAG	9960
TCAATGGAAG CTTATACTCC AGGTGAATTG CCTTCTTTTG ATTTCTTAGA AGGGCGTTAT	10020
GCTAGGATAG AGGCTCTTTC AGTGGA AAAAG CATGCGGAGG ATTTATTAGC TGTTTATGGC	10080
CCTGATACGC CTCGGGAGAT GTGGACCTAC CTCTTTCAGG AGTCAGTAGC AGACATGGAG	10140
GAACTGGTCA GCCTTTTAAA TCAGATGTTG GCTCGTAAGG ACCGTTTTTA TTATGCAATC	10200
ATAGACAAGG CAACTGGTAA GGCTTTGGGA ACTTTTTCCC TCATGCGAAT TGATCAGAAT	10260
AACCGAGTAA TAGAAGTGGG AGCTGTCACT TTTTCTCCAG AGCTCAGGGG GACACGGATA	10320
GGAACAGAAG CCCAGTATCT CTTGGCTTGC TATGTCTTTG AGGAGCTTAA CTATCGTCGC	10380
TATGAGTGGA AATGCGATGC TCTTAACCTG CCATCCAGAC GAGCAGCGGA ACGTTTGGGA	10440
TTTATTTATG AAGGAACCTT CCGTCAGGCA GTGGTTTATA AGGGGCGTAC AAGAGATACG	10500
GATTGGTTGT CTATGATTGA TAAGGACTGG CCTCAAGTCA AAGCTCGATT GGAAATATGG	10560
TTGCGTCCTG AAAACTTTGA TAAAAATGGA CGACAGCACA AGAGCTTGAG AGAACTTTAA	10620
GAGGTGTTGA GATGATTACT ATTAAAAAGC AAGAAATTGT CAAGCTAGAG GATGTTTTCG	10680
ATCTCTATCA GGCTGTCGGT TGGACAAACT ATACCCATCA AACAGAGATG CTGGAGCAGG	10740
CCTTATCTCA TTCATTAGTA ATTTATCTGG CACTTGATGG TGATGCTGTG GTGGGCTTGA	10800
TTGCTTTGGT TGGAGATGGT TTTTCATCAG TTTTGTACA GGATTTGATT GTTTTGCCTA	10860
GCTATCAGCG TCAAGGGATT GGTAGCTCCT TGATGAAAGA GGCTTTAGGA AATTTTAAAG	10920
AGGCCTATCA AGTCCAGCTG GCGACAGAAG AGACAGAAAA AAACGTGGGA TTTTATCGTT	10980
CTATGGGCTT TGAAATCTTA TCCACCTATG ACTGTACAGG AATGATTGG ATAAACAGAG	11040
AAAAATAAAA AAACCTGTTT GTTCTTAAGC AAAGTTTAAG GATGGTCTAG TATCATATAG	11100
TCATTAAATA AAGACCTCCT AACTTTATTT AATAAAATCC TAACTTTTT TCATCACAAT	11160
CTCCTAATGA AGCCACCCAA TCAGGTGGCT TTTTTCGGT ACGACGGCA TGTCGTATAT	11220
CTGAGGTGTA AGTCCTCAGC CTGACTATCG TGAGGTAGCA GGGAGAGGAA GGGATAGCGA	11280
AATCGTGGCT CTACGAACAG GAACGTGATA GTAAGGCGTA TATAGCGGAT AAGGAGGCTT	11340
CAAACTCTAA AGTCCAAAAA GGTAGTCGTA ACCTATATGT GTAAATCACG AGAGTAATTG	11400
AATTCGGACT AAGGTTTGTG TGAAAAAGAT AAATCTTTCT AGAGTCTAAA GACTCTGCGT	11460
CAGATTTCCT ATTTTCACTG TAACCTTTTA ACGTCCTCAT ATCTTGATA AACGAGGAAA	11520
GATGTACGAC TTATCCCGTG AGGTTTCATG AGCGCTGAAA GCGTAGTAAC AACGAATCAT	11580
GAGAAGTCAG CCGAGCCCAT AGTAGTGAGG AAATCTCCGT AATGGAAGTG GAGCGAAGGG	11640

1101

GTGAATACTC AAACAGTCTG GGGAGAGACT GTTTGAGGTC TGTGCTAGA AAGAGAAAAC	11700
GACAGATCGA AGTAATCCTA CTTCACTTGT GTCTGTAAAA TGAGTGGTCT GATAGAACTG	11760
GACTTTGAGG	11770

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAAACTA CTTTCTTAGT ATAACACTTT CAGAATCATT GTCAATAGAA ATGACTTGAT	60
TTTTTCAATT TTTTCAAGCT ATTTCCAAGG GTTGTAAGAT CGTCCCTGAT TCTGCAAGAT	120
AAGTAGTAAA CTAACACTA AAAACAAGGT TGCCAAGAGC AAGGTAATAT AGTCTCCTTT	180
TTTCAAGGCC TGATACTAT ACCATGTGCG TTTTCTCTCT TTCCCAAAGC GGCGAACTCC	240
ATGGCAGTCG CAATGGTATC AATGCGTTCT AGCGAGCTAA AAATCAAGGG CGTAATAATG	300
AGCAGATTGC CTTTGATTCT TTGCATAAGA GAAGCTTTCT TGGATAATTC CATCCACGC	360
GCCTCCTGAG ACATCTTGAT AGTAAAGAAT TCTTCCTGCA AATCTGGAAT ATAGCGCAAG	420
GTCAGGCTGA CAGAATAAGC AATCTTATAG GGCACACCAA TTTGATTTAA ACTGGAAGCA	480
AACTGACTAG GATGGGTTGT CATCAAAAAG ATAATAGCCA GAGGAATGGT GCAAAGATAC	540
TTAATGGCCA AATTTAGCAG ATAAAAGAGC TCCTGGCTGG TTAGAGTGTA GACACCGATT	600
CCCTGCCAAA TCACACTTCT CTCTCCATAA AGTCCAACCC CATACTCGGG AGAAAAGAGA	660
TAGACCATCA AAACGTTTAA AACGGCAAAT ATCGTCGCAA AAACGGCTAC AAAGGAAACA	720
TCTTTAAAGC GAATTTCTGA TAAATAGAGG AGAAAGACTG AAAAGATGGC AATCAGCAAG	780
AGCATTTCTGG TATCATAGCT AATCATGGCC GCCAATGATA CCAGAATGAA AAAGAGAAGT	840
TTCCCAGCTC CTGACAAGCG ATGAATCACA GTATCTCTAT GCTGGTAACC GATTAATTTA	900
GCTTGCATCC CTCTCTCCTT TCTTTGTAAA ATGCCGTTAA ATCCAGTGGA TCCACATCTA	960
GTTCCTTAGC CAAGTTAAAG ATGGAGGTTT CTTTGTAGAT GGCTTTTACT AACAGCTCAG	1020
GATCGCTCAA CAGACTGGCT GGAACAGTAT CGGCAATCAA TTCTCCATCC ACCATGACAA	1080
GGACCCGGTC TGAATAATCC AGCATCAATT GCATATCATG GGTAATCATG ACAATGGTAT	1140
GCCCTTTTGT ATGTAACCTC TCGAGAAATT CCATAATCTC AGTATAGTTC TTCTGATCTT	1200

1102

GACCTGCAGT CGGTTTCATCT AGGAGAATAA TTTCAGCTCC TAAGACCAAA ATTGAAGCAA	1260
TGGTGACACG TTTTCTCTGA CCAAATGACA GGGCAGAAAT AGGCCAATTA CGGAATTCAT	1320
AAAGTCCACA GATTTTCAAG GTTTCATATA CTCTCGTTTC AATTTCCTTC TCATCCACAC	1380
CTCGCAAACG GAGCCCTAGA GCCACCTCAT CAAAAATCAT ATTGGTTGAA ATCATTGTGAT	1440
TAGGATTTTG TAGCACATAT CCTACTCGTT CCGCCCGCTC TGCAACAGAA TCGCCTTTTA	1500
TATCCTGTTT TTCCCAAAGA TAGCGTCCTT CCGTCTGAAT AAAGCTACTT ATAGCCTTGG	1560
CTAGAGTTGA TTTCCCTGCT CCATTTTTC CGACAATAGC AATCTTTTCA CCCTTTTAA	1620
TATCTAAATG TAGGGATTTT AAAATCGGTC TATCATCATA AGAAAAAGAT ACTTCCTCTA	1680
GTCTAAAGAG TGA CTGCAAT GCTGGGGTTT CTTTGGCCAG TTCATTCTGC AACTGAACCT	1740
GACCTTTTGA GATAGACAAG TTATCCAGAT TCGCTAATTG TTCTTCCTTG ACTAAGTCCA	1800
CACCTAATTG ACGGAGAGTC GTTAGATAAA GGGGTTCTCG AATCCATTT TGAGTCAATA	1860
AATCAGTCGC AAGCAACTGG TCAGGGCTCC CATTAAAAAG GATACGACCA TCGTTTATCA	1920
AGACAATCCG ATCCACAGGG CGATGCAGAA CGTCCTCCAA ACGGTGCTCG ATAATAAGAG	1980
TCGTGCTCCC CTCTTCCTTA TGAATCTGGT CAATCAATTC GATAATATCC TGACCTGACT	2040
TGGGATCTAG ATTGGCGAGT GGCTCATCAA ACAAGAGAAT CGGACTTTCA TCAATCAAGA	2100
CACCAGCCAG ACTGACTCGC TGCTTTTGTC CACCTGACAA ATCCTGAGGA CGCTGATCCA	2160
GTAAAGGAAG AAGGTCCAGC TTTTCAGCCC ATTTATAAAC ACGACCTTTC ATCTCATCTA	2220
GGGCTGTCAC ATCATTTTCC AGAGCAAACG CCAAATCTTC TGCCACAGAC AAGCCAATAA	2280
ACTGCCCATC TGTATCCTGC AAAACTGTGC TAACCAGATG AGACTTATCA TAGATGCTCA	2340
TATCAAAGGC TACTTGACCC TTTATCAAAA ATTCTCCATA TGTCTGACCC TTGTAAATAT	2400
TGGGAATAAT CCCATTCAAA CACTGACCCA AGGTAGATTT ACCTGACCCA GATGGTCCAA	2460
CAATTAAGAC TTTCTCTCCC TTGTAAATGG TCAAGTCTAT CCCTTGCAAG GTCGGTTCTT	2520
GTTGTGTTTC ATACCGGAAA GAGAAATCCT TCCACTCAAT TaTAGCTTCT TTCATCTTAC	2580
TCTCTTCATT CGCTTCTTAG ACTTCTATTT TATCATAAAT CAAGCCCTTC TTGCAGTCTC	2640
TCCTCTTAAA ATCTTAGCGC CAAAAAGATT CCTATCCTAG CTTACTTGCC TAACTAATCT	2700
ATAAACATCG AAAAAGACTA GTTGCCAGC CTTCCCATC ATTTTATACT CTTCGAAAAAT	2760
CTCTTCAAAC CACGTCAGcT TCGCCTTGCC GTAGGTATGG TTAGTGACTt CGTCAGTTTC	2820
ATCTACAACC TCAAAACCAT GTTTTGAGCc TGCTTCGTCA GTTCTATCCA CAATCTCAAA	2880
ACACTGTTTT GAGCAACTGC GGCTAGCTTC CTAGTTTGCT CTTTGATTTT CATTGAGTAT	2940
TAGTCCTTTT TCAAACTTCC TGCACGAGTT TGGGTTCTG CATAGGCAAG TAAGAGAAGA	3000

1103

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GTTCTGCAA TAGCTACAGA TACACCATTG GCAATTCCTG CAACAATCCC TTGTGCAAAT 3060
ACTTTTTCTG CCGCTTCTTG ATAAATCACA ACATCTCCAA GTGGTGCCAA GACACCCCAA 3120
ACAAGGGCAT TTGCAAGTAG TTGAATGAGA TAAAAAATAA GAATATCTTT CCAGTCAAAA 3180
ACACCATTGA TCACGCGAAC GTACTTTCTA AAAAGTCCCA CAACTAAACC AAAGAGTCCG 3240
CTAGCGATAA TCCAAGTCCA CCATAGACCA TAACCAACAA GAGAGTCCTT GATTGCATGA 3300
CCAATCAACC CGACAAGCAA ACCGATAATC GGTCCAAAAA TAATAGAAAG TAGCGCTTGT 3360
ACCGCATACT GAAGCTGGAT GCTTGTATTT GGAACAGGGG TTGGAATGTT GATCATCCCG 3420
ATGACGACAA AGAGGGCAGC GCCAATTCCG ACAGCAACAA CTGTGTTAAT TGTAATTTG 3480
ATTTCCATAC TATTCTCCTA TTTTATCCTT CTATTTTCTT TATTTCAATG GTCCAAGATG 3540
AACCGACACC TACATTATAG GCCTTGGCAA AGGAACCTTG GTTGATAGCC AAACCTAAAC 3600
GATAGAGAGA GTTGATGTAA AGGATGGGTT GCCCAATTCT CACATCTGCA AATGATTTGC 3660
CATAGACAAC CTGATTTTGA TAGACCAGCA TATCAGCATG ATAGATGGTC ACTTCAAAAC 3720
GATCACCAAA TTCTGGTTCC AGCTTGTAAG ATTCTTCCCG TGTGATAGAG GTCCAAAGCG 3780
AACCGAAACG CACATCCAGA ATATCAATGG CTCCCTTCAC CAGATGATCT TCTATGATGG 3840
TCGCTACGAC TGGAAGCTCT ACAATCTGTT CCACACTGAG CTCTGGCCCT ACTTCCTCAA 3900
AAGTAATGTG ACCACTGGCC AGTTTAGCAC CAGTATAGGC ATAGACATCA CGACCGTGGA 3960
AGGTATAAGA ATGCTCTGTG TTTTGACGCC TATTGGCCAC CTCAGAAATC TCACGAATGG 4020
CTACAATGCC AACGTGTTTC TTGATAAAGG AAAGCGTCCC ATTATCTGGC GTGACAATGT 4080
ATTGATTTTT TGCAGTCTTG GCAACTACAC TCTTACGTTT CGAACCGACA CCTGGATCGA 4140
CAACCGATAC AAACGTCGTT CCCTCAGGCC AGTAATCCAC CGTCT 4185

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(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2069 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

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TGATAGAGTT AAAGCCGCTG AGTCATTCAA TCCATCTCCA ACCATCAAAA TAGTGTGACC 60
TGCTTTCTGC AGTTTCTCTA CTAACCTCAA TTTCCCATCA GGTTCAGT CTGTATAGAC 120
CTGATCAAAG GGCAATCTT TGAATAATC CTCTGTCCTA ATCAAGGTGT CTCCTGTTGC 180

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		1104	
CAGAATCAAT	TTTTyCCCCT GTGCCTTAAG TTTATCCAAG GCTGTTTTTG CTTCTTTTCT	240	
CAAAGGAGTA	TGAATGCAGA ACATTCCAAT CAATTCATTT TGATAAGCCA AGAATAAGAG	300	
ATTGTAGTGA	CTCTTGTA CTTC AATTAA AGCATT TTGT TCTGAACTGA TATGAATCTG	360	
CTCATCCTGC	ATCAAGACAT AATTCCCAAT AAGAACTGGT TGGCCATCTA TATGAGATTT	420	
GATCCCCTTG	CTTGCGATAT ATTGGAGTTT CCCATGCATT TCCTCATGTT CAATTCCTC	480	
TATCTCAGCT	TGCTTGACGA TGGCATTAGC AATAGGATGA TAAATGTGTT CCTCAAGACA	540	
GGCACTGATT	CTGAGAATAT CTTCTCACT ATAGTCTCCA AAAGGTAACA CCTTTTCAAC	600	
TATAGGATAA	CTAGTTGTGA TTGTTCTGT CTTATCAAAC AAGAAAGTAT CAACTCCAG	660	
ATATTTCTCC	AGAACATCTC CATCCTTAAT CACCATTTC ACGTTCAACC CTTCTTGAT	720	
AACTGTCAAA	TAAGCTACAG GAGTAGAGAT TTTC AAAGCG CAGGAGAAAT CGACCAATAG	780	
GAAAGAAATA	GCCTTAGAAA AAGAACCTGT CAATAGGTAA GTCAGCCCAG CCCCCAAGAA	840	
ATTATATTTG	ACGACTTTAT CCGCCATCTT GATGAAATAG CGTTGTTTCG TTTCTTGTT	900	
TTCTTCAGAT	TTCTTCATCA ACTCAATCAG CTGTAAAATA CCGCTGTTCA TCTGATTATC	960	
TGTTACACGA	ATGCGTAACT CTCCAGTTTC TAATACTGTA TTTGCACAAA CCAAATCAGA	1020	
CTCTCTTTT	TCAACTGGAA AACTCTCTCC TGTCAAGGAA CTTTCGTTGA CCATACCTAA	1080	
ACCTGAAACT	ACTTGTCAT CAAACAGAAT TTCATTTCCT TGAGATAAGA TCAAGACATC	1140	
TCCTATTTGA	ACATCGGAAC TCTTGATACT AACAACCGTA TCGCCCTGTA CTAGGAATAC	1200	
ATCGCTCTCT	TTTGCAAGAA GACTCTGTTC TAAATCTGTT GCAGTTTTTT TCAAGGACCA	1260	
CTGATCTAAA	TGATCCCCA AATCAAGCAT AAACATGATA TTGCTAGCTG TCTTGATTG	1320	
GTTCATAAAC	AAAGACAATA AAATAGCCGA ACAGTCCAAG ACTTCCATCG TTAGTyCCTT	1380	
ACGCGCTAGT	GTTTGATAGG CTTCTCTAAT ATAACCCAAA GCCTGATAAC AAGTCCATAT	1440	
ATAGCGAATA	GGATACGGCA CAAACTACG AAAAAGTACA CGCTTAACCG CTGCACCTGA	1500	
AACAATAGAA	TAAGCACTCT CTTCTCTACG AATGGGAAGA GTCATCAACT CAGAACTTT	1560	
CCCTTTATCA	ATTCTTTTAA AAAAGGCTTC TGCATTATCT AATACAGAAA AGCCTTCTTT	1620	
TATGCGTAGA	GTAAAGTGCT GTTGATCCAT GTAAAAGTGG ATAGACTCAA TCCCCTTTTC	1680	
ATCTCTCGCC	AAGGAACGAA GATAGTCTTG AATATCCAAG GTAAGTGAAA AAGAAGATGA	1740	
TAGTCGGATA	TGTTGGTATC CTCTATGTAG CACTTTAAAA GACATATTAT TCACCTATAA	1800	
GGCTATCTAA	TTGCTCTTCT TTTTCTCTT GCTCGTACAA ATATTTGGCA TCTTGCAAGA	1860	
CATCGTCTCC	ATGTTGCTTC ACAACAGAAA CAGATGCATC TAGCTCGTCT TTCAACTTGT	1920	
AAGCCTTAGC	CAAAGCTTTA GAATAACCTT TTTTAGCTTC CTTACTTGCT AAGATTTTCA	1980	

1105

AACCAAGGGT ACCAAATGCG ACACCACCCA AAAATAATGA AGATTTTTC GCAACTTTTG 2040
CAACGGTTAA TACTTCTTTT AACATAGGG 2069

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AAATCTTGCG CAATAAAGCT CATCTCCATC TCCCGATTGA AACAGTCACT CCCCCGACTG 60
TTTCAACGTC CCAAGACATA ATCTTAGGCA GATTTCTAAA ATTACACTCA AAGTGGAAAGT 120
CATTGAGCTT TCGAATGACA GTTGAAGTTG AAATGGCCAG CTGATGGGCA ATATCGGTCA 180
TAGAAATCTT TTCAATTAAC TTTTGCGCAA TCTTTTGGTT GATAATACGA GGAATTGGT 240
GATTTTCTT GACGATAGAA GTTTCAGCGA CCATCATTTT CAAGCAATGA TAGCACTTAA 300
AACGACGTTT TCTAAGGAGA ATTCTAGTAG GCATACCACT CGTTTCAAGG TAAGGAATTT 360
TATAGGGTCT TTAATGTCTA GTAATTTTGT GATAAAATGT AATTGTTCCA TATGATTCTT 420
TCTAATGAGT TGTTTGTGCG CTTTTCATTA TAGATCTTAT GGGACTTTT TTCTACCCAA 480
AATAGGCTCC ATAATATCCA TAGGGAATT ACCCACTACA AATATTATAG AGCCCAAAGT 540
TTTAGGTCGC TTGATAATAT GCGTTTTTTG AATTTTATAG ACTGCTCGTT TAACTCTAT 600
TTACTTCGTA CCTTCTGGAG CGAGACGGAA TATTAGTCAC ATACAAAATG AGTACTATTA 660
GGATTTTATT TTCATGTACA ATTTCAGCCA GTCTTGTTAT AATCAGCCTA TAGGAATCAA 720
GGAGGTGACT CTTATGGCTG TTTTGTGTC TTTGGATGGA ATTGTGGTAG AAGTCCTTGA 780
TGTCTTTTCT TCTTTTAATG GGGATAGTGA GTTTTCTTG TGTATAGCAT TTTGAATCTG 840
GAATAGGACG CCATGACTGC TAAAGATTT CTATAAATTA ATTTGATTTT CCTAATCAAT 900
TTGTTTCATAT CTTATTTTCAT TCCACTATAA ACGTCTTAAA GACAAGAGTC AGTTTGTAT 960
GGAACGCTCT CAGTTCGAGG AGATGTTCCA ACTTCAAAGT AGTCGCTTGA CGACGCAAGA 1020
AAAATTACAA TTGTTTACCT CTGTGTTTGC TGGCCGTTAT GATGTTTATG CTAAGAAATT 1080
TATCAATGAA CAAGGGAAAA TTCAGTATTT TCCTTCCTAT GATTATGGTT GGAAGCAGTT 1140
GCCACCTGAA AAACGGAGTT TCCAGACATT GACGAACTCC GTTTTGAAAT CTCATTTTCG 1200
TGGGGAGGCA GCTATCGGTA TCTTTCCTAT GCACTTAGAT GATAGCTGTT ATTTTGGT 1260

1106

ACTGGATTTG GATGAAGGAG ATTGGAAAGA AGCTGGTTTA ACCATTCGAA GAATAGCCAG	1320
GGAACGCCAG ATGGAAGCCC ATTTAGAGAT TTCTCGTTCG GGTCACGGAC TCCATATTTG	1380
GTCTTCTTTT GAGGAAGCGA TTCCGAGTCG AGAGGCTCGC TTGTTTGGAA AGAACTGAT	1440
AGAACTGGCA ATGCAGGAAA GTATGCAACT GTCCTTTGAT TCTTTTGATC GCATGTTTCC	1500
AAATCAGGAT GTCCTTCCTA AGGGGGGATT TGGAAATTG ATTGCCTTGC CTTTCAAGG	1560
AGAAGCTTAC CATCAAGGGC GAACGGTCTT TGTGGATGAA CAGTTTCAGC CTTATGAAGA	1620
CCAATGGAGG TATCTACAAG AAATTCAGAG GATTTCAACT GCTAAAGTGG CACTGTAAAT	1680
CCAAGAGGAG TTAGGCAAGC AAGAATTGGA TAAGGAGTTG AAGGTCGTTT TATCCAATAT	1740
GATCCAACCTT GAAAAATCGT CTGTGACATC CAAGGCACTT TTTTCTTGAA AAATATGGCT	1800
TCCTTTTCTA ATCCCGAATT TTATAGTAGA TTGAACTAG AATAGTACAC CTCTGCTTCT	1860
AAAACATTGT TAGAAATCGA TTGACTTTC CTGATCGATT TGTCTGTGTA TTATTTTATT	1920
TTACTATATT TAAAGCAGGC TATGCGACAG CCAACCTATC AAATTCCTGA GAGAATGTAT	1980
TTATTTGGAG AATCCGATCA TTATTTATGG TTGCCAAGAG GTTTGCTGTA TCCATTGCAA	2040
GATAAATTTA AGCAGGTATC TGTGGAAGAT AGGAGAAAGG TACAAAGGTC TATTAGCGTG	2100
GAATTTAAGG GAGAACTCAC TTTTGAGCAA GAGTTAGCCC TGTCAGATAT GACTTCTAAA	2160
GAAATGGT TACTTCATGC GGAGACTGGT TTTGGGAAGA CCGTTTTAGG TGTGCTCTT	2220
ATCTCTGAAC GGAAACAAA AACAATTATT CTAGTCCATA ATAAGCAACT CTTAGACCAA	2280
TGGCTAGATC GCTTAACTG CTTTTTGA CTTCGAAGAGG AGGAGGCTAT CCGTTATACG	2340
GCATCAGGTC GTGAAAAGGT AATCGGCTAT GTTGGGCAGT ACGGTGGGAC TAAGAAATGG	2400
CTGAGTAAAC TGGTTGATGT CGTTATGATT CAATCTCTAT TTAAGTTGGA AAATAGTCAA	2460
AGTCTTTTGG ATGAGTATGA GATGATGATT GTGGATGAGT GTCATCATGT CTCTGCCCTG	2520
ATGTTTGAAA AAGTTGTGTC TCAGTTTAGA GGAAGTATC TTTACGGTTT GACGGCTACG	2580
CCTGAGCGTA AGAATGGTCA TGAGCCTATT GTTTTTCAGA GAATTGGTGA GATACTCCAT	2640
ACTGCTGATA AGAGGGAAAC GGATTTTAAA CGGCAATTGC AATTAAGATT CACTTCTTTT	2700
GGTCATTTGG AAATGAAAA GACCAAAGCA AGTAATTTA TACAGCTTAG TGATTGGATT	2760
GCTACTGACT CAGTGAGGAA TCAGATGATT CTCAAGGATA TTCTAGCCCA AGTGGCAGAA	2820
GGACGGAATA TCTTGGTTTT AGTTAATCGA ATTCAACAGA TAGATGTCTT TGAAAAATTA	2880
TTGAAAGAGA AAGAGGTGA TGAAGTTTAC ATTATTAGCG GAAAAACCA AGTCCGAGAG	2940
AGAACGAGTT TACTGGAGAC GTTAGAACAG TTAGATAAAG GGTTTGTTTT GTTGTCTACT	3000
GGAAAATACA TTGGCGAAGG TTTTGACTTA CCTCAGTTGG ACACGCTTAT CTGGCAGCA	3060

1107

CCCTTTTCTT GGAAAAATAA TTGATTCAG TATGCAGGTC GGATTCATAG AAACACAAG	3120
GATAAGTCTT TGGTGCGTAT TTTCGATTAT GTGGATATTC ATGTTCCCTTA TTAGAAAAAG	3180
ATGTTTCAGA AACGACAAGT AGCTTATCGA AAGATGGATT ATCGTGTCAT CGAGGGTGAG	3240
GAGAAACAAT TCGTTTATGT TGATAGTAGA TATGAGAAGG TGTGAGAGA GGACTTAGCA	3300
GGGAAAGAC AGGAATGTCT GCTTATTTTA CCTTATGTGC ACCAGACAAA ACTGATGAAT	3360
TTTCTAAAAG AATTAGGAT TAGTCAAAT GAGATATGTA TACCAGAGAC GGTGCAAAT	3420
AAAGCATGGC TAGACCAAGT GAAGAGCCAG AAAATTAAAG TGTCTTTTAC TCAATCAAAA	3480
ATAGTAACGC CTATTCCTTT GGTGAATAAG ACTATTGTTT GGTATGGTGC AATGCCATTA	3540
TTAGGGAAGG TAGATGAGAT GACCATATTA CGTTTGAAT CAGCTAGTAT AGTTTCTGAA	3600
CTAGTGGCAG GTTACGATA GAGAAAATTT TAAAAAATTT CTATGTATGA TTTTCATTTT	3660
TTTAGTGAGA CTGTTGCCAT TATCACATTC GAATCACACA AAATAAAAAA ATTTTATAA	3720
GTACTTGACA AATAGATTGA AATATCATAA AATAAAAACG GTTACAGAGT TATTAATTAT	3780
TTAAGCTTCA TGTCACCATT AAAAATTGAA ATAAAAGGAT GTTATCACTA ATACAAGTGA	3840
GCAGGAACCT ATTTAATCAC ATCAGAAGAA GTTCTTGTAT GTTTTAAAGT AGGTTCCCTT	3900
TATTTTAAAA GGGAAATTTT ATGATCATAA AACGAATACT AAACCACAAT GCCGTAATTG	3960
CGCAAAGTAA AAAAGATATC GATATCTTTC TTTTGGGAAG GGAATAGCT TTTGGAAGAA	4020
AAACTGGAGA TAAAGTAAAT CCAATTGATA TTGAGAAAAG TTTTCTCTC AAAAATAGAG	4080
ATAATATGAC CCGTTTACA GAGATGTTA TTAACGTTCC TTTGGAGTTG GTGTACATCA	4140
CCGAAAAAAT AATTAACCTA GGTAATAA CATTGGGTAA TAATTTTGAT GAAATTATCT	4200
ATATTAAATTT AACGGATCAT ATTTCTTCGA GCATAGAACG TTATAAAGAA GGGATTATTA	4260
TTTCGAATCC CCTACGCTGG GAAATATCGA AATATTATAA AGAAGAATTT GAACTTGGGA	4320
AAAGGGCTTT ACAAATAATA AAAAAAGAGT TAGGTATTGA ACTTCCAATT GACGAAGCTG	4380
CATTCATAGC GCTACATTTT GTTAATGCTA ATTTAGAAAA TAATTTTCAA GAGTCGTATA	4440
AAATCACTGA AATAATTATG GGAATTGAGA AAATCATTC AAGATTCTAT TGTACTGAGT	4500
TTAACCAAGA TTCTATTGAT TATTATAGAT TCATAACTCA TATGAAATTA TTTGCCCATC	4560
GCTTGGTTGA GAATACAAC TATTGTGACG ATGATGA	4597

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1108

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

CGGCTTATTT ACTACTTGTT CCATCATATA TGGAAATATGC ATGAAACCTG CTCTCATATT	60
AGGGAATTTT TTATCCACTA AATAAGAGC TTGGTACATC AAATGATTGC AAACAAAGGT	120
TCCTGCACTA TTGGATACAA CTGCCGGAAG TCCCTGTTTT TTGATAGCTT GTACCATCGC	180
TTTGATAGGT AAACACTAA AATAGGCCGA TGCTCCATCA ATACGAATCG GTGTATCAAT	240
TGGTTGATTG CCTTCGTTAT CAGGTATGCG AGCATCATCT TGATTAATAG CCACTCGTTC	300
AGGTGTTAAG CCGGTCCTGC CGCCTGCTTG TCCAATACAA AGTACAGCAT CTGGTTGATA	360
TCGTAATATT TCTGCCTCTA AAACCTCTGA CGACTTATAA AAAACCGTTG GAATTTCTAC	420
CCAGCGAACT TCAGCCCCAT TAATCTCAGA TGGTAATAAT TTTACAGCCT CCAAAGCTGG	480
ATTAATCTTT TCACCTCCAA AAGGATTAAA ACCTGTAACC AATATTTTCA TTTTATTTTC	540
CTTTACTAAA ATGCGAGAAA GTACATTAAG AATATGTGAA TAACAATCAT TACTAGAGCA	600
ACACCTGCTT GAGCCTTTAT AACGCCATTC TGATCTTTCA TATCCATCAA TGCTGCTGGT	660
AGAGCGTTAA AATTAGCAGC CATTGGGGTC AATAAGGTCC CACAATAACC TGCTGTCATG	720
GCAAGAGCAC CAGCCACAAT TGGATTAGCT CCCAGAGCAA ATACAAAGGG AACTCCAACA	780
CCTGCTGTAA TAACGGTGAA TGCTGCAAAA GCATTTCCCA TAATCATTGT GAATAGAACC	840
ATTCCAAGAA CATAGGCCAA AACTCCTATA AAGCGACTAT CTGAAGGAAC AATACCGCTA	900
ATCAGATGAG AGATAACATC ACCAACACCT GCTACAGTAA AAATAGCCCC CAAAGCCCCT	960
AATAATTGAG GAACAATCCC ACTTGTTGAA ACTTGCTGAG TCATTGATT ATTTTCTGAT	1020
AACAGACTCT TAGGGTGACT ATTGTAATC ACAAGAACAG AAATTGTAGC AAACAAGGCG	1080
GCAAGGCTAA TCGAAATCTT GCTAAATCTT GGAATCATT GCGCTAAGAC CAACGCAAGT	1140
ATTGCCATCA GCATAACTGG AATAAAAATT TTATTTTTCAC ACCTGTTAGA TTCAATATTG	1200
GCTTTCATTT CATCTAAGGA TGGCAAGGTT CCGATACGGA CTTGCTTAAA CAATGTTAAC	1260
AGCGATAATA GGATTACAAT AATACCAATA CTCATATTG GCATATAGGA ACCACCTATA	1320
AACGTAATAG ACAATAGAGT CCAAAATGCA GATGTCCCAA GTCGAACTGG GTTTGTTTTA	1380
TCTTTATAAC TACAATAGGC TGTATGGAGA AATTGACAAC CAATCACAAT ATAGGTCAAC	1440
TCTAATAGTT GCTTTGCCAA CTCTGTCAAT TTTGTTCTCC TCCCCTAGTC TTTTGTGATA	1500
TCAATTTTTT ATCAAATAAA TAATTATAAA TCCCCACTAC AATAAGTGTT ATAACAGCAA	1560
CAATAATAGA TGTAAGGCA ATCCCTGCAT AATTGCTTTC ATAGCCTAAC TGATCTAATG	1620

1109

TTCCCCCTAT CAAGAGGACT CCCCCAGCAC CTACAAACGT ATTTTGAGCA AAGAAATTTT	1680
CAAAATTTTC ATTGCGAGCC GCACGCGCTT TTATTGTCTC ATCTTCAACC TCTGTAACT	1740
TTCTACCTAA TTGAGACTCT GCAGCTGCTT CTCCCATAGG TTGAACCAAA GGTCTGACAA	1800
ACTGAGGGTG TCCTCCTAGA CGAATTGAAA AGAAACCAGC TAACTCTCGA ATAAAGAAAT	1860
AAACTGTATA GAAGTTTCCA ACTGTCAGAC CTTTAATCTT TCGAATCAAA TCGATTGATC	1920
GTTGCTTGAG TCCAAAGGTT TCTGACAGCC CCACAAGAGG CAAGGTAACC ATAAAAATCG	1980
TGAGCACTCG CTGATTGCTA AATTCTTTTC CCAAAATCTC CAAAATTC ACGAGAGAAA	2040
CACCTGAAAC TAAAGCTGTA ACCAAACCAG CTAAGACTAC TGTGCAATT GTATCAAATT	2100
TTAAATATA ACCCACAACA ATGATTGCTA TTCCTATTAA TCTAATCCAC TCCATATCAA	2160
ACTCCTTTAT ATTCAAAATG ACAGTATTTT TAAATTTTA TCAAGATCAA TACCATTCTT	2220
TATTTAATGT GTTTTCTAG TTCTTTTGG TATTGCTAT TGGATTCCAA TTTTCTTTT	2280
TGCCATTTT TAAAAACCTC GTTATATCT TTTGTTGTAA CAATATCTTT TTGCAATTC	2340
ATTCTTTTAA AGATATATGG ATCCCCCTA ATACCAACTT GTGAGTATGG TTTTGAGAAT	2400
GGTACTACGT TACTTACAAC TGGAGAACCA CCAGATGAAG CTGTTGGCAT CAATAATGAA	2460
CTATCTGTCG ACCAAGCTTG AGCTTTGGCA TATTTTTCAT ATCTTTTCTC TAGGTCAGTG	2520
GTCTCAGAAA CAGCATCTTC TAACAATTC TTATATTTAT CCAAACCAGG TTTAGCTACA	2580
ACATCCTTAT CTTTTCCTTT CGTAATACCA AGGTGTTTCA TGGCAGAACC AGATTTTGGA	2640
TCTATAATAT TCAAGTGAGA CGCTGGATCT TGATAGCTTG GAGCCCATCC TGTACTGTTC	2700
AAATCATAGT CTTTTTGAGA AGGAGCAACA TTGCCGTATT TATCATTTTC CATCAAACCA	2760
TCAATAACAT TTCCAATAAC GTCTGTCTC GATGTTGAG TCGCTATACT GTAGCCCAAT	2820
GATGCTGGAT CTAATGCATA GACATAAGAA AATGTTGTCG GTGCATCTGC TTCTTTATCA	2880
GTTTTTCAC AAGCCACTAA AATAGCTGAC GTGCTCAGGA CCACTCCTGC TGTAAAGAGC	2940
CACCTTTTCT ATTTCATAAA GAATCTCCTT TGGTTTATTT TAATCTACTT TTACAATCCA	3000
ACCTTCTGGC GCTTCAATAT CGCCAACTG AATACCCGTC AATTCATTAT ATAATTTACG	3060
CGTCACAGGA CCTACTCTG TTTCATAA GAATACATGG AAATCATCAC CATGTTGAAT	3120
ACCTCCAATT GGAGAAATA CCGCTGCTGT ACCACAGGCA CCTGCCTCTA CAAAACGGTC	3180
AAGATTATCA ATTGGAACAT CACCCTCAAT AGGAGTTAAT CCCAAGCGAT GTTCTGCCAA	3240
ATAAGCAAG GAATACTTGG TAATAGATGG CAAGATAGAT GGAATCAATG GTGTTACAAA	3300
TTCATTATCA GCTGTAATTC CAAAGAAGTT AGCTGATCCG ACTTCTTCAA TCTTTGTATG	3360

1110

AGTTGATGGG TCCAGATAGA TAACATCTGA GAAATGACGT GACTTGGCCA TTTTTCCTGG	3420
TAAGAGACTT GCAGCATAGT TTCCACCAAC CTTAGCCGCA CCTGTACCAT TTGGTGCTGC	3480
ACGGTCGTAC TCATCCTGAA TCAAGAAGTT GGTGGGACC AAACCACCTT TAAAGTAATT	3540
TTCAAAGTGGC ATAGCAAAGA TGGTGAAAAT GTACTCTTCT GCCGGTTTTA CCCCATAAT	3600
ATCTCCGACA CCAATCAAAA GAGGGCGAAG ATATAAGGTT CCACCTGTTT CGTATGGTGG	3660
TACGTATTCT TCATTGCGAC GGACAACTGC TTTACAAGCT TCTACAAACA TGTCTGTCGG	3720
AACCTGTGGC ATCAAGAGAC GGTACATGT ACGTTGCAGA CGTTTAGCAT TTTCATCAGG	3780
ACGGAACAGT TGAACACTGC CATCCTTAGT ACGATAAGCT TTCAAACCTT CAAATGCTTG	3840
TTGTCCATAG TGAAGACTTG GAGAAGACTC TGAAATATGC AAAGTTGCAT CCTCTGTAAG	3900
CTCTCCTTGA TCCCATTTGTC CATTTTGTGA ATGAGCAAGA TAGCGATAAG GTAATTTTAT	3960
ATAGGAAAAA CCGAGGTTT CCGG	3984

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8703 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TATCTAATTA TTGGTTTTTA TCGCTGACCT TGGCTATTGT TGGGGTTGTT TTACCCTTGT	60
TGCCTACAAC ACCTTTCCTT TTGTTGTCTA TTGCTTGTTT CTCCAGAAGT TCCAAGCGAT	120
TCGAAGATTG GCTTTATCAT ACCAAGCTCT ATCAAGCATA TGTAGCTGAT TTTCTGAGA	180
CCAAGTCTAT TGCGCGTGAA CGAAAGAAAA AAATCATCGT CTCTATCTAC GTCTTGATGG	240
GAATTTCTAT TTATTTTGCA CCTCTTTTAC CAGTCAAAAT CGGTCTGGGT GCTTTGACCA	300
TCTTTATTAC TTATTATCTC TTCAAGGTCA TTCCAGACAA AGAATAGTTA AACAGTAGT	360
TATTTGCCTT GATAAAATTG AAAGCATATT CATAACAATA TGATATAATA AAATTGAAGT	420
AATATTCAAG GAGAATCAAA TGATTTACGA ATTTTGTGCT GAAAATGTGA CTTTACTTGA	480
AAAAGCGATG CAGGCTGGAG CTCGTGGAT TGAAGTCTGT GATAATCTAG CAGTTGGTGG	540
GACAACACCC AGCTATGGAG TGAATAAGGC AGCGGTTGAA CTGGCAGCTA ACTACGATAC	600
AACCATCATG ACCATGATTC GGCCACGTGG TGGTGACTTT GTCTATAATG ACCTAGAAAT	660
TGCTATCATG CTAGAAGACA TTCGTTTGAC TGCTCAGGCT GGAAGTCAAG GGGTTGTATT	720
TGGAGCTTTA ACTGCTGATA AAAAGTTGGA TAAGCCTAAT CTGGAAAAGT TAATTGCTGC	780

1111

ATCAAAAGGA ATGGAAATTG TCTTTCACAT GGCCTTTGAT GAACTAAGTG ATGAAGATCA	840
AGCGGAAGCT ATTGACTGGC TCAGTCAAGC CGGTGTCACT CGTATCCTAA CTCGTGCTGG	900
TGTGTCTGGC GACTCCTTAG AAAACGTTT TGTTCACAT CACAGAATTT TGGAGTACGC	960
TAAAGGTAAA ATTGAAATTC TACCAGGTGG GGGGATTGAC CTTGAAAACC GTCAAACCTT	1020
TATCGACCAG GTGGGGGTAA CACAATTGCA TGGTACTAAG GTTGTTTTTT AAAAAATAGA	1080
AAGGAACTGC TAGCTTTGGG TAGCAGTTT CACTTATGTT TGAAATTTTT AAATCCTATC	1140
AATTTAATCA AGAAAAGGCT CATGATTATG GTTTTATAGA AAATAGCGAA GTCTGGACAT	1200
ATAGTTGCCA GATTTTGCAA GGTGACTTTG TCATGACTGT GTCCATCACT GCTGATAATG	1260
TGAACTTTCA AGTCTTTGAC CAAGAGACTG GTGACCTCTA TCCTCACGTT TATATGGAAA	1320
GCATGAGGGG AAGTTTGTG GGAATGTCC GTGAGGCTTG TCTGGAGATT CTTTACCAGA	1380
TTCGGAAGGC TTGTTTGTG GTGCAAGATT TTATCTGTCA TCAGACTAAG CGTATCATGA	1440
CTCAAGTTCA GGAAAAGTAT GGAACCAGT TGGAGTATCT GTGGGAAAAA TCGCCTGATA	1500
CAGCTGTATT GCGCCATGAA GGCAATCAAA AGTGGTATGC CGTCTTGATG AAAATCTCTT	1560
GGAATAAGCT GGAAAAGGC AGAGAAGGAC AAGTGAAGC AGTCAACCTC AAGCATGACC	1620
AAGTAGCTAA TTTGCTTTCA CAAAAGGGA TTTATCCAGC CTTCCATATG AGCAAGCGCT	1680
ACTGGATTAG TGTGTCCCTT GATGATACTT TATCAGATGA AGAAGTACTG GAATTGATAG	1740
AAAAAAGTTG GAACTTAACC TCTAAAAAT GAAATATTTT AATAATTTTC ATGAACTTTC	1800
AATTAGCTAA ATATCTTTA CTGAAGAGAT TTTTAGAAAA TATAGGATTT ACCACACTAG	1860
AGGAATATGG TGCCATCTTC AAATACCTGA TTGAGAATGT CAAGACGGAT CGTCAGATCA	1920
TCTATTCGCC TCACTGTCA TATGACCTCG GAATGGCAGT GGCAAAATAGC CTTGCTGCTG	1980
TCAAGAATGG TGCAGGACGT GTTGAAGGGA CTATCAATGG TATTAGGGAG CGAGCTGAAA	2040
ATGCTGCTTT GGAAGAAATT GCAGTGGCTC TCAATATTCG CCAAGATTAC TACCAAGTAG	2100
AAACCAGTAT TGTCCTAAAT GAGACCATCA ATACGTCAGA AATGGTTTCT CGCTTCTCTG	2160
GTATTCCAGT TCCTAAAAAC AAAGCCGTCG TTGGTGGCAA TACCTTCTCC CACGAATCTG	2220
GTATTCACCA AGATGGAGTC CTTAAAAATC CTCTCACTTA TGAGATCATC ACACCTGAAT	2280
TGGTTGGTGT TAAGATTCTG CTGGAATAAT TATCTGGTCG CCATGCTTTT GTTGAGAAAC	2340
TGAGAGAATT GGCCCTAGAT TTTACAGAAG AGGATATCAA ACCACTCTTT GCTAAGTTCA	2400
AGGCACTGGT CGATAAGAAG CAAGAAATCA CAGATGCAGA TATTCGAGCT TTGGTAGCTG	2460
GAACCATGGT TGAAAATCCA GAAGCTTCC ACTTTGATGA TTTACAACCT CAAACTCATG	2520

1112

CAGATAATGA CATTGAAGCG CTCGTTAGCC TAGCCAATAT GGATGGTGAG AAAGTCGAAT	2580
TTAATGCGAC AGGGCAAGGT TCCGTTGAAG CAATCTTTAA TGCTATCGAT AAGTTCTTTA	2640
ACCAATCTGT TCGTTTGGTG TCCTACACTA TCGATGCGGT AACAGATGGA ATCGATACCC	2700
AGGATCGGGT TTTGGTCACT GTTGAAAACA GAGATACAGA AACCATCTTT AATGCAGCAG	2760
GGCTTGATTT TGATGTGTTG AAGGCTTCTG CTATTGTCTA TATAAACGCT AATACCTTTG	2820
TTCAAAAAGA GAATGCAGGT GAGATGGGAC GCAGTGTTC TTACCACGAT ATGCCTAGTG	2880
TGTAAAGGAG AAGGCTATGG CAAAGAAAAT AGTAGCTCTA GCAGGAGACG GAATTGGCCC	2940
AGAAATCATG GAGGTGGTT TAGAAGTTCT GGAGGCTCTA GCTGAAAAA CAGGTTTGA	3000
CTATGAGATT GACAGACGAC CGTTCGGAGG TGCAGATATT GATGCAGCAT GACCTCCCTT	3060
ACCTGATGAA ACCCTTAAGG CAAGTAGGGA AGCAGATGCT ATCCTACTAG TAGCTATCGG	3120
TAGTCCTCAG TATGATGGAG CAGTGGTTCG CCCTGAACAA GGCCTGATGG CTCTCCGTAA	3180
GGAACCTCAAT CTTTACGCTA ATATTCGTCC TGTAAAAATC TTTGACAGTC TCAAGCATTT	3240
GTCACCACTC AAACCTGGAAC GAATTGCTGG TGTAGACTTT GTCGTGGTGC GTGAATTGAC	3300
AGGCGGGATT TACTTTGGAT ATCATATTCT TGAAGAGCGC AATGCGCGTG ATATCAACGA	3360
CTATAGCTAT GAGGAAGTGG AGCGGATTAT TCGCAAAGCC TTTGAAATTG CAAGAAATCG	3420
CAGAAAAATC GTTACTAGTA TCGATAAGCA AAATGTTCTA GCGACCTCAA AACTCTGGCG	3480
GAAAGTAGCT GAGGAAGTCG CACAGGATTT CCCAGATGTA ACCTTGGAAC ATCAGCTGGT	3540
AGACTCAGCT GCTATGCTTA TGATTACCAA TCCTGCTAAG TTTGATGTTA TTGTAACGGA	3600
GAATCTTTTT GGAGATATTT TATCTGATGA ATCAAGCGTC TTATCTGGTA CACTTGGGGT	3660
TATGCCATCA GCCAGTCATT CTGAAAATGG ACCAAGTCTC TATGAACCTA TTCACGGTTC	3720
AGCACCTGAT ATTGCAGGTC AAGGAATTGC CAATCCTATT TCCATGATTT TATCAGTTTC	3780
CATGATGTTG AGAGATAGTT TCGGACGTTA TGAGGATGCA GAGCGTATCA AACGTGCTGT	3840
TGAGACAAAGT CTGGCGGCAG GAATTTTAAC GAGAGATATA GGAGGTCAGG CTTCAACAAA	3900
GGAAATGACG GAAGCTATTA TTGCAAGGTT ATGAAGTTAG ACGAAAAAAT TACTCTAGTC	3960
CTTTTGATTT GGAATGTCAT CATTTTCTTG ATTTATGGTA TTGACAAATC TAAGGCAAGG	4020
AGAAGAGTTT GGCATATCCC TGAGAAAATC TTAATTATTT TAGCCTTTAC TTTTGGTGGT	4080
TTTGGTGCCCT GGCTAGCAGG AATCATCTTT CACCACAAGA CTCGAAAATG GTACTTTAAA	4140
ATAGTTTGGT TTCTTGGGAT GGTGACCACA CTAGTAGCCT TATATTTTAT TTGGAGGTAA	4200
TGGATGGCAG GGTCTTCGAG GGAATACGCT GCTTGGGCTC TAGCGGACTA TGGTTTTAAG	4260
GTCGTGATTG CAGGATCTTT CGGTGACATT CATTACAATA ATGAACTCAA TAATGGCATG	4320

1113

TTGCCAATCG TTCAGCCTAG AGAGGTTAGA GAGAACTAG CCCAGCTAAA ACCAACCGAC	4380
CAGGTAAC TG GACTTGGA ACAACAAAA ATCATCTCAC CAGTTGAAGA ATTCACCTTC	4440
GAGATAGATA GCGAGTGGA ACATAAACTC CTAATAGTT TGGATGATAT CGGTATTACC	4500
TTGCAGTATG AAGAGTTGAT TGCTGCTTAT GAAAAACAAC GACCAGCCTA CTGGCAGGAT	4560
TAGAAAAAAT AGAAAAGGAG ATATAGTAAA CTGAAATAAG ATGTAAACAA ATGAATTGGA	4620
GCTTAACATC CATTTCCAGC AATTTTCTAG AAACCTACAGT GGACTATTCT GGATTCAACA	4680
CATTATAAAA TTATGACAAA ACACATTCAC AAGAAGGCTA CGACATTTTA AAAGGTGAGG	4740
GCGGATGTAT CGTTGCCCT ACTAAAGTTG GTTACATTAT CATGACCAGT GACAAGGCAG	4800
GACTTGAGCG TAAGTTCGCA GCCAAGAAC GTAAGCGTAA CAAACCAGGT GTTGTCTCT	4860
GCGGTAGCAT GGATGAAC TT TCGCTTTAG CGCAACTCAA CCCAGAAAT GAAGCATCT	4920
ACTAAAAACA TTGGGATGAA GATATCTCTC TTGGTTGTAT CCTTCCTTGG AAACCAGAAG	4980
CCTTTGAAAA ACTCAAAGCA TACGGGGATG GCCGTGAAGA ACTTATTACT GATGTACGTG	5040
GTACTAGCTG TTTTGTATC AAGTTTGGA AAGCAGGTGA ACAATTGGCT GCCAAGCTTT	5100
GGGAAGAAGG TAAAATGGTC TACGCCTCAT CTGCTTCAAT GACAAAACGA TTGAACTCG	5160
CTATGAGCAA GGTGTAATGG TGTCTATGGT CGATAAGGAC GGCAAACTCA TCCCAGAACA	5220
AGGAGGAGCA CGTTCAACTT CACCAGCTCC AGTTGTGATC CGTAAAGGC TTGACATTGA	5280
TAAAATCATG ATGCACCTGT CAGATACTTT TAACTCATGG GACTACCGTC AGGTTGAGTA	5340
TTATTAGGAT AGAGAAGAAG TCTAGTGTTA TGAGATATTA AAGCTCCTAA CACTGGGCTT	5400
TTGTTTAGAA TTTCTTTCT TTTCTATAG GATATGGTAT TCTATGTAGA AAATATATGT	5460
TAATAAGTAA TGCCAATATT TAAACATCAT TAGTAAAAGG AGTTAGATTG ATGAATAAAA	5520
GAAAAGTTAG TTTAGAAGAT TTTTATAAAT GGTATAGTCT AAATAAAGAA GAGTTATTAA	5580
ATAAGGCAAC TGTTGGTGAA AAGTTTAATG ATAAATTAAA AGAAGAGTTT CTCCAGGAAT	5640
GGCCTTTGGA TAGGATTTTA ACAATGTCAA TCGATGAATA TGTAATAGGA AAGGGACAGC	5700
AAAATAAGTC TTTATGCTAC GCTCTTGAGA AGGGAAAATA CAAAAATCTA TTTCTTGGA	5760
TTTCTGGTGG CTCAGCTCA AAATTTGGTA TTTATTGGAA TAAAAAACA AACAAATATA	5820
AAGATCAAGC TAATAATGAG ATTCAGAGT TGGATCAGCG ATTTTCAAAA TTAAATCAG	5880
ATTTGTATGA AATTATCAA GAAGGTATTC GTTTTAACTT TGAAAATCCT ATTTTGTATA	5940
TGAAAAGATC AACAAATGAA TTTATTGGTC GTTCTGCTAT GGTGACAAAA TTACTTTGTA	6000
TCTATACTGA GGGAGATCCT TTCTTTGGTG TAAATATTAA TAGTCAGAAA GAATTTTGGA	6060

1114

ACCACTTTGT TTCTCAGACA AATCAAGGTG GACCTTATCT GCAAAATCAT AAAATAATTG	6120
AACTGGTGTC CAAAACCTAT CCTGAGTTGG AGCCATCGAA ATTAGGAACT ATGCTTTTGTG	6180
AGTATTCTAA GCTTTTATG GAAAATAAGG AAGACAATAG TACAATGGAT TCATCAAACA	6240
ATTTTCGTCA TCAATTAACT CAATCTCTAT TAAAGTCTCC AAACCTCATC CTCGCGGTG	6300
CTCCTGGCAC GGGAAAACT TATCTTGCTA AAGAAATTGC TAAAGAATTA ACGGATGGCA	6360
ACGAAGATCA AATCGGATTT GTACAATTC ACCCATCATA TGATTATACG GATTTTGTAG	6420
AAGGTTTAAG ACCAGTATCA AATGGGGATG GAGCTATGA GTTTAGGCTA CAGGACGGTA	6480
TTTTTAAAGA TTTTGTGAG AAAGCAAAAG AAACCCAATT GATTGGAGGA CAAGATAATT	6540
TTGATGAGGC TTGGGATCT TACTTAGAAT ATATAAATGT TGCTGAAGAA AAAGAATATA	6600
TAACAAAAAC ATCTTACTTA TCTGTTAATA GTAGACAAA TTTGTCAGTA AATTATGATA	6660
GTGGTGTTCC AGGATGGTCA CTACCTAGCA AATATGTTTA CGAGTTGTAT AAAGATAAAA	6720
ATTATAATAA GCAAGAATAC TACAAAAGTG GTGGAAAAAC TGTCTAGAA ACATTGAGAA	6780
AGAGATTGG TTTGAAAGAC TATGTTTCCC CAACAGAAAT TGATACTGAT AAGAATTTTG	6840
TCTTCATCAT CGATGAGATC AATCGTGGG AGATTCTAA GATTTTGGC GAACTCTTTT	6900
TCTCTATCGA CCCC GGCTAT CGTGGTGAAA AAGGAAGTGT TTCTACCCAA TATGCAAATC	6960
TACACGAAAC TGATGAAAAG TTCTATATCC CCGAAAATGT TTACATCATC GGAACATGA	7020
ATGATATTGA TCGTTCAGTG GATACCTTTG ATTTTGCTAT GCGTCGTCGT TTTGTTTTG	7080
TTGAAGTTAC TGTCGAGGGT CAAGCTGGCA TGTTGGATAA AGAGTTGAAT ATCCATGCAG	7140
AAGAAGCAAA AATTCGTCTA AGAACTTGA ACGCTGCTAT CGAAAATATT CAGGAATTAA	7200
ACAGTCATTA TCATATTGGA CCAAGTTATT TTCTTAAGTT GAAGGATGTA GATTTTGA	7260
ATGAATTACT CTGGTCTGAT TATATTAAGC CTCTCCTAGA AGACTACTTG CGAGGTTCTT	7320
ATGATGAGGT TGAACTTTG GAaACTTTGA AAAAAAGCATT TGATCTGACA AATAATGAGC	7380
AAAAAGATCA GGCAGTAGCT GATGACAATG AAGGCGATGA AAACGATGAT GCGGATTACT	7440
GATAATCAAC ACAAGATTAT TAAAGAAAA TTTGTTGAAG AATATCCTAA ACTAAGCAAT	7500
CCTCTTTTAG ACAGAACCTT GGAAAGTCTA TCCCAAGATG AACGTATTTT CATTTTCCA	7560
AATGATTWGA CTCATACTCC TGATTTGGAT AAGGACCAA AGATTTTGA AACAGTCAAT	7620
CAGAAAATCA AGACAGGGAA CGTGATTGGT TTTCTTGGAT ATGGTCAGGA AAGATTACG	7680
ATTTCTCAC GATTTTCTGA TGAGAGTAAT GACCACTTTT TGCATTATCT CTTAAACAAG	7740
GTCTTCATA TCAATCTCAC TAGTTTAGAT GTTGCTTTGT CTCGTGAAGA GAGGCTTTAT	7800
CAACTTTTGG TGTATCTCTT TCCCAAGTAT CTACAAGCTG CTATTCGAAA AGGTCTTTAT	7860

1115

AAGGAATATC ATCGATTTTC TCATAACGAC AGTCATGTTA AGGGAGTGAT TGATGTAAGA	7920
AACCATCTCA AGAAAAATCT TCCTTTCACG GGAAATATTG CCTACGCAAC GAGAGAGTTC	7980
ACCTATGATA ATCCCTCAT GCAGTTGGTC CGTCACACTA TTGAATACAT TAAGAATCAG	8040
AAAAGCATTG GTCAAGGGGT ACTAGATAAT CTCTCAACTA GTCGTGAAAA CGTATCTGAA	8100
ATCGTGCGTG TAACGCCCTC TTATAAACTA GCTGATCGTG CTAAGATTAT TCGGGGAAAT	8160
CAATCTAAAC CTATACGTCA TGCATACTTT CACGAGTACA GAAACTTACA AGAACTTTGT	8220
CTGATGATCC TAAACCAAGA AAAGCACGGT TTAGGGTATC AAGATCAAAA AATCTATGGT	8280
ATTCTCTTTG ATGTTGCCTG GCTTTGGGAA GAGTATGTTT ACACCTTGTT GCCAAAAGGT	8340
TTTGATACATC CCAGAAATAA GGATAAGACG GATGGAATTT CAGTATTTTC TGTGGGAAA	8400
CGAAAAGTAT ATCCAGATTT TTATGACAGA GAACGAAAGA TTGTTCTAGA TGCAAAATAT	8460
AAAAAAGTGG AATTGACTGA AAAAGGAATC AACCCTGAGG ACTTATTCCA GCTGATTTCC	8520
TATTCTTATA TTTTAAAGC TGAGAAGGCT GGACTGATTT TTCCTAGTAT GGAGCAGTCA	8580
GTAAATAGTG AAATAGGAAA AGTAGCTGGC TATGGAGCTC AATTGAAGAA GTGGTCTATT	8640
CGAATCCCTC AGAATGCCTC ATTCTATAGT ACATTTTGTA AAATGATGGA AAATTCAGAA	8700
GAG	8703

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

CATCACCAGT TTTAGATGGC TTAAACAGTG AAATTATTGC TTTTAATCTT TCTTGTTCCG	60
CTAATTTAGA ACAAGTACAA ACAATGTTGG AACAGGCATT CAAAGAGAAG CACTACGAGA	120
ATACGATTCT CCATAGTGAC CAAGGCTGGC AATATCAACA CGATTCTTAT CATCGGTTCC	180
TAGAGAGTAA GGAATTCAA GCATCCATGT CACGTAAGGG CAACAGCCAA GACAACGGTA	240
GGATGGAATC TTTCTTTGGC ATTTTAAAT CCGAAATGTT TTATGGCTAT GAGAAAACAT	300
TTAAATCACT TAACCAATTG GAACAAGCCA TTATAGACTA TATTGATTAT TACAACAATA	360
AGAAAATTAA GATAAACTA AAAGGACTTA GTCCTGTGCA GTACAGAACT AAATCCTTTG	420
GATAAATTAT TTGTCTAACT GTTTGGGGGC AGTACACAAG AAAGCGCTTT AAAACCAAGTA	480

1116					
GACCTTTTCA	TAAGGTTTCG	TTGATGTACC	AAGATGAGGC	TGGTTTCGGT	AGAATCAGTA 540
AACTGGGATC	TTGTTGGTCT	CCAATAGGAG	TAGGTCCACA	TGTCCATAGT	CACTATATAC 600
GAGAATTTTCG	CTATTGTTAT	GGAGCTGTTG	ATGCCCATAC	AGGCGAATCA	TTTTTCTTAA 660
TAGCTGGTGG	ATGTAATACT	GAGTGGATGA	ACGCCTTTTT	AGAAGAGCTT	TCACAAGCTT 720
ATCCAGATGA	TTATCTTTTA	CTCGTTATGG	ACAATGCTAT	ATGGCATAAA	TCAAGTACCT 780
TAAAGATTCC	GAATAATATT	GGTTTTACCT	TTATTCCTCC	ATACACACCA	GAGATGAACC 840
CATTGAACAA	GTGTGAAAG	AGATTGTA	ACGTGGATTT	AAGAATAAAG	CCTTTCGAAC 900
TTTGGAAGAT	GTCATGAATC	AACTCCAAGA	TGTCATACAA	GGATTGGAGA	AGGAGGTGAT 960
AAAGTCCATC	GTTAATCGGA	GATGGACTAG	AATGCTTTTT	GAAAACAGAT	GAGTATAAAA 1020
TTGAATTGCT	TATAAAAAAG	CTCCATACAC	TGGATGTGTA	TAGAGCAATG	GGGCTTTATT 1080
TGATATAGAG	TTCTTGGTTT	TTTAGGACAA	TTTCTCGGAT	ACTTGCAAAC	TTTTTAAGTT 1140
TTTTTGATTTT	TTCTGGATGA	GTGACGAGAG	TGATAACATA	ACCTTCCTTG	CCCATACGAC 1200
CAGTACGGCC	AGCACGGTGT	GTGTAGGTTT	CGCTATCTCT	AGGAATATCA	AAGTTTACGA 1260
CACATTCTAG	GCTATCGATA	TCAATTCCAC	GAGCCAAAAG	GTCAGTTGCA	AGAAGCAGGG 1320
TTAGTTGGTT	ATCTTTAAAC	TTTTCTAAGA	TGATTTTCT	AAATTTAACA	TTAACATCAC 1380
TAGCGAGGGA	AACAGCCAAT	ATATCACGAT	ACTGTAGTTT	TTCCCTCGGCA	TTCCCAAGGT 1440
CTGACAGGCT	ATTGAAGAAG	ACTAGACCAC	GGAAATCCTC	TACATGAGCC	AGTTTTCGTA 1500
GCATATCCAC	TCGATGACGT	TGGTCTACCT	GCATGTAGAA	ATGCTGGATA	TTGTCCAATT 1560
TTTGATCAGA	GAGATCAATA	GTGCGTGTAT	TCGGCACAAT	CTTTTCTTGG	TCAAACCTGG 1620
TCGTGGCACT	CATGTAGACC	AGTTGGTGGT	CACGAGGTGC	GTAGTGAGTG	ATTTTTTCTA 1680
CAAAGTGAAT	CTGAGAATCA	TCTAGTAATT	GGTCAAATTC	ATCCAGGATG	ATGGTTTCCA 1740
CATTTCATCAT	CTTGATTTTT	TTAAGTTTAA	TGAGTTCAAA	GATACGGCCA	GGAGTTCCAA 1800
TCAGAAATTC	TGGCCCCTTT	TTAAGACGTT	CAATTTGTCT	TTTCTGACTT	GAACCTGAAA 1860
GGAAGAGTTG	AGCAGTCAAT	CCGATAGCTT	CTGCCCACGT	TTTACATACA	TCAAAAATCT 1920
GTCCAGCAAG	TTCCGTATTT	GGTGCTAGAA	TCAAGAGTTG	TTGGGCTTTT	TTCTTTTGTA 1980
GTCTGAGAAG	ACTTGGTAGG	AGATACGCTA	GGGTCTTACC	AGTTCCGGTT	TGGCTCACTC 2040
CTAGGAGGTT	TTCTCCAGCA	AGAAGGGGCT	CAAATAGTTG	AGTTTGAATG	GGGGTGAATT 2100
CTTGGAAC	GAGTTGGTCA	CTCAGTTCTT	GCCATTTCAGT	CGGTAGTTTG	GTTTTCATTT 2160
TTCTGCCTCA	AATCTAATGC	CAGCAGTCTG	GCGCATGCTA	TATAGTAGCT	CATGAACAGA 2220
GCCTGCATCA	TACAGCCAAG	TTTGGTAGAG	ATTCAGATCT	GTTTGTGGA	TCATGTGTGC 2280

1117

AAATGCAGCG ACTTCCTCAG TCATCGTATG AGGAGCCTGT TGGATAGGAA GCTGGACTTG	2340
ATTTCCCTTGG TGGTCGGTAA AAATAGCTGA GCGAATATGC TCAATCGTGT TGAGAGTCAA	2400
GGTTCCATCT GTTGATATAA TCTCGCAAGG AAGATTGGAA GTGATGTTTT TTCCAGCCTT	2460
GATGTGAAC TATAGTCTG GGTAGAAGAG GATACCATCT CCATTTAGGT CAATGCTATT	2520
GTCAAGCTGT TGAGCATGGT AAGTCGCGTC ATTGGCTTTT CCAAAAAGAC GAACAGCAGC	2580
ATAGAGGGGA TAAATCCCCA AATCCATGAG GGCTCCACCA GCAAAACGGT CTGAAAAGAC	2640
ATTTGGTGTT TGTCCAGCCA ACAAGTCAGG CATCTTGGAA GAGTATTTGG CATAGTTGAA	2700
ATCTGCTCCT AACACTTGCT TATCTGCTAA AAAGTTTGTG ATAGTAGTAA AGGCTTTCTC	2760
GTGGTAATTA CGAGCTGCTT CAAAGATAAA ACAGTTATTT TTTTCAGCTG TTTGAATCAA	2820
ATCAAACCAT TCTTGTGGT GAGAGACAGC TGGCTTTTCG AGAATAACAT GTTTACCAGC	2880
AGACAAGGCA GCTTTGCCT GAGCAAAATG TAAGGAGTTT GGAAGTGGCA TATAGACTAA	2940
ATCAAAAGAA GATTGAAGA AGACTTCTAA TTGATCGAAT AGTTGGATAT TCTGATAGCG	3000
AGAAGCAAAG GTTGCTGCAG TTTCTAGTTT TCTAGAATAG ATTGCGACCA GTTGGTATTC	3060
TCCACTGGTA TGGGCTGCTT CTATGAAATG ATGGCTGATA GCGCCAGTTC CGATGACACC	3120
TAATTTTAGC ATAAATACTC CTTTTCCGAT TTTAAATCCT TCTTTCATTA TAACATAGAT	3180
AGACGGGACT ATCCAACAGA GAGGAGAAAA TTTCAAATAA GCTATTAGCT TTCTTTTCCG	3240
AATAAATAGA TAGAAGCATA GAATCTAGCA AACCTAGATT TAAAAATGTG CTATAATAGA	3300
AGGAGGAAAA GGAGGATTCT CAGACATCTA GGTATCAGCC CAACTAATGA TTTGTCAATT	3360
TATCCGCGAT ATGCTGGACT TGCCAGCAAA AAATGTGACG ATTTTGGAGG GAAGTAACAT	3420
TCACGTCTTG CCTTCCATGC CCTACTCAGC GTAAGATTTC TATACTAGTA TAGACGTCTT	3480
GGCGGAGTTA GATAATGGAA TCCAAGTTAT CATCGAAATT CAGGTTTCATC ATCAGAAATT	3540
TTTCATCAAT CGCCTATGGC CTATCTGTG CAGTCAGGTT AATCAAAACC TAGAAAAAT	3600
TCGCCAACGT GAAGGTGATA CCCACCAGAG CTACAAACAA ATCGCACTAG TATACGCTAT	3660
CGCAATTGTC GATAGTAATT ACTTCTCAGA TGACCTAGCT TTTTCATAGTT TTATAGTAAA	3720
ATGAAATGAG AACAGGACAA ATCGATCAGG ACAGTCAAAT CGATTTCCTAA CAATGTTTTA	3780
GAAGTATAGG TCTACTATTC TAGCTTCAAT CTACTAGAAA TTCCATAGAT AGAAAACTAC	3840
ATAATCTCTA CAGATACGGA TGTGGAGTT GATGTAAGAT GCTTTGGCTT GCTAGAGGAA	3900
TTGTGGATTG CCAAATTGTA TCATTGAAAT TATTGCTCAA ATTTGTTATG ATATAAATAT	3960
GAATAAAAGT AGACTAGGAC GTGGCAGACA CGGGAAAACG AGACATGTAT TATTGGCTTT	4020

1118

GATTGGTATT TTAGCAATTT CTATTGCTT ATTAGGCGGA TTTATTGCTT TTAAGATCTA	4080
CCAGCAAAAA AGTTTGTAGC AAAAGATTGA ATCGCTCAAA AAAGAGAAAG ATGATCAATT	4140
GAGTGAGGGA AATCAGAAGG AGCATTTCG TCAGGGGCAA GCCGAAGTGA TTGCCTATTA	4200
TCCTCTCCAA GGGGAGAAAG TGATTTCCTC TGTAGGGAG CTGATAAATC AAGATGTTAA	4260
GGACAAGCTA GAAAGTAAGG ACAATCTTGT TTTCTACTAT ACAGAGCAAG AAGAGTCAGG	4320
TTTAAAGGGA GTCGTTAATC GTAATGTGAC CAAACAAATC TATGATTAG TTGCTTTTAA	4380
GATTGAAGAG ACTGAAAAGA CCAGTCTAGG AAAGGTTTAC TTAACAGAAG ATGGGCAACC	4440
TTTTACACTT GACCAACTGT TTTCAGATGC TAGTAAGGCT AAGGAACAGC TGATAAAAGA	4500
GTTGACCTCC TTCATAGAGG ATAAAAAAT AGAGCAAGAC CAGAGTGAGC AGATTGTAAA	4560
AAACTTCTCT GACCAAGACT TGTCTGCATG GAATTTTGAT TACAAGGATA GTCAGATTAT	4620
CCTTTATCCA AGTCCTGTGG TTGAAAATTT AGAAGAGATA GCCTTGCCAG TATCTGCTTT	4680
CTTTGATGTT ATCCAATCTT CGTACTTACT CGAAAAAGAT GCGGCCTTGT ACCAATCTTA	4740
CTTTGATAAG AAACATCAAA AAGTTGTCGC TCTAACCTTT GATGATGGTC CAAATCCAGC	4800
AACGACCCCG CAGGTATTAG AGACCCTAGC TAAATATGAT ATTACAAGCG GGGT	4854

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TAAACAGGTG TTAGGTGCTC TAAACTATTA AAATCTAAG GAAATAAGGC TACTTTTCT	60
GGGTCTTGTT CATAGTAGGT GTGGTCTTT TTTTCGAGTG TAGCCCATAG CTTTGAGCGC	120
ATAGTGGATG GTAGTTGGAT GACAGCCAAA TTCAGAAGCT ATTTCAGTCA AATAAGCATC	180
TGGATTGTCA GTAAGATAGT TTTTAAGTCT ATCTCTATCA ACTTTTCTTG GTTTTGTTC	240
TTTTACTTGG TGGTTTAGCT CTCCTGTTTT CTCTTTTAGC TTTAACCAGC CATAAATGGT	300
ATTACGTGAG ATTTGGAAAA CGTGTGATGC TTCTGTTATA CTACCTGTTT GCTCACAATA	360
AGAGAGAACT TTTTACGAA AATCTATTGA ATATGCCATA AGAAGATTAT ACCACATTGT	420
GTAATATTTT TGGTTCATTT TACTATATTT CTAAACACTT AGAAATAATA AAACAAATTA	480
AATATTATTT CTAAATATTT GAAAATAACA TCTATTGTGA TTATACTATC TTTGAGGTAA	540
CTATTATGAA CTATATCAAA AGACCACATT ATTTAGATTT TTTAAGAAAA CATCGTGACC	600

1119

GACCAATCAT CAAAGTTGTG AGTGGAGTTA GACGAGCTGG TAAATCTGTG CTTTTTCAAC	660
TCTATAAAGA GGAGTTACTA GCAACTGGGG TAGACGAGGA TCAGATTATA TTCATCAATT	720
TCGAAGATTT GAGTTACTAT GATCTGCGAC ATTTTCAAAC ATTATTCGCT TATATAAAG	780
ATCAATTAGT TAGCAAGAAA ACATACTATA TCTTTT TAGA TGAAATCAA TATGTTGAAA	840
AATTTGAACT GGTAGCAGAT AGTCTATTCA TCTTAGCAAA TG TAGACCTC TATTTGACTG	900
GATCTAACGC CTACTTTATG AGTAGCCAAT TAGCAACAAA CTTGACTGGT CGGTATGTTG	960
AGATAGAGGT TCTTCCTTTG TCATTGGAAG AATATCTATC AGGTCAATCT CTCACAGAGA	1020
ATCTGAATAC AACAGAAATT TTTAACAATT ATCTCTTTAG TGCTTTCCCT TACTTATGTC	1080
AAACATCATC TTACGATGAA AAAATTGACT ATCTCAGAGG AATATATAAC TCCATACTGT	1140
TAAATGATAT TGCTACTAGA TTGGGAAAAC CAAATCCTAC TATTATTGAG CGCATTTGCC	1200
GAACCTTCT CAGTAGTACA GGTAGCTTAA TATCAACAAA TAAGATTTCG AATACCCTAG	1260
TCAGCCAAA TGTTC AATA TCCATAATA CTTTGAAAA TTATTGACA ACTTTGACAG	1320
ATAGTTTACT TTTTATTCC GTTCCACGTT TTGATGTAAA AGGTAGAGCA TTATTGCAAC	1380
GTTTAGAAAA ATATTATCCC GTTGATTTAG GTTTACGACA TCTCTTATTA CCAGACCAGA	1440
AAGAAGACAT TAGGCATATC TTGGAAAATA TGGTATATTT GGAATTGAGA CGTAGATATT	1500
CACAAGTATA TGTGTGTAAT TTAGATAAGT ATGAGGTTGA TTTTGTGTT GTAACGTATC	1560
TTGGCCACTA CGCTTATTAT CAGGTCAGTG AAACAACACT TGCTCCAGAA AACTAGAAA	1620
GAGAACTTAG ACCACTAGAA GCCATTAAAG ATCAATTCCC TAAATATCTA TTAACAATGG	1680
ATACGATTCA GCCAACAGCC AATTACAATG GAATCGAGAA GAAAAGCATT ATAGATTGGT	1740
TACTAGAAAA ATAGATAAAT ATAAATCATA CAGCTAATTA GATTGCAAC AGTCTGTTAT	1800
CAATGATTCT ACCCAAATCC TAACAAGATA TAGTGAATTT CGAATACGCT ATATAATACG	1860
GACACTTGAA AATAGAAATT GGGGATGAAA GGGGATCTAT AATTTCTGGA AGTACTATCA	1920
AAAATTAATA TCATAGTCTT ATTAGAGAAT AGCATCACCC ACTTTCTCAA ATAAGATTAA	1980
ATTGTAAC TG AATTATAATG AAAAAGAGAC TGAGCAATCA GTCTTTAAAA TCAGAAAAGC	2040
GCATAGTATC AGGTATTGAA CAACCTTGAT AATATGCGTT TTATTATGGA AATATTTGCT	2100
TCATTTTCTC CTGAAATAGA GCTTTTGCTA TCCTATTTT CTCTATTTCT AATGATTTAC	2160
TTCAACTTCT TACCTCTTGG GAAAA	2186

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3236 base pairs

1120

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GTCACACGTT TGACTTCACG TATTTTCATAA GTATAAACTT TATTTTATC GGTTAGATAA	60
ATCTTCATGC CATTTTTAGC ATTATCTAAA GGAGAAAATA ACATTTTATT AGCATTATCA	120
ACACCAAAGA TATGGTGACT AGCTAGACTA TAATTTCTCT CTCCCATTAC TTGCTCGCGT	180
TTCATGTGAC CAGCTCCGTA GAAGAGATTA ACATTATCAA GTCCTTTAAA AATCGGCAAA	240
TTCATTTCCA ATTCAGGAAT TGCAATTCCC CCAATAACTG GTAATTTTGT AGCATCCCAT	300
TGAGAAGTTA GAACAGCTTC CGAAGAGATA GCTTTGACAG AATCAAAGTC AAAATTGCCT	360
TCTGTATCCT GATTTTCTTC TAATTTTCT TTTGATACCT GGCTAACTTG ATACTTATTG	420
GTATTCAGCA CTATGAAAT ATTTGCAATT TGAGTATTAA AAATCAAAGC CAGTGACAGT	480
AATATCAGAA ATCCTGCTAG GATATTTGTC AGCAGATTTT TTCGCTTGTT TTTCTTTTTA	540
TTATTTTTTT GAGACATTAT GCTTCACCTT CTGTTTCGTT TTCTGTCCCA ACTTCTCTTT	600
TTTCTGCCAC CGCAACCGTT GTGAAAGTCA CTATCTGAGC ATCTTGATCC AGGCGCATTA	660
CTTTAACTCC CATAGTTGCA CGTCCTGTTT GTGAAATATT GGCAAGATTG GTTCGAATCA	720
TGACACCTGT ATCAGTGATA ATCATCAAAT CCTCATCCCC TTGAACAGTC ATAAGACCGG	780
CCAGCAAGCC ATTTTTTTTCG GTAATTTTAG CTGTCTGCAT TCCCTTACCA CCACGACCTT	840
TTGTTGGGTA TTCAGTAGCG ACTGTACGCT TACCATATCC TTTTCTGTG ATAATAAGAA	900
CCTCATCTTG ATCAGTAATC AAGCTGGCAC CAACAACCTG GTCTCCTTCA CGAAGGTAA	960
CACCTTTCAC ACCAGTGGCG ATACGGCTCA TACCACGAAC GGCTGATGTA TTAAAGCGAA	1020
CTGCATAACC AAACCTGGTA CCAATGATAA TATCCATATC TCCTTCTGCC AACAGACAT	1080
TGATTAATC ATCTTCATCC TTTAAATTCA GCGCTTTGAG ACCATTTTGA CGAATATTGG	1140
CAAACCTCCT AACACTGGTT CTCTTCACAA TACCGTGACG GGTGTAAAG AAGAGATAAG	1200
CATCATCACT GCGATCAGAC TCAACATTGA TAACCGTCTG AATACTTTCT TCTTCATCCA	1260
ATTTCAAGAG ATTGACTACT GGTAGCCCTT TGGCAGTCCG ACCATACTCA GGAATTTTCA	1320
AACCTTTAAG ACGATAGACA CGTCCCTTGT TTGTGAAGAA GAGCAGATGA TCATGGGTGC	1380
TAGTTGACAC TAACTCACGA ACAAAGTCAT CATCTTTCAC TCCCGTTCCT TGGACACCAC	1440
GACCCCCACG TTTTGTAGCA GTGAACTCGT CCTGATCCAA ACGCTTAATG TAGCCTCTGT	1500
TAGAAAGGGT AATCAAGACA TCCGATTCTT CAATCAAGTC CTCATCCTCG AGACTCAAGA	1560

1121

CCTGTCCAAT CATCAACTCT GTACGGCGCT TATCAGAAAA TTTACGTTTA ACTTCATCCA	1620
ATTTCGTCTTT GATAATTTGA GAAACACGTT CAGGCTTAGC AAGAATATCT GCTAAATCCG	1680
CAATCAGAGC CAAGAGGTCA TCATACTCAG ATTGAATCTT ATCGCGTTCC AAACCTGTCA	1740
AACGACGAAG ACGCATATCA AGGATAGCTT GACTTTGACG TTCAGAAAGC TTAAACTTGC	1800
TCATCAACTC AGCTTGAGcT TCCGCATcCG tTTCAC TAGC ACGGATGATA CGAATCAyTC	1860
GTCGATATGG TCTAGCGCAA TCAAGAGACC TTCTAAGATA TGAGCGCGCG CTTCCGCTTT	1920
TTCCCTTATCA AAACGTGTAC GACGAACAAC CACTTCTTTT TGGTGCTCGA TATAAGCATC	1980
CAAAATCTGA CGAAGAGACA AAATTTTCGG TATACCATTT TGGATAGCGA GCATATTGAA	2040
ACCAAAATTG GTTTGCATTT GGGTCATTTT GAAGAGGTTA TTGAGAATAA CATTTGGCTGA	2100
GGCGTCGCGC TTGACTTCAA TAACAAATCG AACACCTTCA CGGTTTGA CTACACGTAC	2160
TGCTGTGATA CCCTCAATGC GTTTTTCCTG AACCAAGCGA ACAATATGCT CATGCACCTT	2220
GGTTTTATTG ACCATGTAAG GAAATTCTGT TACAACGATA CGCTCACGAC CAGTCTTAGT	2280
CGTTTCAATC TCTGTACGAG AACGTAGGAC AATCGAACCT TTACCTGTTT CATAAGCCTT	2340
ATGGATACCT GATTTCCCCA TGACAAGAGC ACCAGTTGGA AAATCTGGTC CAGGCAAGAC	2400
TTCCATCAAG TCCTTGGTAG TCACTTCAGG ATTATCCATG ACCAACTTCA CTGCATCAAT	2460
gGTTTCACCC AGATTATGAG GTGGAATATT GGTGGCCATC CCAACCGCGA TACCAGTTGC	2520
TCCATTAAAC AAAAGGTTTG GAAAACGCGC TGGCAAGACC AAGGGTTCCC GTTCATTGGC	2580
ATCATAGTTA TCAACGAAAT CAACTGTATT TTTGTTGATA TCACGAAGCA TTTCCAGAGC	2640
AATCTTGCTC ATACGTGCCT CGGTATAACG TTGAGCGGCA GCACTATCTC CATCCATGGA	2700
ACCAAAATTC CCATGACCAT CTACAAGCAT GTAACGGTAG CTCCACCATT GAGCCATACG	2760
GACCATGGCT TCATAAATAG AGGAATCCCC GTGTGGGTGA TATTTACCCA TGACATCCCC	2820
TGTAATACGA GCAGATTTTT TATGGGGTTT GTCTGGGGTC ACACCAATT CATTCATTCC	2880
GTAGAGAATG CGACGGTGAA CAGGTTTTAA GCCATCTCGA ACATCAGGAA GAGCTCGCGC	2940
TACGATAACA CTCATGGCGT AGTCGATAAA ACTTGCCTTC ATCTCCTTTG TCAGATTGAC	3000
ATTCACTAAA TTTTATCCT GCATTAATAA ATGCCTCATT TCACAATTAG TAAGTAACAA	3060
CATTATACCA TAAATTCCCA TCTATTTCAG CCTCTAAACC ACTAAAACGT TTACATCGAG	3120
AACTATAAGG CATATTCGTG ACAAAGTTTT TTAAGTGA TAGAATGAAG TTGTCTAGGG	3180
AAAACCCCTA ATAGAATAAG GAGATGGTTA nACAATGACT CTGACTAACA CACAAA	3236

(2) INFORMATION FOR SEQ ID NO: 181:

1122

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

AGGTCCTGAA GTATTGGAAC AGGAAGGTCA AGAGTTTTTG GAACATTTCA AAAAACTCTT	60
GGAGTCAGTT GAAGTAGTAG CCATCTCAGG TAGTCTGCCA GCTGGCCTTC CAGTTGATTA	120
CTATGCGAGC TTGGTAGAAC TTGCTAATCA AGCTGGCAAG CATGTAGTCT TGGACTGCTC	180
AGGTGCAGCA CTCAGGCTG TTCTTGAATC ACCCCATAAA CCAACAGTCA TCAAACCAAA	240
TAATGAAGAA TTGTCTCAGC TTCTTGGAAG AGAAGTTTCT GAGGATTTGG ATGAATTAAA	300
AGAAGTACTT CAAGAACCTT TGTTTGCAGG GATTGAATGG ATTATCGTTT CACTTGGTGC	360
CAACGGTACT TTTGCCAAAC ATGGTGACAC TTTCTACAAG GTAGATATTC CTAGAATTCA	420
GGTGGTAAAT CCTGTTGGAT CTGGAGACTC TACTGTGGCA GGAATTTCTT CAGGACTTCT	480
TCACAAAGAA TCGGATGCAG AATTACTCAT CAAGGCAAAT GTCCTTGGTA TGCTCAATGC	540
TCAAGAAAAA ATGACTGGTC ATGTCAACAT GGCCAACTAT CAAGCTCTAT ATGATCAATT	600
AATAGTAAAA GAGGTATAAA ATGGCTTTAA CAGAACAAA ACGTGTACGC TTAGAAAAAC	660
TTTCTGATGA AAATGGTATC ATCTCAGCTC TTGCATTTGA CCAACGTGGT GCTTTGAAAC	720
GCCTCATGGT TAAACACCAA ACAGAAGAAC CAACTGTGGC CCAAATGGAA GAACTTAAAG	780
TCTTGGTAGC AGATGAATTG ACTAAATATG CTTTCTCTAT GCTTCTTGAC CCTGAGTATG	840
GACTTCCAGC AACTAAAGCT CTTGATGAAA AAGCTGGTCT TCTCCTTGCT TATGAAAAAA	900
CAGGTTATGA CACAACAAGC ACAAACCGCT TGCCAGACTG CTTGGATGTT TGGTCTGCAA	960
AACGTATTAA AGAAGAAGGT GCAGATGCAG TTAATTTCTT GCTTTACTAT GATGTAGATA	1020
GCTCAGACGA ACTCAATCAA GAAAAACAAG CCTACATCGA ACGCATCGGT TCTGAGTG/G	1080
TGGCTGAAGA TATCCCATTC TTCCTTGAAA TCCTTGCTTA CGATGAAAAA ATTGCGGATG	1140
CAGGTTCTGT AGAATACGCT AAAGTAAAC CACACAAAGT TATCGGCGCT ATGAAAGTCT	1200
TTTCAGACCC ACGCTTTAAC ATTGATGTTT TGAAAGTTGA AGTTCCTGTT AACATTAAAT	1260
ATGTTGAAGc KTCGCTGAAG GTGAAGTAGT TTATACACGT GAAGAAGCAG CAGCCTTCTT	1320
CAAAGCGCAA GATGAAGCAA CGAACTTGCC ATACATCTAC TTGAGTGCTG GTGTATCAGC	1380
TAAACTCTTC CAAGATACTC TTGTATTGTC TCATGAATCA GGTGCCAACT TTAACGGAGT	1440
TCTTTGTGGC CGTGCTACAT GGCAGGATC AGTTGAAGCT TACATCAAAG ATGGTGAAGC	1500

1123

AGCAGCTCGC GAATGGGCGC ACAACTGGAT TTGAAAACAT TGACGAACTC AACAAAGTTC	1560
TTCAAAGAAC AGCAACTTCA TGGAAAGAAC GCGTGAAGA AAGTCCTCCT AGTTTAGGAA	1620
CATGAATCTA AAAAAATTTA AAAAAAGTTG TATGTAAAGG CTTACAAAAT AACTTACTTG	1680
TGCTATACTT AAATCACAAG TTAATATGAA TTAGAAAGTA ACTATATGAA GTATAATAAA	1740
AATAGGATAT AGTTTATTTT ACGAGCTAGG AAGGAAAAAT ACGGAAACAA TATTGCCAGA	1800
ATAAACTATA TTTAGATGCA CATTTTCATTC ATTGTTTTAT AAAAGGAGAA GATAAACGGC	1860
TACTAAAAAG AGTTTAAAG CGTTAGTTGT AGGACTAGGT ATTGTTTCAA TATTCTTATC	1920
AGCCTTACCT ATGGTTAGTG GTTCTGTATT TGCAGATAGT GCCCTAACTA CAGTAGATAA	1980
AGCAAATGAT ATTGTTTGA ATGTTGATGG GAATAAATTT TATAATGTTT CGGTTTCAGA	2040
AGATATTGTA AATGCTGGTC AAATTTTGA AGATTATTTT TATGTAGATA AATTTGGAAA	2100
TATAAATTTA AAAGGCACTC CTGAAGAGTT AGCAAAAAAT ATTGGTATTT CTGTACAAGA	2160
AGCAAGTTTG ATGTATGGAG CTGTAAAAGA GTTACCCAAC GTTTACGAAA GAGGTCTGT	2220
AGGTTTTCGT TTCAATCTTG GTCCTCAAGT GAGGGGGATG GGTGGCTGGG CTGCTGGAGC	2280
TTTCGCTACT GGATATGCTG GATGGCATT GAAACAATTT GCGGTTAATC CTGTTACATC	2340
TGGATTTGTT GCTGTAATAA GTGGTGCAT TGGCTGGGCT GTAAAACTG CTGTAGAAAA	2400
TTATTGGACA GTTGCTGTAG CTACAGTAGA AGTGCCGTTT GTGAACCTTG TTTACACCAT	2460
AGATTTACCT TAGAGTTAT TTCTTTATGA ATCATTCTTT TAAAAAATA ACTGTATTTT	2520
GTTTTATAGT TTCTTGTTT CTTTGTATT TAGACTTAAT GAATTTTAAA AATGTAGCTA	2580
CTTTTTTATT TTTCTGTCTT CCTGTTTTG TTTTGATTTA CAAAAATAA TAAAAACAGA	2640
GCCTCTGTTT GATGAATTTT AGAACATAGT TAAGTTTTAA AAAAAGTTGT ATGTAAAGGT	2700
TTACAAAATA ACTTACTTGT GCTATACTTA AATCACAAGT TAATACAAGG TGAGTGTTAC	2760
TAAGTAATAT TAGGCATGAT CACAGGTGAA TTAGAAATCA GCTGATTTTC TAGTTCATTT	2820
GTGGTCATTT TTTGTACTTA TATACCTTTA AGATATAAAA GGAGGTTGAC ATGTATCGAA	2880
TTCTAAATCC AATGAATCAC AATGTCTCGC TTGTCAGAAA TGATAAGGGA GAAGAGGTGA	2940
TTGTAATTGG TAAGGGAATT GCATTCCGAA AGAAGAAGG GGAATTTGATT GCTGAAAATC	3000
AGGTTGAGAA AATCTTTCGG ATGAAGACCG AAGAGTCCAG AGAAAACTTT ATGGCTCTTC	3060
TCAAAGATGT TCCGCTTGAT TTTATCACAG TGACCTATGA AATCATTGAT AAGCTATCAA	3120
AGAAATATCA TTATCCGATT CAAGAGTATC TCTATGTAAC CTTGACAGAT CATATTTACT	3180
GTCTTATCA AGCTCTAACT CAAGGAAGGT ACAAGGATAG TAATCTGCCA GATATTTCCG	3240

1124

CTAAGTATCC TGTCGCTTTT CAAATCGCAA ATGAAGCTTT TGAAATTTAC CGTCAGAAGC	3300
TAGCAGATCA TTTTCCTGAG GACGAAATTA TTCGGATTGC TTATCATTTT ATTAATGCTG	3360
AAGGTGAAAA TGAAGTGGAA CTTGTGGAGT CGATTGATAA GAGGAAAGAA ATTCTCAGGA	3420
ATGTTGAAGA AGTTTAAACG GACTATGCAA TTCAACGAAC TAAAAAGAAT AACCATTCTT	3480
ATGATCGCTT TATGATCCAT TTGAATTATT TCTTGGATTA TTTAGACAGA TCTAGAGATG	3540
ATAACCAATC ACTTCTGGAT ATGGAAGATC ATATTAAACA ATCCTATCCA AAAGCCTTCG	3600
AGATTGGTTC CAAGATCTAT GATGTGATTA CGCAACATAC GGGTCTTGAT TTGTATAAAA	3660
GTGAACGAGT TTATCTAGTT CTACATATCC AACGTTTATT GTCATAAAAA TTTATTTAAA	3720
ACTATATAAG GAGAATTCTA TCATGAATAG AGAAGAAGTA ACATTGTTAG GTTTTGAAAT	3780
CGTAGCCTAT GCTGGCGATG CTCGTTCAAA ACTATTGGAA GCCTTGAAGG CTGCTGAAGC	3840
TGGTGATTTT GAAAAAGCGG ACGCTCTGGT AGAGGAAGCT GGTAGCTGTA TTGCAGAGGC	3900
TCACCACGCG CAAACAAGTC TATTGACTAA GGAAGCTTCA GGTGAGGACT TGGCTTATAG	3960
TGTAACCATG ATGCATGGCC AAGACCACTT AATGACAACT ATCTTGTTAA AAGATTTGAT	4020
GCATCATTTA ATTGAACCTT ACAAGAGAGG AGTTCAATAA TGAATAAACT AATTGCATTT	4080
ATCGAGAAAG GAAAGCCTTT CTTTGAAAA CTATCTCGTA ATATCTATCT TCGTGCATAT	4140
CGTGATGGTT TCATTGCAGG TATGCCTGTT ATTCTCTTCT CAAGTATCTT TATCTTGATT	4200
GCCTTTGTAC CAAACTCATG GGGCTTTAAA TGGTCTGATG AAGTTGTAGC CTTTCTGATG	4260
AAACCTTATA GCTATTCTAT GGGTATTCTG GCTCTCTTGG TAGCTGGTAC AACAGCTAAG	4320
TCATTGACTG ACTCAGTAAA CCGGAGCATG GAAAAAACCA ATCAAATCAA GTATATGTCA	4380
ACATTGTTGG CAGCAATTGT TGGTTTGTG ATGTTGGCAG CTGATCCTAT CGAAAGTGGT	4440
CTAGCTACTG GATTCTTGGG GACAAAAGGT TTGCTTTCAG CCTTCCTTGC TGCCCTTGTT	4500
ACTGTAGCCA TCTATAAGGT TTGTGTTAAG AACAACTGCA CTATTCGTAT GCCTGACGAA	4560
GTTCCACCAA ATATCTCACA AGTCTTTAAA GATGTGATTC CATTCACTCT ATCTGTTGTT	4620
TCTCTTTATG CTCTTGACTT ATTAGCACGT TATTTTGTG GTTCTAGTGT GGCAGAATCA	4680
ATCGGTAAAT TCTTCGCACC ACTCTTCTCA GCAGCAGACG GATACCTTGG TATTACCATT	4740
ATCTTTGGTG CCTTTGCCTT CTTCTGGTTT GTTGGGATTC ATGGTCCATC TATCGTTGAA	4800
CCAGCTATCG CAGCTATTAC CTATGCCAAT GCCGAAGTTA ACTTGAACCT TCTCCAACAA	4860
GGGATGCATG CAGACAAGAT TCTTACTTCT GGTACACAAA TGTTTATCGT TACCATGGGT	4920
GGTACAGGTG CGACATTGGT CGTTCCATTT ATGTTTCATGT GGTGACAAA ATCGAAACGT	4980
AACCGTGCAA TCGGACGTGC TTCAGTAGTT CCTACCTTCT TCGGTGTAAA TGAACCAATC	5040

1125

TTGTTTGGTG CACCTCTTGT TTTGAATCCA ATCTTCTTCA TTCCATTTAT CTTTGCTCCA	5100
ATTGCAAACG TATGGATTTT CAAATTCCTT ATTGAAACTC TTGGAATGAA CTCATTCACT	5160
GCTAATCTAC CATGGACAAC TCCAGCTCCA CTAGGTCTAG TTCTTGGAAC TAACTTCCAA	5220
GTGCTATCAT TCATTCTTGC TGCCCTTCTA ATCGTGGTTG ACGTTGTCAT TTACTATCCA	5280
TTCCCTTAAGG TCTATGATGA ACAAATTCCT GAAGAAGAAC GTTCAGGTAA GTCTAATGAT	5340
GAATTGAAAG AAAAAGTTGC TGCAAACCTC AACACTGCAA AAGCGGATGC TATTCTTGAA	5400
AAAGCGGGTG TCGATGCAGC ACAAATACC ATCACTGAAG AAACAAATGT CCTCGTTCTC	5460
TGTGCAGGTG GAGGAACAAG TGGTCTCCTT GCAAATGCTT TGAATAAGGC AGCAGCAGAA	5520
TACAAATGCC CTGTGAAAGC AGCAGCAGGC GGCTATGGTG CTCACCGTGA AATGTTACCA	5580
GAGTTTGATC TTGTTATCCT TGCCCTCAA GTTGCTTCAA ACTTTGAAGA TATGAAAGCA	5640
GAAACAGATA AGCTCGGTAT TAACTAGCG AAAACAGAAG GCGCTCAATA CATCAAATTA	5700
ACTCGTGATG GAAAAGGTGC TCTTGCAATC GTACAAGCGC AATTCGATTA AGGCTAGAGA	5760
CTCTGAAATA GTCTCCCATC GTTACGGAAA TCGCTATGGC GAATTTCTTA TTATTAATTC	5820
GTCGGTAAAA AGATATCGTT TTTACCTCCT CATGTCACAA TTCGGTGACT TGGTACAAGA	5880
AGTGAGATGG AGAAGGATGG CTCACTGACT CCTCTCCTCT CACTTTTACT TTATTTAAAT	5940
CAAGAAATAG GTGAAAAAA TGACAAAAC ACTTCCAAA GACTTTATTT TTGGTGGCGC	6000
AACAGCTGCT TATCAAGCAG AAGGTGCTAC ACATACTGAT GGAAAAGGAC CAGTTGCTTG	6060
GGATAAATAT CTTGAGGATA ACTACTGGTA CACTGCCGAA CCAGCTAGTG ATTTTACAA	6120
TCGATATCCA GTTGACCTCA AGCTAGCAGA AGAGTATGGT GTCAATGGTA TTCGAATTTT	6180
TATTGCTTGG TCACGTATTT TCCCGACTGG TTACGGCCAA GTAAATGCTA AAGGTGTTGA	6240
GTTTTATCAT AATTTATTTG CAGAGTGCA CAAACGTCAT GTTGAGCCTT TTGTAACCTT	6300
TCATCACTTT GACACGCCAG AAGCTCTCCA CTCAAATGGA GACTTCTTAA ACCGTGAAAA	6360
TATCGAACAT TTTGTAGACT ACGCTGCCTT CTGTTTGA GAATTTCCAG AAGTAAACTA	6420
TTGGACAACC TTAAATGAAA TTGGACCAAT CGGTGATGGT CAATATTTGG TTGGGAAATT	6480
CCCTCCAGGT ATCCAGTACG ACCTTGCCAA AGTCTTTCAA TCACACCACA ATATGATGGT	6540
GTCTCATGCA CGCGCGGTAA AATGTACAA AGAGAAAGGC TATAAAGGGG AAATTGGTGT	6600
TGTTACAGCC CTGCCAACTA AATATCCTCT AGATCCTGAA AATCCAGCAG ATGTTCTGTC	6660
AGCTGAGTTG GAAGATATCA TCCACAATAA ATTCATCTTA GACGCAACTT ATCTAGGTCG	6720
CTATTCAGCT GAAACCATGG AAGGTGTCAA CCATATCTTA TTAGTCAATG GTGGTAGTTT	6780

1126						
GGATCTTCGT	GAAGAAGATT	TTACAGCATT	AGAAGCTGCA	AAAGACTTGA	ATGATTTCCCT	6840
AGGAATCAAC	TACTATATGA	GTGACTGGAT	GGAAGCCTTT	GATGGAGAAA	CTGAAATTAT	6900
CCATAATGGT	AAAGGTGAAA	AAGGAAGCTC	TAAGTATCAA	ATCAAAGGTG	TTGGTCGTCG	6960
TGTAGCTCCT	GACTATGTAC	CACGCACGGA	TTGGGATTGG	ATTATCTACC	CTCAAGGTTT	7020
GTATGACCAA	ATCATGCGTG	TGAAGAAAGA	TTATCCTAAC	TACAAGAAGA	TTTACATCAC	7080
TGAAAATGGT	CTCGGCTATA	AAGATGAGTT	CGTTGATAAC	ACTGTTTACG	ATGATGGTCG	7140
TATTGATTAC	GTGAAGCAAC	ACTTGGAGGT	TTTATCTGAT	GCGATTGCAG	ATGGAGCTAA	7200
TGTAAAAGGT	TACTTCATTT	GGTCATTAAT	GGATGTCTTC	TCATGGTCAA	ACGGTTATGA	7260
GAAACGTTAT	GGTCTCTTCT	ACGTAGATTT	TGAAACTCAA	GAACGTTATC	CTAAGAAATC	7320
AGCTCACTGG	TACAAGAAAG	TAGCGGAAAC	TCAGATTATA	GACTAGTAGA	ATTAGTCATT	7380
AGATATAGAA	TTTTAGTGAG	TCAAAAAGAT	GTTCAAAGAT	TTTATCCAAT	CTATTTATGA	7440
AAAAAAGTTT	ATATTATAAA	TTTCGAAAAA	TGCTCTCAAA	TACCGTGTTT	GACGAGTGAA	7500
GAATTGAAAA	GTCTTGAAAA	ATGGTATGTC	TCGACTGGTA	AAGAATGGAT	TTGTCATTCA	7560
GATGATGAGC	TGGAAGAATT	TAAAAATCTA	TTTTTAAATT	TTATCAATCC	TGAAGAATGG	7620
GATACTATCT	CCTTTGATTC	AGATTTTATG	CCGTTTCAAC	AATCGTAACC	AATTTCTCAA	7680
AAAAGTTAAA	TCTTATATTT	AGTACTCTGT	AAAACCTCTA	TCTAATCACG	TTGCTTATAC	7740
TCAATGAAAA	TCAAAGAGCA	ACTTTAAACT	AGGAAGCGAG	TCGCAGATTT	CTCAATGCAT	7800
AGCTTTGAGG	AATTGGGCAA	AAAGTCTTTG	ATATAGAAAA	ACGCATAGTA	TCAGGTGTTT	7860
CAACACCTGA	TACTATGCGT	TTTATTGTGG	GAAGATTTAC	TTTTTTTCTT	CTGAAATTGA	7920
GTTGTTACCC	AGGCTCTTTC	AGTTTATTAA	GGCTTGATGA	CTTTAATGTG	TTTAGATAGC	7980
TTAAAAAGGA	TTGAATCACT	TAGTTTAGAA	TCTGAAACAA	TAGTATCAAG	ATTTGATACA	8040
TTATAAAAAG	TATAAAAATC	AAACTTATTG	AACTTGCTAT	GATCTGCGAG	TAAATATTTT	8100
TTATTAGAAT	TATTTAAAGC	GATGCGTTGA	GCCTCTCCCT	CTTCCTCGCT	AAAAGTAGCT	8160
AGAGCTCCGT	TTTGAATACC	ATTACAGCTA	ACGAAAGCTT	TAGAAAATTG	GAGATTAGAG	8220
AGATTTTGTA	GGGTCAATGT	ACCAACAAAA	GCACCTGTAA	TATCGCGATA	ATTTCCACCT	8280
ATTAAATCA	AATCTGTAA	TTTTCGTTTCG	CTTAAATCA	GAAAAACAGG	TAGACTGTTG	8340
GTTACGACGC	GGATATTGTC	AATAGGCAAC	TCACGCGCAA	AAAACCTCTAA	TGTTGTTCCCT	8400
GGTCCAATGA	AAATAGTTTC	TCTTTCTTCT	ACTAGACTGC	CTGCAAAATG	GGCTATTTCT	8460
TGTTTTTCTG	CCGTTTGAGG	GGCTTGTTTT	TCAATATTTG	ATCGCTCATT	AGTCAAAAGG	8520
GAGTTGGTTC	GAAGTTTTTC	AGCTCCACCA	TGCACACGAA	TCAGCAAATC	TTTATCAGCT	8580

1127

AATTCCTGTA AATAGCGCCT TGCAGTCATA TCTGAAACGG CTATTTTCGTC CATAATCTGT 8640
 TTAACGTGA T 8651

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AATCTCCAAT CAGTGCCACT TCAGCTACAA AGAAGAGGAG GATAATAACT CCGTTCACAA 60
 GGACAGACAA GAATAATTGA TAGAAGGAGT CGGTTTCACT TGCTTGACTT GGTCTGTAA 120
 TGATwTGGAG ACTGGCAAGC AGAATGATTC CAATGCTAAT CACACACAAG AGGGCTGTAA 180
 ATCGTAGGCT ATCAAAGAAA GCAAAGAAAC TAGCAATAGC AGTGAGGAmG ATTGGAATTG 240
 CCAAGAGTTG ACTATATTGT TGGAGAACCT TGTCTAGCGT CCAGTCCTTT TCCTGGTGGA 300
 TAAATCGTCT CACAACGAAA CTACCCAAGA GGAATGAAAA GAAGAAGAGT GTTGTGCGCTA 360
 CTAGGATAGA GATGATAGAA AAAAGAGTTA AAGGAGCTAG CTGCTCAGGG AAGCGACTGT 420
 TAATGCTTGC TATATGTCCA TAGTAAGCAT GTTTGATGTG ATAGATACTA AAGAAAAAGG 480
 AAGATGCAGA AAACAGAATG AGCAAGAGAA AGGCTGTGTA ACTGTGTGTG ATACTTGTTT 540
 CCAACTTACT TGTAGGAGAT TTGATCGCTT CCACTAGCCA AGACCAAAAA TCAAGCACTT 600
 GCTCTTTCCA TTTATCCCTA GATTTTGGAG CTTGGTCGGG GATATAAGGA CTTTCTAAAG 660
 ATTTACTGAT AAGAAGTGGC TCTTTCGTGG TTGCTTTTGT CTGAGGAAGA GCTTCTTGGC 720
 TCTCTTCAGC TATAGTGA CTCTTCTGTTT CTTTAGAAAG GTCTGGCTCT TCTTCAGTAG 780
 AATTAGATGC CTTCTTTTCT TCTATTTCTG TTCTCGCTTC ACTGTCTTCA GGAGCTTCAA 840
 TTTTCTCTTC TTGCTGGCTT TCCAATTGCA CTTGAGCTTG AGGGACTTCC TCCTCTAACT 900
 GAGTATTTTT TTCAATTGGT GTATCGAGAT CGGCTATCGT TTCTTCAGCC TTGTCTGCAA 960
 CCTCTTGAGC TTGCTCTTCA GGCTTGTCT TGCTTGTGT TTTTACAAAA TCATTACTTT 1020
 CAAACCATTC TTGTTTCATG GTAGAACCTC CTTTTTAGTT AGATAAATAT GTTTCCATAG 1080
 TAGCAAAATGT AAGCGTTTTT GTCAACGTCT GCTTGGTGTG GATATTAGAT CAATATTATC 1140
 ATCAGATCTC GCAATGAGTT GATCCTTGAC ATCGGTTTTT TCAGTTTGT AAGGGTTGCT 1200
 TAATCCGTA CCTCTTGATT CAGGCTTTTC TCTTGTGAAT TGGAAGATAG AACCATAGTT 1260

1128

GCTTGAGATG TCCCAGTTAA TTCGTTGGCT TTCTTTCTGG TCTAGGATGA TTCTGAGATA	1320
ATCTTTGGCA GTCAGTTCAA CCTTGCCATG GACTTGGATA TTTTCAGCGT GGAAGTGATT	1380
CTCTGTTGAC TCTAGCTGAC TATCTGTAAG AACTGTATCA AAGATATTAA CGATATTGGG	1440
CGTTGTGAGT TTACTGTTTT TGATACGACT TCCTTCAATT CGGAGGATAT AGCTGTTTGT	1500
ATTGAGGGTC GCATTTTCAA GGCTAGCATT TATGATGGTG GTTTGTCCGC GATTGGCTGA	1560
GATGTTGATC CCTTTTAGAG TTCTCCCTTT TGCTAGTCGG AGAATAACTT CTTCAAAACG	1620
ACTAGAGTAG CTACTTGCGA TATGAAGAAT CCCACCAATT CCAGAAGAGA GAAACGGAGT	1680
TTCAGACAGT TTCTTATCAG TGAGACTCAG AGTTCTATCG TTCTGATTGG TGATAAGATC	1740
ATGGTGAGCA GAAAGAGATG GATGGTAAGA AATGTGGATT TGATCATCGA AAGAGTCTGT	1800
GATGGTGAGC GTGTGTTGGT GGAGAGTAAT TTCTAGGTTT TCGACTTCCT TGCCAAAGGT	1860
TAGCTTTTCC GTACGGCTAT CATAGACAGG TTCTTTGGAC ATGGAAAGTA GGCTCTTAAT	1920
CCCGTCAGAT TGGATACCTA CAAAAGCAG GATAAAGCCG ATAACGGTAG TCACCACACC	1980
AAAGATGAGA AATCCTTTTG TCCATTTACG CATGCTGATT ACCTCTCTTT CCTTTTTTAA	2040
GAACAAATG TACCAGACGA ACAATGAGTA GACCGAAGAA GCGAGTTGCA TAGGAAATGC	2100
CAAGTAAAC TAGCGAAGAA GCACCGATAG CCAGTAAACC AGAACCAAAA ATCAAGATAA	2160
AGGCTGATTT GGCTTGGGCG AGGACAGTGA AACTTTCAAC TAAAAATAGG AATCCGCCGA	2220
TGATACCCAG TATGGAAACT GCAAAGAAAG CCAGAATGAC AGTCAAAGCG GCTACAAGAA	2280
TTGCGAACAG GGTCACGAGG ATGGCGATTC CCAGAGGAAT GCCGATAGGT GCTGCAAGGA	2340
GGGCTAACAA GGCGATATGT AAAATTTGTC GGTATTTTTT TTGAGCGGGT GCTTCATTGA	2400
TTTTTTTATC GAGAAGATTG GATAGAAGTT CGTGGGCCGC TTCTTTGGGA GTTCCCAAAC	2460
TAGCGATGAG TTCTTCTTCT CCTTCGACTC CAGCATCGTC AAAGAGCTCT CTGAAATAGT	2520
CCATGGCTTC GATACGGTCA GCTTCAGGTA GTTTCTTGAG ATAGAGTTCT AGCTGAGTCA	2580
GGTATTCAGT TCTTGTCATG GCGGATACTC CCTTCTATGA TGCCATTGAT GGTGTCTGTA	2640
TAGAGTGCCC ATTCATCTTT TAGGGTCAAG AGCTGCTCTA TACCACCGTT TGTCAAGGAG	2700
TAGTATTTGC GCATGCGACC TTGGAAGTCT CTAGAATAGG TTGTCAGAAA GCTATGCGCT	2760
TCCAATTTTT TGAGAATGGG ATAGAGTGTG GATTCTTTGA TATTAGCGAT CAGCTTAATG	2820
GTTTGGCTAA TCTCATAACC ATAAGAATCA CCCTGCTCCA GTACAGCCAA GATGAGAAAT	2880
TCAATCAAGG CAGAGGATGT TGGAAAGTAC ATGGGAAACC TCCTTTTCTA ATGTGTAAGA	2940
TTTTTATATA TAATTTTCT ACACATACAT TGTACATCTA AAAGAAAGCC CTGTCAAGAG	3000
AAATGTGTAA AATTTTATA TATAAAAAAC TTCTAGCTAA AACTAGAAGT TTAAAGGATC	3060

1129

TTATCCGCTC TGTCCACTGT AAAGAGGGCC ACAGTCATCA GGATATCGAT GAGCAAGAGG	3120
GCAGCTACAG ATGGTACCCA AGAGTGGAAC AGGTCAAAAC TGTAACCAA GAGGGTTGGC	3180
CCAAAGGCTG CTAGGATATA GCCTCCTGTT TGAGATAGGC CGGACAATTG GGCTGCTTTT	3240
TCAGGGGCGC TTGTCTTGAG TGAAAAGTTG ACCATGAGAT AAGGGAAGAG GGCACTGGTT	3300
GCGGTTCCGA TGAGGAGATG GATGGCAAGC CAGTAAATGA AATTATTGAT TGGGAAAAAG	3360
AGCATGGAAA TGCCGACCAC ACCAGCTAGT GAAACCAGAG TGAGCATGAG CTGACGGTTG	3420
CGAGTAGATA AACTGGTTGT CAGGCTTGGG ATGGTCATTG AAAAAGGAAT GCTAATCAGA	3480
GATAAGATAG AAGTCAGCAA GCCAGCTTCG TGA CTGGATA GACCTGCATG GATAGACATG	3540
GTAGGTAACC AGGTCAATGAC GGTGTAAAAG ATCAAGGATT GAAAACCTGA AAAGATAATA	3600
ATTGCCCAA CCTGTTTATT ACGCATGACC TTTATTGAC TTTTGTGTTT GGTGTGTGGA	3660
GCTAGTCTAT GATTATAGCG GTGATTGGG AGCCAGACCA AAAAAGTGC TAGACAGAGT	3720
AACGTGAGGA GAAGGATAAG TCCTTTCCAA GAACTGGCTT GTGTAATGGG CACAGCTAGA	3780
TAGGAA	3786

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3054 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TCAGCTAAAA AACATTGCTA AATTGATTGA AGCTGGTGCT ACACATTCCG ATTCAACTTC	60
TCACACGGCG ACCACCAAGA ACAAGGTGAG CGTATGGCAA CTGTTAAACT TGCGGAAAAA	120
ATTGCAGGTA AAAAAGTTGG TTTCCTTCTT GATACAAAAG GACCTGAAAT CCGTACAGAA	180
TTGTTGGAAG GTGAAGCTAA AGAATATTCA TACAAAAC TGAAAAAAT TCGTGTGCA	240
ACTAAACAAG GAATCAAATC AACTCGTGAA GTGATTGCGT TGAACGTTGC TGGTGCTCTT	300
GATATCTATG ATGATGTTGA AGTTGGTCGT CAAGTTTGG TTGACGATGG TAAACTTGGT	360
CTTCGTGTGG TTGCTAAAGA TGATGCAACT CGTGAATTG AAGTTGAAGT TGAACCGAT	420
GGTATCATCG CTAAACAAA AGGTGTGAAC ATCCCTAACA CTAAATTC TTTCCAGCT	480
CTTGCTGAAC GCGATAACGA CGATATCCGT TTCGGTCTTG AACAAGGTAT CAACTTCATC	540
GCAATTTTCAT TCGTACGTAC TGCAAAAGAT GTGAACGAAG TTCGTGCAAT CTGTGAAGAA	600

1130

ACTGGAAACG GACATGTTCA ATTGTTTCGCT AAAATCGAAA ACCAACAAGG TATCGATAAC	660
TTAGATGAAA TCATCGAAGC AGCTGATGGT ATTATGATTG CTCGTGGTGA TATGGGTATC	720
GAAGTACCGT TCGAAATGGT TCCAGTTTAT CAAAAAATGA TTATCAAGAA AGTCAATGCT	780
GCAGGTAAAG TTGTTATCAC TGCAACAAAC ATGCTTGAAA CAATGACTGA AAAACCACGT	840
GCAACTCGTT CAGAAGTATC AGATGTATTC AACGCTGTTA TCGACGGAAC TGACGCTACA	900
ATGTTGTGAG GCGAGTCTGC AAACGGTAAA TACCCACTCG AGTCAGTAAC TACAATGGCT	960
ACAATCGACA AGAACGCTCA AGCTCTTCTT AATGAATACG GACGTCTTGA TTCAGATTCA	1020
TTTGAGCGTA ACTCTAAGAC AGAAGTAATG GCTTCTGCTG TTAAAGATGC TACTAGCTCA	1080
ATGGATATCA AATTGGTTGT AACTCTTACT AAGACAGGTC ATACTGCACG TTTGATTTCT	1140
AAATACCGTC CAAATGCTGA CATCTTAGCA TTGACATTG ACGAATTGAC AGAACGTGGC	1200
TTGATGTTGA ACTGGGGTGT TATCCCAATG TTGACAGATG CTCATCTTC AACTGACGAT	1260
ATGTTTCGAAA TCGCTGAACG TAAAGCGGTA GAAGCAGGTC TCGTTGAGTC AGGCGATGAT	1320
ATCGTTATCG TTGCTGGTGT GCCAGTAGGA GAAGCTGTTT GCACAAACAC AATGCGTATC	1380
CGCACAGTAC GTTAAGAAAA ATATAAAAAC CTATCATATC CAGCTTTAGA GCTTGTGTGA	1440
TAGGCTTTTT GTATAGAGGG TAAGAAATAG GCAAACTTT CATAATGGAT TGATACTCTT	1500
CGAAAATCTC TTCAAACCAC GTCAGCGTCG CCTTACCGTA TATATGTTAC TGACTTCGTC	1560
AGTTCTATCT ACAACCTCAA AGCAGTGCTT TGAGCAACTG CGGCTAGCTT CCTAGTTTGC	1620
TCTTTGATTT TCATTGAGTA TGAAATAAGA TATGCACAAA TTGATTAGAA AGTCAAATGA	1680
ATTTCTACAA ATGTTTATAG AATCGTAATG TACTTGCTA GATTGATCT GATATATTTT	1740
CGATTTAATG ATATGGTATT TAAACCTCC AAAGTAGCTT ACTCCATTCT TTTACTTACG	1800
TGAGTGTAGA TGTTATTTAC TGTTTTAGCG TTTTGTGTT CCACTCTAAC CATATAGCA	1860
TTCTTCTCAG CTAGTGTACT AAGGAGTGTG TGCCTGAAAA TATGGGAACT AAGGGGCTGG	1920
TTTATCGGTT TCTCTAGTTT AGTATTTGCC TTTTGCAAAG TGATCTTAAA TGCCTTTCTC	1980
TAAATTTACA TATCACTATT GTTTAACAAA ATCTAATCTA TTTTAGGTCA CTTATTCTTT	2040
TTTTGAAATG TAGAATGAAC TTTTCAAAG TTTTTCGAAT CTTTTAAAAT CTGTTTGCTT	2100
TATATCGCCA TTCTCCCCC TTTTTAATT CTCCCTATAT AGCCTGACAG CTTTCCCGAT	2160
GGTACGAATA TGGTTGCTTT CGTCTAGGTG GATGTCGGG TATTCGGGAT TGAGTTTITT	2220
TGAGGCAGCC TTGGCGGAGT TTCTTGACAT AGTTAGTGCC GTCTACTTGG AAGATGCCGA	2280
TGGTATTATA GTCAATCTGT GGGGTATTCT TGATAAATAG GTAGTCGCTG TTTCTTATCT	2340
TTGGCTCCAT GGACTTGCTG ACGACATAAG CGATTGGGTC GTAGTCGTCT GGGATAATGG	2400

1131

AAACTCCATA TCTAAATCGT TGTCCTGTCAT CGAGCGGCTA CCTGCAGAGA TAAACTACCT	2460
AACACGAGAG TAAGTAGTCT GTCTGTAGTC GTCCAGTCTG ATGATTTTTC CGATACTTCG	2520
TTTTTCTGAT CATACAGTTG CCTCTCGGCA TAGGTCAGAA CTTTACCTTG TCTGGGTGGT	2580
TCCCGTTGGT CGTAGATAGA TTGGATATCG CTAGGAGAAT CCTTTTGAAC TGGAGGAAAG	2640
AGGGCATCGA TCAAGCTACT GAATACTTTA ACTAAGTCAA ATATAGTATT TTTCTTAGTA	2700
GACCTAACCC TTTTTCATA ATTTCTAATG GTGTTTTTAC TTATACCTAT CTTAGTACCC	2760
AATTCCTATT GAGTCCAACC ATTACTAGTC TATATTGTTT TATAGTTGAT TGAGTTTGGA	2820
ATAGTACGCT GTAGCTGCTA AAACATTTCT AGAAATTAAT TTGACTTTCC TAATAGAGTT	2880
GTTTCATATCT TATTCAATC TATTATGTTT TTCACCTCTA ACAATCGCAA TCTCTCTTT	2940
ATCCATGAAT GAAATCGCTT TCTATTTTTC TAAGTAAAGC ATAACACGAA ATCCACGAAA	3000
ATGAAAACCT TTGTTGTGTT TTCGTAAAAA ATTTGTTGAC AGAGCACGAA ACGC	3054

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TGTGATTTTC yGAAAATTG GTAAAATATA TCTTAATCAT TTTCAGGAGG AAAAAATTT	60
GACAAGATAT CAGAATTTAG TAAATGGAAA ATGGAAATCA TCTGAACAAG AAATTACGAT	120
TTATTACCA ATCAATCAAG AAGAATTGGG TACAGTTCCA GCCATGACTC AGACTGAAGC	180
TGATGAGGCT ATGCAAGCTG CGCGTGCAGC CCGCCAGCA TGGCGAGCTT TATCAGCAGT	240
TGAACGTGCG GCTTATTGTC ATAAAACAGC AGCTATTTTA GAACGCGATA AGGAAGAAAT	300
TGGTACTATC CTTGCCAAAG AAGTAGCAA AGGGATTAAA GCAGCAATTG GAGAAGTAGT	360
GCGTACAGCA GACTTGATTC GTTATGCTGC TGAGGAAGGT CTCCGTATCA CTGGACAAGC	420
AATGGAAGGT GGTGGTTTTC AGGCAACAAG TAAAAACAAA CTGGCTGTTG TCCGTCGTGA	480
ACCAAGTTGGT ATCGTGCTAG CGATTGCTCC CTTTAATTAT CCAGTTAATT TATCTGCTTC	540
TAAAATTGCA CCTGCCTTGA TTGCAGGGAA TGTGGTCATG TTTAAGCCAC CAACACAAGG	600
TTCCATTTCT GGACTCTTGT TGGCTAAAGC ATTTGAAGAA GCAGGGATTC CGGCAGGTGT	660
TTTCAACACC ATTACAGGTC GTGGTTCAGA AATTGGGGAT TATATCATTG AGCACAAAGA	720

1132

AGTCAACTTC ATCAACTTTA CAGGTTCAAC TCCTATTGGA GAACGTATTG GTCGTTTAGC	780
TGGTATGCGT CCTATCATGT TGGAACTTGG TGGGAAAGAT GCAGCTCTTG TACTAGAAGA	840
TGCAGATTTG GAACATGCTG CCAAGCAAAT TGTTCGGGA GCCTTTAGCT ACTCAGGACA	900
ACGTGTCACG GCCATTAAAC GTGTCATTGT TCTCGAAAGT GTAGCAGATA AATTAGCTAC	960
TTTGCTTCAG GAAGAAGTTT CTAAATTAAC AGTTGGTGAT CCATTTGACA ATGCTGATAT	1020
TACACCTGTT ATTGACAATG CTTACGCCGA CTTCAATTTGG GGCTTGATTG AGGATGCACA	1080
AGAAAAAGAA GCTCAGGCTC TTACACCAAT CAAACGTGAG GGCAATCTTC TCTGGCCAGT	1140
GCTTTTGTAC CAAGTTACAA AAGATATGAA AGTGGCATGG GAAGAGCCAT TTGGTCCTGT	1200
TTTACCAATC ATTCGTGTGG CTAGGTAGA GGAAGCTATT GCCTTTGCCA ACGAATCTGA	1260
ATTTCGCCTT CAATCATCAG TCTTTACAAA TGATTTCAAA AAAGCCTTTG AAATTGCTGA	1320
AAAACTTGAA GTAGGTACAG TCCACATTAA TAATAAAACC CAGCGTGGTC CAGATAATTT	1380
CCCATTCCCTT GGTGTCAAAG GTTCTGGAGC TGGAGTGCAA GGAATTAAAT ATAGCATTGA	1440
AGCGATGACA AATGTCAAAT CCATTGTTTT TGATGTGAAA TAACGTGTAA AACCAGGAAA	1500
TTGTTTTCTT GGTTTTATTT TTTTGCTATA AAATAATAAT AATTATAGAA AAAATACGAA	1560
CTTTTGGTA TTATAATAGA TTGAAACCGG	1590

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4848 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

CCTGCAGTTG TCAGACCTGT AATTTTCTTT TTATCTGTAA TAAGAATCGT TCCAGCGCCT	60
AGAAAACCCA CACCTGATAT AACTTGAGCT CCTAATCGTG TAGGATCTCC TGTCCCAAAT	120
TTATAAGATA CGTATTCATT CGTCATCATA ATCAACATG CAGCTAGACA AACATACTA	180
TAAGTTCGGA TGCCTGCAGG CTGGGATTG CTCCCTCTCT CTAAACCAAT TATACTACCA	240
ATGACTACTG ATAAAACAAT CCTGACAACT ATTTCAATAT TTGATAACCC AAGACTAGTG	300
GCTGTCTATG TTATTTCCTT ACTTTACGCC CCGGTCTTTG TGTGAAGTAT AATACCGTTC	360
CAGAAATAAT CATCAGAACA ATTGATATAA CAAATACCAG AGCTTGTGCA TTAGATGTTG	420
CTGTTTCATC ACCTGCAGAT CGAATCGTAA TACCTAATGG TTGAGCTAGG GGATGGTAAA	480
GGAATACAGA TAAGTCGAAG TCAGTTAATA AAGAGTTAAA GTTTAAAGCA ATAACAGAGA	540

1133

GAACAACCGG TAAAATAAAT GGAATGATAA CCTTCATCAT AGTATAAAAA GGTGAAGCAC	600
CCATACTTCT TGCTGCATCT TCCATCTCAT CATCAACACT AAATAAAATA GCACGTACCA	660
TTCTATAAGA AAATGGGATT TTTACAACATA TATATGCAAT AAGTAGAATT ACCAACTAC	720
CTACCAAAAT CTGATTCAAG ACAAGAAATT GTGGCTGATT AAAAGTAAAT AATAAACTTA	780
CTGCTAAAAG TGTACTTGGT AGTAACCAAG GAAGTAGAGC ACCATATTCA AATAAGAAAT	840
CAAAACGAGA TTTATGTTTT CTGACAACAC GAGCAAATAC AACTGCGAGA ATTGTTGCTG	900
TTGTCGCAGC AATAATAGAA TAAATAAAGC TGACCAAGAA TGGAGAGAAT GCCGCACTAT	960
TACTAAAGAA TAAGCGATAA TTTTCTAAAG TAAAGTTTGA TAATGTTAAG TTACCTGTTT	1020
GAATTGCAAC TGGATCTGTA AATGAGTATA ATACTATAAA AATTAGTGGA AGCATGAAAA	1080
CTGTGAACAA TCCATATGCT ACAATGTGAG CAATGATATT CCAAGGCTTA GACGCAATT	1140
TTTGTTTTTT AAGAGGCGCT TTAGTCTTAG AGATAGAAAT ATAATTCCA CCTTTTTCTA	1200
TCTTATTCAT GATAGTAAGC AAAATTGTAG TTGCAATACC TAAATAAATT GCAAGTAGGG	1260
CAGCTAAATC ACGAGAATTC CCCATCCCTG CAAATGTAAT AATCATTGGA TTTATAGTTT	1320
GAAATTCTTT ACCACCAACA ATCATGGGTG CTGCTACTGC AGATAAACCA CTAAGAAAAA	1380
CCATAATAGT AAGTGCAAT AGAGTTGGAA TTAAGGTTGG TAACACTACT TTTCCGAAAA	1440
CAGTAAATGG TTTTGCTCCC ATATTTGAG CAGCCTCAAT AGTGTGATAG TCAACGCTTC	1500
GAATTGTATT TGTAAAAAC AATGTATGAT TAGCAGTTCC TGAAAATGTC ATAATGAATA	1560
AGACTGCACC ATACCCAATA AACCAGTTAG GGTCTAAAGA AGGGATAACA TTTTGTAATA	1620
ATTTTGTAAT CAATCCATAA GGACCATAGA CAAATTTATA TCCAGTCGCT AAAACCACTC	1680
CTCCATAAAT TAAAGAGGTC ATATAACCTA ATTTTAAAT TTTAGCACCT TTAATATCAA	1740
AGTACTCTGT AAATAGAACA CAAAGAATAC CTACGACATT AACTGTAATA ATGAGTGAAA	1800
ATGCTAACTT AAAACTGTTC ATAATACTCT GAAGTGCCCT CTGAGATTTT AGAACACGAT	1860
GTACAGCATC AAGGGAAAT TCTCCTCCTT TTACAAATAC ATTCACTACT AGATCAAAGT	1920
TTGGATAAAT AATAAATGTT ACTAAGAACC AGATTAACCC TAAACGAATA AGCCAATCTT	1980
TTAAATTTAA TTTATGACGC ATACTGCACC TCCTTAAAT TGCAGAACGT CTGATGGTGT	2040
GATAAATAAT TCCCACTTT CTCCGACAGA TCTAATAGCA GCCTGACTAT CAATACTTGT	2100
TACATTAAGA ATCTGACTTT CAGAACTTT TATTGTATAG TGAATTGTAA CTCCAGAAAA	2160
CTCAACATCA ATAATTGTCC CTTTGAAT AAAATCTTGT TCAGTTTCAC GATTGAATCG	2220
AACCTTCTCT AATCGAATGT ATCCTTTTTT ATCCTCTAAG AAAACGCTTG TATTTTCAA	2280

1134

TAATACTTCG TGGACTGTTT CATCGGTCAA AACATTAATA TCTCCAATAA AATCACATAC	2340
AAATTCAGTT TGAGAATTAT GATAAATCTC TACTGGTGTA CCGACCTGTT CGATGTATCC	2400
ATTGTTAAAG ACTGCAATTC TATCAGATAA AGTCAAGGCT TCCTCTTGAT CATGAGTAAC	2460
ATATAAGTA GTAATACCTA ACTCTTTTGT AAGTCTTTTC AACTCTTTTC TCAAATCTAC	2520
ACGTAATTTT GCGTCAAGGT TTGACAATGG TTCATCTAGA CAAAGAATTT TAGGTTCAG	2580
AACCAGAGCA CGAGCCAATG CTACCCCTTG TTGTTGACCC CCAGATAATT CTGATACATT	2640
ACGCTGTAAC TGTGATCAG AGATCTTAAT TTTTGCTGCC ACTGCTGATA CTTTAGCTTT	2700
AATAACATCT GGAGCTACCT TCTTAACPTT TAAACCAAAT GCAATATTAT CAAAAACAGT	2760
CATAGTTGGA AATAGCGCAT AAGATTGAAA TACAATACCA ATTCCACGCT TTTCAGGTTT	2820
CAATGAGTG ACATCTGTTT CATTAACCTC AATACTTCCT GATGATGGAT CTAGAAAACC	2880
TACCAATGCT CTCAAAGTAG TTGATTTACC ACATCTGAA GGCCCAAGAA ATGTAAAAA	2940
TTCCCTTCA TGTATATCTA AATTCAGATT ATCAATTGCA ACAAATCAC CATATTTAAT	3000
TTGAATATTA TCAAATTTAA TCATCTCACT AACTCCCTCT ATTACTAAAC CAAAAGCCTC	3060
TCTTTATTTT TTCCATAAAT TTAGAAATAA TAGAGAGACT TGGACATAAA AATTAACCTT	3120
TATTTCTTAT TGTACGTATT CTAATTCAGC TTTTCTTACC CATTCATCCA AATGCTTTCC	3180
AACAGCTTCC CAGTCAATAT TTTGTGGTTT CACTTGATCA ACAAATTTCT TCGTATCTTC	3240
AGGTAGATCT TTGAGGGCAT CTTTATTGTC AGGAATAGAT CCAAAGTTCT TACTATATTC	3300
TACTTGAATT TCTGATTGAC CAAACCAATC AATAAATTCT TTAGCTAACG CTTGTTTTTT	3360
ACTAGTGCTT AAAACCATAG TTTGTTTCACT TACAAATGGT ACACCAATCT CAGGAGTCAT	3420
AACTTTGAAA ACAACATTTT GTTCTTTTGT TCCAACTAAT GCACCAGAAC CCCACATCAT	3480
TCCATATTGT ATTGGATCTT CTTTGTCTAA CATCTTAACA ATTGAACTTT CTCCCTTTTG	3540
AAGAGTGAT GCATTTTCA AATATTCTTT TGCTACTTCC CAACCTTTTT CGGAAACACC	3600
TAATTCACCT TTATCATCAA GGTATCGAAC TAAGATACTT GCTAGAATTG CCCGTCCTGT	3660
ACCTCCTTGA AGACCAGAAA TTGAATATTT ACCTTTTATC TTACTACCTA ATTCAGTCCA	3720
ATCTTTAGGC ATTTCTTTTA CATCAGGCGC CCCAATTAAA ACTAATGGTT GAACAATCAC	3780
AGGATTATAA TAATTATCTT TATCTGATAA AGATTGATCA ATTTTATCTA ACCATTTAGG	3840
CTTGTAAGT ACTAGTAATT TTTGATCTCT AATTTTATTT GAATCAACAG CACCAATTCC	3900
AAATACCATA TCTGCAACTG CATTATTCTT CTCAGCAATA ACACGGTCTG CTAATTGAGC	3960
GCCAGCGATA TCAACCATTT TTATATTAAA ACCAGCTTCT TTTGCTTTAG CAGTTAACCA	4020
ATCACCACGA CCATTTGAGA CTGAGTTCGA ATAGATAACT AATTCCTGAC TTTTATCAGC	4080

1135

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TTTTTCTTCA GATGAAGAAG CAGTCGTAGA ATTTGAACCT CCAGAGCAAG CAGCAAGTGT    4140
AGTAAgAGCA ACTCCCGTTG CAAGTACAGT AGACCAAACCT TTCATTTTMT TCATGATAAG    4200
TTCTCCTTTT TTATTATTTT ATTTAAATTT TTCGTGATAT GGAACAAATT GTCTCATATC    4260
TTCAAATACA GTATAGTCAA TACGGTTTAC AGTAATAGTT GGAATCTTCT CTAATAAAAT    4320
TTCAGTTAAT TCTGCTCTGA CTTTAGTAAA CTCTTCTTCC TCCTCTTCGG TTAGAGGAAT    4380
CCGAAGATAC CCAATTGAAA TATGGAATTG ATATCTATCA TGATTAGGGA AACAAACACC    4440
TGCTTTTTCT GAGACATAAG TACGAATTC TTCTAATCTC TTTGCAGAAG CTTCACTGTC    4500
AGGTTCAACT AGTATGTTTT GTTTTCCCAT TTCAGTTATA CGCATATGAA TTTCTTCATC    4560
CAACAATGGA AAAATTTCAA GTTGTTTAGC AAAGTAATCA TGTATTCCT GTAAAGGTGT    4620
ATCTAGAGGA AGATTACTGC TCCAAAATC gttCACGATT TTCATGGCAC AACAAATCAA    4680
TTACAGTCAT GTGAATAGAA TTCCTTGAG TTAAGTAAA CTTATCGATA AATGGTAATT    4740
CTCTATAACG TGATTGAATA ATATCAACAA CTTCCATCAA ATCTTGTTTA GTATAAGAT    4800
TTGCTACAAC TGTATCCCA GGGAAATGAT TAAATCCCC ATCTCTCGG    4848

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(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3763 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

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GTTATAAGCA ACACCTTCTT GCTTGCCATA AGTTGTGAAA TGGGTAGAAT CGATATCTAC    60
AATGAGTTGG TTTAGCTGGT GAAACTGTAA AAAGAATTCG ACCAATTCAA GGTGAGGCA    120
TCGCAAACTA TGGACTGTTT CCTCGTCAGT TCTGGAAAGA AACCGGGATA AGGTTGGCTG    180
TGAAGCAAGC TGCCCTCCTT CCAATAATTT TGGAAAGTAG GCATCAGCTG ACAATTCCTT    240
ACAAGCATAG TCCGTTCCAT AACCTGTTAA CAGTTGAAAG AGGAAGTGA CAAGGATATC    300
TGAATCCGAA TAACGACAGT AGCGGCGTTG GTCATTCTGT ACTAAATACT TAGAAATCCG    360
CTCTTTTAGT TTCAACTGGG AAAAAAGTTC CTGAAAAAG ATAAGACCAC CATACTGGGT    420
TAAATGACCT CCATCGAAAG ATAGTTGGTA AAAAGACTTG TTTTGGAAGT GATGATTGG    480
TAAACTGTTC ATGTGAGTTT CCTTCTTTT TGTGTTTTTT TCTACACTTA TACCATAAAG    540
GGGAACTCT TTTTGTCTA GTAAAAACA CCCATTGGGT GAAAAAGAA ACCATCCAG    600

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1136					
ATCTAAGCTA	AGGCAAGGAT	TCTGGATGGT	TTTTAGATT	GGGGTGAATA	ATTGGGGATT 660
TAGGAGAAAT	GATGGTATCT	TCCAAATCAA	AATCAACTTC	ACTCCATAGT	CTCAACTGAT 720
TGATTTTCCC	ATCTTGATAG	GTCACATCCT	TGTCAAGGAT	AAACTGAGTC	AACACCTCAT 780
GTTGACCTTG	ACACCTGATG	TCATCTACCA	AGAGCCAGAC	ATCCTCTACC	AACATGAGGA 840
TTTTTCTCCT	GTGAAGATAA	GGCAAATCAG	GTTCTGCTGA	CCAATAAGCC	CCCTCAATAT 900
AATGCACTCC	CTCCCTTTCT	TTATGGTGAC	AAAACAGGGA	GTGAGGATAG	TATTCATATT 960
CCCAGGATCC	CGTGATTCTT	TCCGGAGCTT	TCCCATCTAC	AATGCAGGTC	GAATGACTCC 1020
AAGCACTCTT	TAAGAGATAA	CGTTCATATA	TCTCCCGATA	AGAATAACGC	CCAGCATCTA 1080
TGAAAATAGG	TTGGCCTTGA	TACTGTAAAG	AAAAACTATT	CTCGTCACTA	TGACTATGGG 1140
CACCTTCTAG	CGGACCATTT	TTGAAAAATA	GATAACGATG	TTCATCCTTA	ATGCAGACAT 1200
GTCAGAGTC	TTCAAAGATC	ATGGACTTAG	GCTGCCAAGC	TCTCTTTTCA	AATTCCTGCA 1260
GTCGCTTGAC	CTTTTCTCGC	CCCAGGAACA	AGAGGCTAAG	CAAATCAACT	TTAACATCCA 1320
GACCGTTAAG	AAGGTCTTCC	TGGTTCAAAA	CCACAGCAGA	CAGGCTCAAA	ATTTCTGTCTG 1380
TTTCTGTAGA	ATCGCTATCA	CCAAAAGCCA	AAGTCCGTCC	ATCTAAGCCT	GTCATCATTT 1440
GAATATAGGT	CGCCATCTTT	TCCAGCAACT	CTTGGTAACT	ATCTTGCAAG	TCTGGAAGCA 1500
AGAGACACAA	ATCCAGCAAG	GCTTTATAAA	CCTCTACATG	ATAGAGAATC	GACTGTTCAA 1560
ACTGGCTTCC	ATCTCCTAAA	ATCTGTGTCT	CAATTTGCTG	TTTCAACTCC	TCTGAAGCAA 1620
AATGGTAAGC	TTCTTCTAGA	TCCATCTTAT	CTGAAAAGAA	ATGATAGATA	GCAAGCATCG 1680
GAATTGTTTG	TAAAATCCCC	CAGTTACTAA	GGGTGTACTT	GGCGCGATAG	TAGCTTTTCA 1740
TAAAGTCAAT	CTGCTTTTCT	AGACTGACCA	AAATTTTCTC	TAGTTCTTTC	TCCTCTAGCA 1800
AGTCAAATTT	CAAGAGGAGC	AAGAGTAGTT	TCAACCAAGT	AAAGGAACGA	ATACCCGTAT 1860
CCAAGGTCTT	AGTCATCAAG	GATTGAGGAG	AAAATTCTCT	CACCTGCTCA	ATCCAATCAA 1920
ATAGAAAGAA	CTTGCACTTT	TGAATATAGT	CCTTATCTCC	TTCTACCAGA	TACCCTATCA 1980
TAAACTGCAA	GAGATATTCT	TGTCGATTGA	GCATATAAGA	CCATTCTGGA	TCATCTTCAA 2040
ATACTTGATC	CCATACCATC	GGCTGGATTT	GATGGATTTT	TGAACAAGGC	TCCATATCCC 2100
AAGGACTATC	AAACATAAAA	CGATTGTCCA	TCAAGCGTTC	AAGGGAAGTC	TTGACTTTCT 2160
CATAGTCTTT	TGAACAGTGC	GACAAGATAT	AATCACGACA	TTGATTTCCA	TCGACTCTTT 2220
CAAAAAATTG	TCTTCTTTCT	TCTTTCATTA	TCTATTACCA	GAAAAAGAAC	TACTTAAAAA 2280
GCAGTCTTTT	TGTCTTTCCC	ATTACACTTT	CCTTTTCTAC	ATGGATGACC	ACACCTTTTG 2340
CAATCTGCAA	GGAGACCAAG	TCATCTTGGA	TAGAAATGAT	TTTTCATGA	ATTCCAGACA 2400

1137

ATAACAACAC TTCATCACCA AATGTTAAAG AAGCTAAATA CTCTTGTCGT TGCTCCATCT	2460
GTTTGCGAAG CAACTTTTGC TGACGAATAG AATGAAAGCT TGACAGTAAA AGGGGACTCA	2520
CTGCCAAGAC AATCACTATT CCATAAAACA ATGTTGTATC CATTAAGCTA TAATCTTAAG	2580
CCAGCTTCCG ATAATCCGA TGATAACTGT TAAAATAACG AGTTTATATG TTGTCCATTT	2640
CTTTTCTTTG ATCAAGTAGT AAATAAAAG TGTAATAGG GCTGGTAGAA GAGCTGGAGC	2700
AACCTTATCA AGCATTCCTT GAATACTTAC GATACTTTGT TTAGCGTCTG CTTTAACTTC	2760
CCCTGCAGCA AAGGTAATCG GCACCATAAT CTTAACAGAT GTCGCTGCCA AACCAGCAAT	2820
TACGtTACAC CGATAATATT GGCAATACGA GAAATCGTTG CCATCTGTTC GCTTAGTTTA	2880
TCAATCACAG TTGTTCCCTAG TTTGTATCCA TACAGACCAG TTGACAATTT AATCGCTGTT	2940
AAAATCGTAT TCATCGCAAG GAAGAACAAG ATTGGACCGA CAACCAAGCC TTCTTGAGCA	3000
AACGAAGCTG CGATGGTTGA GAACAATGGA GCTAAACAGA ATTGAGAAAAG AGAATCCCCA	3060
ATACCTGCCA ATGGTCCCAT CAAGGCCATC TTGATGCTAC GTGTTTCTTT TGCCGGACGG	3120
CCATTTTCCA ACATTACAAG ATGCAAGCTG GTAATAAAAG GCAGGAAGTG TGGGTTGGTA	3180
TTATAGAATT CACAGTTTTC TTCCAAGGCT TGGTAGAAAC CTCCTGATC CTCTCCATAG	3240
TGTTTTTTCA AAGCAGGATA CATCACATTG GCATATCCCA ACCCTTGATA GTTACTATAG	3300
TTAAATCCAT TTTGACAAAA GAATGCCCGC AAAGACGTTT TAAGATAATC ACGTTTGT	3360
AATTTGTTAG ATCCAGTCAT CGTGTGCTTC CTCCTTACC ACATGATCCG CTGTTTGTGG	3420
CTTGTTATAA AATTCAATCA AAGCAAAGAT AGTACCTACA ATTGCAATAC CAATGTTGG	3480
GATGTTTAGA TAAGCTGCAC AAACATATCC CAACAAGACA AAGGGAATCA ACTCTTCTT	3540
AGCCATCACT GACAAGATCA TCGCAAAACC GATAGCTGGG AGCATTTTAC CAGCAACTGT	3600
CAAACCTGTA AGTAATACCG GTGGAATGTA GTCTACGAGT TTCAACAAGG TATCCATTGA	3660
AAGGGCACCA AGCAACCCAA GGTAAATCCA ATAAAGGCAA ACAACCAAAT TGTTGCATTT	3720
AGAGTGAAC TAAATTTCTT CAAATTATGG TTTTCAAGT GCT	3763

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5053 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

1138

CAATCTCTGA GTATGTGCGG TCAATACTAw CAAAGGGAAT yCCTGACGTC AAGTAATGTT	60
CAATTGGmCT ATAGGTAATG GCAACCACTC CATCAACTTT ATTATGACGC AACATCTCCA	120
GATAGTCTTG CTCTCTATTT GTACCATTGA TAGAACATAA GAGTAATTTG TTATTTCTCT	180
TATAGACTTC ATTTTCCACA TGCATAGCAA ATTCTGAAAA GAAGGGATGC CAGATACTTG	240
GTACAATGAT TGCAATCGTT TCTGTTTCGAT TTTTTTTCAT TCCTCTAGCG TAGTAATCTG	300
GAATGTAATT CAAAGTTTAA ATCGCTTGTT CCACTTTTTT CAAAGTTACT TCTTTAATGC	360
CTTTTCTTTT ATTAATTACA CGTGAAACAG TTCCAACACT AACTCCTGCT TCTAAAGCAA	420
CATCTTTCAT GGTAATTGAT TTTCTTTGTT CTACCATATT ATCACCTCCT TTCAATATAT	480
AGTATCATGC AAATGCTTTT TAAGCAACTA TTTCTCAATC ATTTTTGGCC AGATCATTTA	540
TCCCATCATG AATAAAATCA CTCCAATTAG CTTTGTAAAA TACTTCAATT TTCATGTGTA	600
AACATCTACA TAAAACAGGA AAAGCCTTGG TTCATGGCT TTTTTCGTAT CTTCTATAAA	660
AAAAGCAAGA GTTTTAGATG GCTATAAATC TAGATGTACA TTTTGCTTAA ATGATTGAAG	720
GTCTTTTCTT AACAAAAACA CCCCCAAAAT TAGACTTTTT CTGTCTAACT TTTGAGGTAC	780
AGTTCAAACG CGAAATAGCG TTTTTTTGTT ATTTTTGGTT ACTCATCTAA TCGAATAAAC	840
ATCATGGCAT TTAACAAGTA TATGAGTGAG ACCGTGTTTA TATTATTTGA ATAGATGAGT	900
CTCTATTTTT CAATAGGAGG AATAATAAAA TTAGAAATAA TGATATCATA AGGTGAATCT	960
TCTAAAGATT CCTTTGATAA TTCTAATTCA GTCCAAACTT CCAGTTCAAA ATTATGCTA	1020
CAATAATAAG AAAGTGCTCT TGCAACGAAT TTTGCATGAT ACTGATCAAA ATTACTCATA	1080
ACTAAAACCT TTAGTTTAGG CTGATTTTGT AGCAAATTAA TCACCAAATG TTTGGTATGA	1140
GTGATGAAGG TATAAGATAG ATGATTTACC ATCATTGAAC TAGAACAAAC CTCAAGAGTC	1200
TCTAAATAGT GAGAAAGCTC TTTTTTTATA TCTGAAACAA ATTTTGGAAG AATATTTTGA	1260
AAGTTCCTGA TTGTATTCCC TTTTGTGATCA AATAAAATAA ACTCAGTAAA CAACTCTTGA	1320
CGATACAGAT GTCCGGTATT ATGCAGATGC CAAATCAGAT TATCCTTATT CTCCATTTCA	1380
ATCTGATACT TGA CTGAAAT CTGATCAATA AAATCACTCA ATAGATGGTA AGATTTTTTCA	1440
ACATAACTAT CCTTTTAC GCATTTTATA AAGAGACTTT CATCTATGAA AAACATTTTT	1500
TGAAAGTAAG ACACAAATAA TTGGCAAACA ACTTCTTCAT CTAAAGAGAT ATTGTATTCT	1560
GATTCAAAAC TCTGAGCAAC ACCTTCTATT CCTTCTGCCT GCATTAAAAA ATCCAAACTT	1620
TGGTCGTTAA AAGAATCTTT ATCTACTTCC ATAAAATGAC CAAACTTTAT TCTATATAGG	1680
TCGTAACTA GGAGCAACTT TAGCATTTCTA TGCCTTGACA AATTCATTGG AAAGCTTGTT	1740
TCCTTATAAA CCAATTCTAA CAATTGAGAT AGTGGCTCTG ATGAAAAATT TTCAAATGGC	1800

1139

CATTCTAGGA AATAATATTT TTCTGAAAA TATTGTGCAA AAAAGTAACG AATGTCTCTC	1860
TCATTTCCAA TGATTTGAAC AGGGGTCAGA CTAACCTCAA ATTGAAATTG CCTTTTAATC	1920
ACTTTATTGA TTGGGCTAAT AATACGATAG AGCGAAGATG AACTGATATA AAATTCCTTTA	1980
CAAATACTCT CAGCTTGACA ACCTTCATTA AAGAAGATGA ATTCTAAAAT CGAAAAATGA	2040
GTTGAATGTT TAAAGAAATG ATGGTAAACC ATTTCAATAT CACTATCATC GGTATTAATA	2100
ATGCGTATAC CATTAGTAGA AGAATGAAAA ATCAAGTCAG GAAAAGCAGA TTTAACATGG	2160
GATAGATCAT CTTTGACTGC ACGTTCTGTA CAATTTAATA ACTCTGCTAG TTCAGAACGA	2220
TGAAACCAAC GTTTATGTTT AAATAATAAT TCTAATAATT CTAATTGCCT ATGACTTTTTT	2280
TTAGATAATA AATCTCTCAT GAATATCTTT CTCTCTTTAT AAATTATCGG ATTAAACCTC	2340
TTGCAATTAT ACCACAAAGA ATAGGTATAG CATGATATAA CGACTTTTCC TAAATCTTT	2400
TATTTCTGAT AATAACACTA CGGAGACAAT ATATAAACAA TTTTCTTATT TTACCGTCTA	2460
TTGAGGGCGT GAATACAGAA TCAAATTCOA GTCTAAAGAT TATATTTTTA ATTTTAAAAA	2520
TTATATAATA GCAACAATTA AAGAATTGA TTTTTTAAAA TTATATAATA ATAACAATCG	2580
AAATAATGA CTTTCTCTATA TTAAAGTTAT ATAATAGTAA TAATCAAAGA AATTGATTTT	2640
TTGATATTAA AATAAAAAAG GAGGGTAGGC AGTGTGTGTA TCAATTATTG CTGGGGTCT	2700
TATTGGTCTC TTGGCAGGTA AAATCACTAA AAAAGTAGTT CTATGGGAAT CATCGCAAAT	2760
GTATTCGCTG GTTTAGTCGG GGCATATGCA GGACAATCTC TTTTAGGTAG TTGGGGTCCA	2820
GCAATCGCTG GAATGGCTTT GCTCCCATCT ATTGTAGGTG CAGCGATTGT GATTACTGTA	2880
GTGTCATTCT TTACAGGTAG AAAGTAACT TTTCCGCTAGT AAAGTTAGCA AACTATTTTT	2940
AAATCAATGA CGGAAAAAT AGTTTAAATG TTAAATCGAA AGGATTGTAT ATGTCAAAAG	3000
CAAAGAAAAT ATGTTTCATT ATTTCTGTGA TTTTAATCTT GACAATTTTC CTTCTGTTT	3060
TGATAGATTA TCATCAAGTT AGTGATCTAG GTATTCATCT ACTTAGCTGG AGACAGAACT	3120
CCGTAGTTGA ATTCTATCTT GCTAGATATG TCTTTTGGGG GACAGTGGTT CTATCAACTT	3180
TAGTTTTATT ATCCATTTTA GTTGTGATGT TTTATCCTAA ACGTTACTTG GAAATCCAAC	3240
TTGAACTAA AAACGATACA TTAAATTAAG AGAATTCGGC AATCGAAGGT TTTGTTAGAA	3300
GTTTGGTGAG TGATCATAGA TTGATCAAGA ACCCACTGT TCATGTAAAT TTACGAAAAA	3360
ATAAATGTTT CGTTCATGTA GAAGGTAAAA TTCTTCCTTC AGACAACATC GCTGACAGAT	3420
GCCAAATAAT TCAAAATGAA ATAATAATG GATTGAAGCA GTTTTTTGGT ATTGAGCGTC	3480
AAGTAAACT TGAAGTTGCA GTAAAAAAT ACCAACCATA ACCTCAAAAC AAAAAGACTG	3540

1140

TTAGTCGTGT GAAGTAAGGA AGTAAAAAAT GGAATGGCTT AAACAATATC GATATCCAAT	3600
TATCGCTGGT CTCATAGGCG TATTTCTGGC TTGTTTGATG GTCTCCTTTG GCTTCTTCAA	3660
AACAATATTT GTATTGATTT TAGGAGCACT GGGAGTTGCA GCTGGATTAT ATATCGAAAA	3720
AAACTATATA GATAAATAAA AAAATAAAAA TTAATAATTT AATTAAAGGA GTTTCATATG	3780
TCAAACGAAA AAAACACAAA CACTAACGTA GAAAAGAAAG ATGCTACTGT TGTAGCTCAC	3840
GAAATCAAAG GGGAACCTAC TTACGAAGAT AAAGTTATCC AAAAAATCAT TGGTCTTTCA	3900
CTAGAAAAACG TTTCAGGTCT TTTGGGAATC GATGGTGGTT TCTTCTCAAA TCTTAAAGAA	3960
AAAATCGTTA ACAGCGATGA CGTAACAAGT GGTGTTAACG TAGAAGTTGG TAAACACAA	4020
GTTGCAGTTG ACTTAAACGT TATTGTTGAG TACCAAAAAA ATGTTCCAGC TTTATATTCA	4080
GAAATCAGAG AAATCGTATC TTCAGAAGTT GCTAAAATGA CTGACTTGGA AATTGTTGAA	4140
ATCAACGTAA ACGTTGTCGA CATCAAACT AAAGAACAGC ATGAAGCAGA CTCAGTAAGC	4200
CTTCAAGATC GCGTATCTGA CGTTGCTGAA TCAACAGGAG AATTCACCTC AGAACAATTC	4260
GAAAAAGCTA AATCTGGTCT TGGATCTGGT TTCTCAACTG TTCAAGAAAA AGTTAGCGAA	4320
GGTGTAGAAG CTGTTAAAGG TGCAGCAAAT GGTGTAGTAT CTCACGAAAA CACTCGTGTA	4380
AACTAAGATA AAATAATAT AACAGGAGAA ATTATCATGT CAGTAGAAGA AAAATTAAAT	4440
CAAGCTAAAG GTTCTATTAA AGAAGGTGTT GGGAAAGCCA TCGGTGATGA AAAAAATGGA	4500
AAAGAAGGTG CAGCTGAAAA AGTTGTTTCT AAAGTAAAAG AAGTTGCCGA AGACGCTAAA	4560
GACGCTGTAG AAGGTGCTGT AGAAGGTGTT AAAACATGT TGAGTGGCGA CGATAAATAA	4620
GGTAAAAAGT TACTTTATCT TTTTAGTAAT ATTAGTCAAA AGAGTCTGAG TCAAGATGAT	4680
TCTCAGAAAA CAAAAAGCTA GAGATTCCCA ATTGCGGAAC TCTAGCTTTT TAATTTTGCC	4740
TCTTTCTCTT ATTATATTTT AGCAGGTGTT TGGCCATGAG TACGAATCCC ATGTCAATTC	4800
TCACTTGACG CTTACCTCTC AGATGACATC TCTTATAACC CAAACAAACC TTTATCTGCC	4860
CAAAGACAGA TTTCATATCA ATCTTACGTT TAGCGAAAAT TTGTCTACCC TTGGAAGATA	4920
AAAGTGCCGT ATATTCTTTA GTTTTAAAC ACTGGTAACG TTCATTATA TACAGTCTCT	4980
TTTGAGGGGC TGATTACGGT TCATAATCGC AGTCAACATT GATTTCAAGG CTGTTTGCTT	5040
TCTATCTCCC CGG	5053

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

AATTCTCTTT TTTCCAACAA AATGTATGAC CTGCACTTGA ATACTTCTCA TTGTTTGTAC	60
ATTCATCTAC TTTCATATAA TCTTTTACAA AATCATAATA TGACATAACA CACTATCCCT	120
TTTAGACAAT ATTCCAATTA GCCTTATTAA TTCAAACTA TTGTATTAGT AATTATAACA	180
GATGTATAAT AGAAAAGCAA TGATAGATAT TATCAATTAA GCGAATTTAT ATCTAAAAGG	240
GATATTAAAG AAAGGAGATA TGCTTATGAA GATTTACAAA AAACATTTTG CTATGTCCA	300
AGATAAGAAA TATCTTGGGG TTTTGGCCAT AATTTTTTCT GCTATATCTG CTGCACTTAC	360
AGTATATGGA TATTATTAA TCTACAAATT TCTAGATAAG TTAATAATTA ATTCAAACCT	420
ATCCGGTGCA GAGAGTATAG CATTAAAATC TGTATTACA CTAACAAGTG GAGCGATATT	480
TTATTTTGTG TCAGGAATGT TTTCACATAT CTGGGATTC AGGCTTGAAA CAAATTTAAG	540
AAAAAGGGaA TCGATGGTCT GGAAAAGCA AGTTTTAGGT TCTTTGACTT AAATCCATCT	600
GGTCAATAA GAAAGATTAT AGATGPCAAT GCTGCACAAA CTCATCAGGT GGTAGCACAC	660
ATGATTCCCG ATAGTTCTCA GGCAATAATC ACACCCGTAC TTGTACTTGC ACTTGGCTTT	720
ATAGTAAGTA TAAGAGTTGG CATAATTTTG CTGCTCTTA CTATAATTGG TGGCTTAATT	780
TTAGGGGCAA TGATGGCGA GCAAGAATTT ATGAAGATAT ACCAAGAATC CCTATCTAAA	840
CTAAGTGCTG AAACGTGTA GTACGTGAGA GGAATGCAAG TTGTAAAAAT ATTTAAAGCA	900
AATGTAGAGT CTTTTAAAAG CTTTTATAAG GCGATAAAAG ATTACTCAA GTATGCTTAT	960
GATTATTCCC TATCTGTAA AAGGCCTTAT GTTTTGTATC AATGGTTATT TTTTGGACTG	1020
ATTGCAATTT TAATTATTCC TATAGTTTAT TTTATGACTA GCTTAGCTAG CGCAAAGGTG	1080
ATTTTACTTG AGCTTATCAT GATTTATTT TTATCAGGAG TTCTCTTGT TTCATTCTG	1140
AGAATGATGT GCACTCCATG TATATTTCTC AAGGAAATTA TGCAGTAGAT ACTTTAGAGG	1200
CGCTTTACGA AGATATGCAA AAAGACAAAT TAGTGCATGG TAATGTCAAT AATTTTAAAA	1260
ACTATAATAT AGAATTTGAG AATGTTAGCT TTGCTTATAA TGATAAAGCT GTCATTGAAA	1320
ATTTATCCTT TAATTAGAA GAAGGAAAGT CCTACGCACT TGTCGGTTCA TCTGGATCAG	1380
GCAAAATCAAC AGTAGCAAAA CTTATATCAG GTTTTACAA TGTTAATAAA GGAAGCATAA	1440
AGATAGGCGG GATAGCAATA AGTGAATATT CTGACGAAGC CTTAATTAAA GCCATTTCTT	1500
TTGTTTTTCA AGATTCAAAA TTATTCAAGA AGAGCATTTA TGATAATGTA GCGTTAGCTA	1560
ATAAAGATGC GACGAAAGAT GACGTTATGA GAGCCTTAAA ATTAGCAGGA TGCGATTTAA	1620

	1142	
TATTAGACAA ATTCCCAGAA AGAGAAAATA CAATCATAGG CTCAAAAGGT GTTTATTTAT	1680	
CCGGTGGAGA AAAACAAAGA ATTGCAATTG CTAGAGCAAT TTAAAGGAT TCCAAAATTA	1740	
TTATTATGGA TGAAGCATCA GCATCTATTG ACCCAGATAA CGAGTTTGAA TTGCAAAAAG	1800	
CTTTTAAAAA TCCTATGAAG GATAAACAG TTATCATGAT TGCACACAGG CTATCTACAA	1860	
TTAAAGACCT TGATGAAATT ATTGTCATGG ATAGTGGAAG AATTATAGAA AGAGGGTCTG	1920	
ACAAAGAATT AATGTCAAAA GATACAAGGT ATAAGGCCT GCAAGAGATG TTAAACAGTG	1980	
CGAATGAATG GAGGGTTTCA AATGAAAGAG TTTTATAAAA AAAGATTTGC TCTTACAGAT	2040	
GGAGGAGCAA GAAATTTAAG TAAAGCAACA CTGGCTTCAT TTTTCGTTTA TGTATATAAC	2100	
ATGCTTCCTG CCATATTACT TATGATTTTT GCTCAGGAAG TTTTGGAAAA TATGGGCAAA	2160	
AGCAATGGCT TTTATATAGT ATTCTCAGTT TTGATTTTGA TAGCAATGTA TATTTTGCTT	2220	
TCTATCGAAT ACGATAAATT ATATAACACA ACCTATCAAG AAAGTGCAGA TTAAAGAATA	2280	
AGGACAGCGG AGAATTTATC AAAATTACCT CTATCTTACT TTTCTAAACA TGACATTTCC	2340	
GACATTTTAC AAACAATCAT GGCTGATATT GAAGGCATAG AGCATGCAAT GAGCCACTCA	2400	
ATACCAAAGG TGGGCGGCAT GGTACTGTTT TTCCCATTA TATCTGTAAT GATGCTAGCG	2460	
GGCAATGTCA AGATGGGTTT AGCTGTAATT ATTCCATCTA TTTTAAGCTT TATATTTATA	2520	
CCTTTATCTA AAAAATATCA GGTTAATGGA CAGAATAGAT ATTATGATGT CTTAAGAAAA	2580	
AACTCAGAAA GCTTTCAAGA AAATATCGAA ATGCAAATGG AGATTAAAGC ATATAATTTA	2640	
TCGAAGGATA TTAAAGATGA CTTATATAAA AAAATGGAAG ATAGTGAGAA AGTACACTTA	2700	
AAGCGGAAG TAACTACAAT TTAACTTTG TCTATATCTT CAATATTTAG CTTTATATCT	2760	
CTTGCTGTG TGATATTTGT CGGCGTAAAT CTAATTATTA ATAAAGAGAT AAATCTCTC	2820	
TACCTTATAG GATATTTACT AGCTGCTATG AAGATAACAG ACTCTTTAGA TGCATCTAAA	2880	
GAGGGCTTGA TGGAAATATT TTATTTATCG CCCAAAATAG AAAGATTAAA AGAAATTCAA	2940	
AATCAAGATT TACAAGAAGG CGATGACTAT AGCTTAAAAA AATTTGATAT TGATCTAAAA	3000	
GATGTTGAGT TTGCCTACAA TAAAGACGCA AAAGTTTAA ATGGTGTAAG TTTTAAAGCT	3060	
AAGCAGGAG AGGTCACTGC TTGGTAGGT GCAAGTGGCT GCGGTAAAAC AACTATCTTG	3120	
AACTTATAT CAAGACTTTA TGATTATGAC AAGGGACAAA TCTTAATCGA TGGCAAAGAT	3180	
ATAAAGGAAA TATCAACAGA ATCCCTTTTT GATAAGGTGT CTATTGTTTT CCAAGATGTG	3240	
GTCTCTTTA ATCAAAGCGT TATGGAAAAT ATTAGAATCG GTAAGCAAGA TGCAAGTGAC	3300	
GAAGAGGTTA AAAGAGCAGC AAAACTTGCA AATTGCACAG ATTTTATAGA AAAAATGGAT	3360	
AAAGGTTTCG ATACAGTTAT TGGTGAAAAC GGAGCTGAGC TATCAGGAGG AGAAAGACAA	3420	

1143

AGATTATCAA TAGCCAGAGC CTTCTTAAAA GATGCGCCGA TATTGATCTT AGATGAGATA	3480
ACAGCAAGCC TTGATGTTAA CAACGAGAAA AAGATTCAAG AGTCTTTAAA TAATTTAGTT	3540
AAAGATAAAA CTGTTGTAAT CATTTACAT AGAATGAAAT CCATAGAAAA TGCAGACAAG	3600
ATAGTAGTTC TTCAAAACGG AAGAGTAGAA AGCGAAGGTA AGCATGAAGA GCTTTTACAA	3660
AAATCAAAAA TTTACAAAA TTTAATAGAA AAGACAAAA TGGCAGAAGA ATTTATTTAT	3720
TAGGAGGACT ACAATGGATA ATAAAAAATT AAAAGTAAAA GATTTAGTAA GCATCGGTGT	3780
TTTTGGCGTA ATTTATTTTG CCTTCATGTT TGGAGTTGGT ATGATGGGCT TGATTCCAAT	3840
ATTGTTCTTA ATATACCCGA CAGTATTAGC CATAGTTGCA GGAAGTGTG TTATGTTATT	3900
TATGGCTAAG GTTCAAAAGC CATGGGCACT ATTTATATTT GGTATGATAT CACCACTTGT	3960
GATGTTTGCA GCTGGTCATA CCTACGTAGT TGTGGTTTTA TCACCTTATAG TAATGATAAT	4020
AGCAGAATTA ATTAGAAAGA TTGGTAATTA TAATTCATTT AAATACAATA TGCTTTCTTA	4080
TGCAATCTTC AGCACATgGA TATGTAGCTC TTTAATGCAA ATGCTTTTAG CAAAGAAAA	4140
ATATATGGAG TGGTCTTTGA TGACTATGGG AAAAGATTAT GTTGATGTAT TAGAAAAGTT	4200
AATAACTTAT CCTCACATGG CTTTAGTAGC CTTAGGTGCT TTCTTAGGAG GAATTCCTGG	4260
AGCATATATA GGCAAGGCTC TATTGAAAA ACACTTTTC AATGGATTAT ATTGTGTGGG	4320
ATACTTTACT CCTTGCCTAA TTTTATGGTG CTATCTGAAT TAAACCCTAT AGTTAAGATG	4380
TTTTTGAGTA TACCTATTGT TATTAGAATG TTTATTTTAC CATTTATGGC AGCAAGCTTT	4440
ATGATAAAGA CCTCGGATGT AGGCGCAATA ATTTCATCGA TGGATAAGCT TAAGATTTC A	4500
AAGAATGTAT CCATACCTAT TGCGGTTATG TTTAGATTCT TCCCATCTTT TAAGGAGGAG	4560
AAGAAAAACA TCAAAATGGC TATGAGAGTA AGAGGGATAA ATTTTAAAA CCCAGTCAAA	4620
TATCTTGAAT ATGTTTCTGT GCCACTACTC ATTATATCAT CTAATATATC AGATGACATT	4680
GCAAAAGCGG CAGAAACAAA GGCAATAGAA AATCCAATTG CCAAGACCAG ATACATTTCG	4740
GTAAAGATAC AGCTAATTGA TTTTGTTTAT GTTTTAGCGG TTGCTGGACT TATTGTGGGA	4800
GGCTTAATAT GGTTGAAATA AAAAATTTAA GTCTTGATTA TGGTGAAGAG CATATATTAG	4860
ATGATATATC ACTATCCATA GCCGAGGGAG AGTGCCTGCT ATTTACAGGA AAAAGTGGA	4920
ATGGTAAGTC ATCTTTAATA AATTCAATCA ATGGACTAGC TGTAAGGTAT GATAACGCAA	4980
AGACAAAGGG CGAAATAATT ATTGATGGTA AGAATATAAA AAATTTGGAA CTTTATCAAA	5040
TCTCAATGCT TGTTTCAACT GTTTTCAAA ATCCTAAGAC ATATTTTTTT AATGTCAATA	5100
CGACATTAGA ATTATTATTT TATTTGAAA ATATCGGTCT TGCAAGAGAA GAGATGGACA	5160

1144

GCGCTTTGAA GGATATACTT GAGATATTCC CGATAAAAAA TCTTTTGAAC AGAAATATAT	5220
TTAATCTATC CGGCGGTGAA AAACAAATTC TTGTCATTGC AGCTTCTTAT ATAGCAGGTA	5280
CAAAGATTAT AGTTATGGAT GAGCCTTCAT CGAATTTAGA TATTAAAAGC ATAAGTGTTT	5340
TGGCAAAGAT GCTAAAGATA TTAAGAGAGA AAGGCATAAG CATAATTGTT GCAGAGCATA	5400
GAATTTATTA TTTGATGGAC ATAGTTGACC GTGTATTTT AATAGATAAA GGAAAGCTTA	5460
AAAAAAGCTTA TACTAGAAGT GAATTTTAA AGCTAGATAA AAATGAATTA AATGCTTTAA	5520
GTTTAAAGAGA TAAAGAATTA AGTAAATTAA AAGTTCCTTA TTTAAAAGAA GGTGGAGAGT	5580
ATCAGATAAA AAATCTTAGT TACAAATTTA CTGATGATGA GTGTTTAAAGC TTAAGAGATA	5640
TTTCGTTCAA GCTTGGGAAA ATTTATGGCA TAATAGGATC CAACGGACGA GGAAATCAA	5700
CGCTTTTAAAG ATGTTTAAATA GGTCTTGAGA AAAAATCAAA AGAAGAAATT TATTTTAAAG	5760
GAGAGAAGCT ATCTAAAAA GAAAGACTCA AAAACTCTTC ACTTGTTATG CAAGATGTAA	5820
ATCATCAATT ATTCACAGAT GAAGTATTCA ACGAGCTTAG ATTAGGAGTA AAGAATTTTG	5880
ATGAAGAAAA GGCGAAAATC ATTTTAAACC CCAATTATTC ACCCCAAATC TAAAAACCAT	5940
CCAGAATCCT TGCCTTAGCT TAGATCCTGG ATGGTTTCTT TTTTCACCCA ATGGGTGTTT	6000
TTTACTAGAC AAAAAGAGT TTCCCTTTA TGGTATAAGT GTAGAAAAA ACACAAAAG	6060
AAAGGAACT CACATGAACA GTTTACCAA TCATCACTTC CAAACAAGT CTTTTACCA	6120
ACTATCTTTC GATGGAGGTC ATTTAACCCA GTATGGTGGT CTTATCTTTT TTCAGGAACT	6180
TTTTTCCAG TTGAACTAA AAGAGCGGAT TTCTAAGTAT TTAGTAACGA ATGACCAACG	6240
CCGCTACTGT CGTTATTCGG ATTCAGATAT CCTGTGCCAG TTCCTCTTTC AACTGTTAAC	6300
AGGTTATGGA ACGGACTATG CTTGTAAAGA ATTGTCAGCT GATGCCTACT TTCCAAAATT	6360
GTTGGAAGGA GGGCAGCTTG TFCACAGCCA ACCTTATCCC GTTTTCCTTC CAGAACTGAC	6420
GAGGAAACAG TCCATAGTTT GCGATGCCTC AACCTTGAAT TGGTCGAATT CTTTTACAT	6480
G TTCACCAGC TG	6492

(2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AACTGAAGGT AAAGGCTTCG ACGCAGAACG TGACGCTGCC CAAGCTGCCC TTGATGACCT 60

1145

TAAGAAAGCT CAAGAAGACA ACAACTTGGA CGACATGAAA AAAAACTTG AAGCATTGAA	120
CGAAAAAGCT CAAGGACTTG CTGTTAACT CTACGAACAA GCCGCAGCAG CGCAACAAGC	180
TCAAGAAGGA GCAGAAGGCG CACAAGCAAC AGGGAACGCA GGCGATGACG TCGTAGACGG	240
AGAGTTTACG GAAAAGTAAG ATGAGTGTAT TGGATGAAGA GTATCTAAAA AATACACGAA	300
AAGTTTATAA TGATTTTGT AATCAAGCTG ATAACCTATAG AACATCAAAA GATTTTATG	360
ATAATATTCC AATAGAATAT TTAGCTAGAT ATAGAGAATT ATATTAGCTG AACATGATAG	420
TTGTATCAAA AATGATGAAG CGGTAAGGAA TTTTGTACC TCAGTATTGT TGTCTGCATT	480
TGTATCGGCG ATGGTACCAG CTATGATATC ATTAGAAATA CAAACATATA AATTTGTAAT	540
ACCGTTCATA ATTGGTATGA TTTGGACAGT AGTTGTATTT CTTATGATCA ATTGGAATTA	600
TATAGGCAAA TACTAAGAAG AGACAAAAAT ATATAAATAT TTCTGTACTT ATAGGATATT	660
TAAAATCAAA ATAAAGTTAA TTTACTTATT TGCAGAGGTT GCAACCCAGC CTCTGTTTTT	720
CGATAAAAAG GGACGGAATC TCATTTGTTT GGGTTTTGTC TCATCAATAG AAAGGAACAA	780
AGAGTGTTTCG TAACTGAACA CGGGTTTCAG AATTTCTTAC TAAATATAAA AGAAAGGAAT	840
TGAACCCGAC CTAAATGGTG GTTCGATTCA GAACATCAAT AGAAAGGAAT AAGGGTGTTT	900
GTAACCTGAAC ACGGGCTATG GACTGTGCCA AAAAGATAGT TTTTCTAGG ACCTAAGCGT	960
CCGTCGTCAA AACTCCTAGA TGGCTGTGTC CGTTTGACGC CCTTTGTATC TTGAATTATG	1020
AACAATACTG AATTTTATGA TCGTCTGGGG GTATCCAAA ACGCTTCGGC AGACGAAATC	1080
AAAAAGGCTT ATCGTAAGCT TTCCAAAAA TATCACCCAG ATATCAACAA GGAGCCTGGT	1140
GCTGAGGACA AGTACAAGGA AGTTCAAGAA GCCTATGAGA CTTTGAGTGA CGACCAAAAA	1200
CGTGCTGCCT ATGACCAGTA TGGTGCTGCA GCGCCAATG GTGGTTTTGG TGGAGCTGGT	1260
GGTTTCGGCG GTTCAATGG GGCAGGTGGC TTCGGTGGTT TTGAGGATAT TTTCTCAAGT	1320
TTCTTCGGCG GAGGCGGTTC TTCGCGCAAT CCAAACGCTC CTCGCCAAGG AGATGATCTC	1380
CAGTATCGTG TCAATTTGAC CTTTGAAGAA GCTATCTTCG GAACTGAGAA GGAAGTTAAG	1440
TATCATCGTG AAGCTGGCTG TCGTACATGT AATGGATCTG GTGCTAAGCC AGGGACAAGT	1500
CCAGTCACTT GTGGACGCTG TCATGGCGCT GGTGTCATTA ACGTCGATAC GCAGACTCCT	1560
CTTGGTATGA TCGGTCGCCA AGTAACCTGT GATGTCTGTC ACGGTCGAGG AAAAGAAATC	1620
AAATATCCAT GTACAACCTG TCATGGAACA GGTCATGAGA AACAAGCTCA TAGCGTACAT	1680
GTGAAAATCC CTGCTGGTGT GGAACAGGT CAACAAATTC GCCTCGCTGG TCAAGGTGAA	1740
GCAGGCTTTA ACGGTGGACC TTATGGTGAC TTGTATGTAG TAGTTTCTGT GGAAGCTAGC	1800

1146						
GACAAGTTTG	AACGTGAAGG	AACGACTATC	TTCTACAATC	TCAACCTCAA	CTTTGTCCAA	1860
GCGGCTCTTG	GTGATACAGT	AGATATTCCA	ACTGTTTCACG	GTGATGTTGA	ATTGGTTATT	1920
CCAGAGGGAA	CTCAGACTGG	TAAGAAGTTC	CGCCTACGTA	GTAAGGGGGC	ACCGAGCCTT	1980
CGTGGCGGTG	CAGTTGGTGA	CCAATACGTT	ACTGTTAATG	TCGTAACACC	GACAGGCTTG	2040
AACGACCGCC	AAAAAGTAGC	CTTGAAAGAA	TTCGCGGCTG	CTGGTGACTT	GAAAGTAAAT	2100
CCAAAGAAAA	AAGGCTTCTT	TGACCATATT	AAAGATGCCT	TTGATGGAGA	ATAATACTCT	2160
TCGAAAATCT	CTTCAAACCA	CGTCAGCGTT	GCCTTGCCGT	ATATATGTGA	CTGACTTCGT	2220
CAGTCGTATC	TACAACCTCA	AAACAGTGTT	TTGAGCAGCC	CGTGGCTAGT	TTCCTAGTTT	2280
GCTTTTTACT	TTATAGATTT	TTTAAGACTT	TCCTAAGTAA	TGACGGACGG	TAGTGACCTC	2340
CTTCGAAGTT	CCATACCTAA	ACTTTGAACC	TAAGTTTTAA	AGTTTCCGGA	CAGCTGAAAC	2400
CAAGCTGTTT	CAGGTGTTTT	CATTACGGCA	GAAAGTCTTC	GATTTAGTTG	TGAAATGGTG	2460
AATGATACTC	TTCAAAAATT	TCTTCAAACC	ACGTCAGCGT	CGGCTTGTC	TGGGTATGGT	2520
TACTGACTTC	GTCAGTTCTA	TCCACAACCT	CAAAACAGTG	TTTGAGCTGA	CTTCGTCACT	2580
TCTATCCACA	ACCTTAAAC	GGTGTTTTGA	GCAGTCTGTG	CCTAGCTTTC	TAGTTTGCTT	2640
TTTGATTTTT	ATTGAGTATG	AATTACCTAA	ATTATGATGC	ATAGTTGATG	GGATATATAT	2700
AATAGATTGA	AATAGAATAT	GAACAAATTG	ATAAGAGGAT	TTTAAAGTAA	TCTCTAACAA	2760
TGCTTTAGAA	ACTATGGTGT	GCTATTCTAA	ATTCAATTCA	CTATAACTTG	TTTACGTTTT	2820
AAAAAAGAGC	CGTCGGGCTC	TTTTTACTTA	TCTTCAGTTC	CCTGCATTTT	TTTTATCACA	2880
GCTAGTCTAG	TCTGGATATC	CTTTTCCAAG	ACCTTAAACT	TGTAAGTCAA	GTCTTCTTGG	2940
TATTCCTTGA	TAAGTCTTTT	TTGCTGGTTA	ATGATTTGCA	GGCTGTTTTG	GATAATATCC	3000
ACATCGTCCT	TGATAGCTTG	AACGCGGTCA	GTGGTATTCA	AGACTTCATC	TGTGATGGTT	3060
TGGCGATTTT	TTGTAACCAG	ATAACTTCCG	GCTGCAGCTC	CTGCAAATAG	CAGTAGGTTG	3120
GATAATTTCA	TAGCAACTCC	TTAAGCGTTT	TTGATGGTTT	CAGCGACTTG	AGCAAGTTTG	3180
TCAAAGTCTG	GTTCGTGGGC	GATAAAATCA	ATCTTGAGGT	CATCGTCAGC	ACTGTAGCGA	3240
GGCACAAGGT	GAACGTGAGT	ATGAAAAACT	GTTTGACCAG	CGACTTCTTC	ACAGTTGGAA	3300
ATGATATTCA	TACCAGCAGC	CTTAGTGACT	TTCATGACTT	TTTGAGCTAC	TTTTGGTACT	3360
TGGGCAAAGA	GTGGCTGGC	GCTCGTAGCA	TCCATCTCCA	AAAGATTGCG	ATAGTGTTC	3420
TTTGGCACGA	CCAAGGTGTG	TCCTAGTGTT	ACTTGAGAGA	TATCAAGAAA	GGCAAGGACC	3480
TGCTCATCTT	CATATACTTT	TGAAGCAGGA	ATTTCCCTG	CGATGATTTT	ACAAAAAATG	3540
CAATCTGACA	TAAAATCTAC	CTCTACTGTA	CTGAATTTTG	ATATAATATA	GCTACATTAT	3600

1147

ACCAGATTG GAGAAAATAT GTTAGAAATT AAAACCTGA CAGGTGGCTA TGTTTCATGTT	3660
CCTGTTTTGA AAGATGTGTC CTTTACTGTT GAAAGTGGC AGTTGGTCGG TTTGATTGGT	3720
CTCAATGGTG CTGGGAAATC AACGACGATC AATGAGATTA TCGGTCTGTT GGCACCTTAT	3780
AGTGGCTCCA TCAATATCAA TGGCCTGACT CTGCAAGGAG ATGCGACTAG CTACCGCAAG	3840
CAGATTGGCT ACATTCCTGA GACGCCTAGT CTGTATGAGG AATTGACCCCT CAGAGAGCAT	3900
ATCGAAACGG TTGCTATGGC TTACGGTATT GAGCAAAAAG TGGCTTTCGA ACGAGTAGAG	3960
CCCTTGTTAA AAATGTTCCG TTGGAACAG AAATTAGACT GGTCCCCTGT TCATTTTTC	4020
AAAGGGATGA AGCAGAAGGT CATGATTATC TGTGCTTTG TGGTGGATCC AAGTCTTTTC	4080
ATCGTGGATG AGCCTTTCCT TGGTCTTGAT CCGCTGGCTA TTTCTGATTT GATTTCAGCTT	4140
TTGGAAGTGG AGAAGCAAAA GGGCAAGTCT ATTCTCATGA GTACCCACGT GCTGGATTCTG	4200
GCGGAGAAGA TGTGTGATGC CTTTGTCAAT CTCACAAGG GAGAGGTGCG TTCCAAAGGC	4260
AATCTCCTGC AACTACGTGA AGCCTTTGAT ATGCCTGAGG CTAGTTTGAA TGATATTTAC	4320
TTGGCTCTGA CCAAGAGGA GGATCTATGA AAGACTTGTT TTTAAAGAGA AAGCAGGCCT	4380
TTCGTAAGGA GTGTCTTGGT TATCTGCGCT ATGTGCTCAA TGACCACTTT GTCTTGTTC	4440
TGCTTGCTCT GTTGGGCTTT CTAGCCTACC AGTACAGTCA ACTCTTACAA CATTTTCTCTG	4500
AAAATCATTG GCCTATCCTT TTGTTGTAG GAATTACGTC TGTTTTACTT TTACTTTGGG	4560
GAGGAACTGC CACCTATATG GAGGCTCCAG ACAAGCTCTT TCTCTTAGTT GGAGAAGAGG	4620
AAATTAAGCT CCATCTCAAG CGTCAAACTG GCATTTCCCT AGTCTTTTGG CTCTTTGTAC	4680
AGACCCTTTT CTGCTGTTA TTGCGCCTT TATTTTTAGC AATGGGTAT GGCTTGCCAG	4740
TTTTTCTGCT CTATGTGCTT TTATGGGGG TAGGAAAATA TTTCCACTTT TGTCAAAGG	4800
CCAGCAAATT TTTCAGTAA ACTGGACTGG ACTGGGACTA TGTTATTTCT CAAGAAAGCA	4860
AGCGTAAGCA AGTCTTGCTT CGTTTCTTTG CCCTCTTTAC GCAGGTCAAG GGAATTTCAA	4920
ACAGCGTTAA GCGTCGTGCC TATCTGGACT TTATTTTAAA GGCTGTTTCAAG AAGGTGCCCTG	4980
GGAAGATTG GCAAAATCTC TATCTGCGTT CTTATCTGCG AAATGGCGAC CTCTTTGCTC	5040
TCAGTCTTCG TCTTCTCTG CTTTCCTTGC TGGCGCAGGT TTTTATCGAG CAAGCTTGGA	5100
TTGCGACAGC AGTGGTAGTT CTCTTTAACT ACCTCTTGCT CTTCCAGTTG CTGGCCCTCT	5160
ATCATGCCTT TGAATACCAG TATTTGACCC AACTCTTTCC GCTGGACAAG GGGCAAAAGG	5220
AAAAGGCTT ACAGGAGGTA GTTCGAGGAT TGACCAGTTT TGTTTTACTT GTGGAATTAG	5280
TTGTTGGGTT GATTACCTTC CAAGAAAAC TAGCCCTTCT AGCCTTACTA GGAGCTGGTT	5340

1148

TGGTTTTACT AGTCTTGAT TTGCCTTATC AGGTAAAACG TCAGATGCAG GACTAACATT	5400
GCTGATACGA CACTAAAAAA GAAGTTGAGT TCAGTCTGTC TCAACTTCTT TTTTGTTACT	5460
ACAGGATAAT GGTGGTCCG TAGAGACTTA TACTCTTCGA AAATCTCTTC AAACCACGTC	5520
AGCGTCGTCT TACCGTACTC AAGTACAGCT TCGGCTAGC TTCCTAGTTT GCTCTTTGAT	5580
TTTCATTGAG TATTAACCTG GTCTTGACTT GGTCAAAGTG GAAGCGGTCA TAGGCCCGCC	5640
AAGCGGCGCG AGTTGGAGCA TCTGGATCAA GAGCGCTGAG TCCCATGAGA AGACTGGAAG	5700
TCTGGTAAAA TTTTCTAGT TCAATCAAGA ATCGATTATC CACTGTTTCA GCCTTGGCTA	5760
GAAAACCAAG AATAGAGTTT AATTGCTCCT GAAAGCGAC GTCGTCAGCG CTTGCCTGTT	5820
TGCATGCTTG GTAGGCTTG TTTAAGTCAG TAATCAAAGT ATGAGCTCTT TTGATGGGGT	5880
CTGTATCTGT CATGGGAATG CCTCCTTTAA TCTGGTGCC AGTCTTACTT CTGGCAACTG	5940
TGTTTTGATA CTGTTAGTTT ATCACTTTTA ATTCTTTTTT TTTATTCAAA TCTTTAATTG	6000
TCATTGAAAT GTCTTGAATT GCGCTGAGTG AATTTTATGA TAAAATAGTT GTAAGCTCAT	6060
CATGATGTTG TAGAAAATAA TCCTTTTAGG AGTTTTCAAA GACTGTTTAG GATTGGGTGT	6120
GCTTGGGCTA GACCTTTTCT GTTATTCTTT TCTTAGGAGG AGAATCCAAT GAAATATATG	6180
ATTATTCAGA CGCAGAAAAC AGTCTATAAA GTAAACATCG ACGATATCTA CTATATCCAA	6240
ACACATCCAA CTAAAGCCCA TACCGTACAG ATTGTTACAG AAGAAGCTAG TTTTAATATG	6300
CTTCAAAATT TAAGTAATCT TGAGAACCA TGTGGGGAAA CCTTGATGAG ATGTCATCGA	6360
AATTGTTTGG TTAATCTTGA TAAATTAAAA TCGATTGATT TTCAAGAAAG AATCCTTTTT	6420
CTCGGAGAAG AAGGTCAATA CGCTGTCAAG TATGCCAGAC GTCGCTATAG AGAAATTCGT	6480
CAAAAATGGT TGAAAGAGGG AGAGTAAGAA GATGAGAATA TTTGTTTLAG AGGATGATTT	6540
TTCCCAACAG ACTAGAATTG AAACGACGAT TGAGAAACTT TTGAAAGCAC ATCATATCAT	6600
TCCTAGCTCT TTTGAGGTAT TTGGCAAGCC GGACCAACTG CTGGCTGAAG TGCATGAGAA	6660
GGGGGCCCAT CAGCTATTCT TTTTGGATAT TGAGATTGCA AATGAAGAGA TGAAGGGACT	6720
GGAAGTGGCT AGAAAGATTC GGGATCGGGA TCCTTATGCC CTGATTGTCT TTGTGACGAC	6780
TCACTCGGAG TTTATGCCCC TGTCTTTTCG CTACCAAGTG TCTGCTTTGG ACTACATTGA	6840
TAAGGCCTTG TCAGCAGAGG AGTTTGAATC TCGGATCGAG ACAGCCCTCC TCTATGCCAA	6900
TAGTCAAGAT AGTAAAAGTC TGGCGGAAGA TTGCTTTTAC TTTAAATCAA AATTTGCCCA	6960
ATTTCACTAT CCTTTTAAAG AGGTTTACTA TCTCGAAACG TCGCCAGAG CCCATCGTGT	7020
TATTCTCTAT ACCAAGACAG ACAGGCTGGA ATTTACAGCG AGTTTAGAGG AGGTTTTCOA	7080
GCAGGAGCCC CGTCTCTTGC AGTGCCACCG CTCTTTTCTC ATCAATCCTG CAAATGTGGT	7140

1149

GCATTTGGAT AAGAAAGAAA AACTGCTTTT CTTT

7174

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CCACCAGGGA AAATCATTGA AGTTGGTAGT CACCAAGAGT TAATGCAGGC GCAAAGTTTC	60
TACCATCATC TATTCAATAA ATAAGGAGAA TGTCATGAAT CCTAATCTTT TTAGAAGCGT	120
CGAGTTTAT CAGAGACGTT ACCATACTA TGCACAGTG TTAATTATAC CTCCTTCATT	180
ACTATTTACT TTCATCTTGA TTTTCTCCCT TGGTGCCACA AAAGAAATTA CTGTTACTTC	240
CCAAGGAGAA ATCGCCCTA CAGTGTCATT GCCTCCATTC AGTCAACCAG TGATAATCCT	300
ATCCTAGCTA ATCATTTAGT GGCAAATCAA GTAGTTGAAA AAGGGGACTT ACTCATCAA	360
TACTCTGAAA CAATGGAAGA AAGTCAGAAA ACTGCCTTAG CAACTCAATT ACAAGACTT	420
GAGAAGCAAA AAGAAGGACT TGAATTTTG AAACAAAGCT TAGAAAAAGC GACTGATCTT	480
TTTCTGGCG AGGATGAATT TGGCTACCAT AATACCTTTA TGAATTTTAC TAAACAATCC	540
CATGATATTG AACTGGGTAT CACAAAGACT AACCCGAAG TTTCAAATCA AGCTAATCTT	600
TCCAATAGCA GTTCATCAGC TATTGAACAA GAAATTACAA AAGTTCAACA ACAAAATGGA	660
GAATATCAAG AGTTGAGAGA TGCTATCATA AATAACAGAG CACGCTTACC AACTGGCAAT	720
CCGCACCAGT CAATTTTGAA TCGTTATCTT GTAGCCTCAC AAGGACAAAC ACAAGGAACT	780
GCAGAGGAGC CATTTTATC TCAAATTAAT CAAAGTATTG CAGGTCTTGA ATCATCTATC	840
GCAAGCCTCA AAATTCAGCA AGCTGGTATC GGAAGTGTAG CAACTTATGA TAACAGTTTA	900
GCAACCAAAA TTGAAGTACT CCGCACTCAG TTTTACAGA CAGCCTCACA GCAACAACCTA	960
ACTGTGGAGA ATCAATTAAC AGAATTAAAA GTACAACCTAG ATCAAGCCAC ACAGCGTTTG	1020
GAAAACAATA CCTTAACCTC CCAAGTAAA GGTATCGTTC ATCTGAACAG CGAATTTGAA	1080
GGTAAAAATA GAATTCCAAC TGGTACAGAA ATTGCTCAA TATTCCTGT CATCACAGAT	1140
ACAAGAGAAG TACTAATCAC TTAACGTA TCTTCTGACT ATCTACCTCT ACTAGATAAA	1200
GGACAACTG TAAGATTAAA ACTGGAGAAG ATTGGAATC ACGGCACCAC CATCATCGGC	1260
CAACTTCAGA CAATTGATCA AACTCCTACC AGAACAGAGC AAGGAAATCT CTTTAAATTA	1320

1150

ACCGCTCTTG CAAAACTATC TAACGAGGAT AGTAAACTCA TCCAATATGG CTTACAAGGT	1380
CGCGTCACTA GTGTAAC TAC AAAGAAAACA TATTTTGATT ATTTCAAAGA TAAAAATTTA	1440
ACACATTCTG ATTAATTTTC AGATAACACT CTATAACTAT TTATTATCTT ATCAAAAAGG	1500
AGAATCATAA CATGGATAAG AAACAAAACC TAACTTCATT TCAAGAACTA ACAACTACCG	1560
AACTCAATCA AATTACAGGT GGAGGATTGT GGAAGATTT ATTATATAAC ATTAATAGAT	1620
ATGCTCATTA CATCACATAA GAACTTCATC ATCCAATACA ACTATAAAAA AATAAGACCG	1680
AGAAACAAGT ACTCTCGGTC TTATTTTTC TCACTTCGTA TGTATCACAG TAAGTACCTG	1740
ACGAAAGACT TGATTTTGAC AGGTGGTATT TAGACTGGTA TTAGGATGGC TTTCCACAAT	1800
CTTCATGACG GTATAGAGAC CAACTCCTCT CTCCTCCCCT TTAGAAGTGG CTCCAAAGGA	1860
GAAGATTTC GAAATATCGA TGCCCTCTTC TTTGATGGAG TTTTCGATGA TAAAGGTCTC	1920
CTGTGCTCCA TTTTAAAA AGGCGATTGA AACATGAGGT TGACTAGCTT CCACACTGGC	1980
TTCAATAGCA TTGTCAAAA GGATAGACAC AATGGTTAGA AAATCAAGTA GACTCATCCC	2040
CTCGACCTGA ATCTCCTCAG GAACTTCGAC ATTAAAGACA ATGTTCTTAT CTCTGGCTTT	2100
TAAAAATTC CCTGCTAGAA GACTTTTGAG GGCTTTATCA CGAATATTTA CCAATCTGCC	2160
CAGGTCATAT TTATTGTTCT GCAATTTCTG ACTGGAATCC TTTAAGACGG AGCCATAGAC	2220
CTCTTTTATC TGCTCCATAT CCTCCTCTTC AATGCCCAGA CGTAAGCTAG TCAAGAGGTT	2280
GGTATAATCA TGACGAAAGC TCCGTACTTC CTTGTAAAGC TCCTCTATAT GCCGACTATA	2340
GCGTTCCATA TCTCTATAGC GCAGGGCCTG CTCTTGTTCC AATCTCTCAT AGAGTTTTTC	2400
CTTCAAATAG GTATCCAATT TCTTGATAAC CCCCATAAAA AAGAGTAGGT AAAAGACTAG	2460
GATGAGATGG CGAACAGTCT TTGATTGAAT ACTTTGTTCA TATTCAAAAA AAGACAGACT	2520
TTCCATGACT AGATAGTAGC CACCCATTAT CCAGTTAATC TGAGTCAGGG ACTTTTGAAA	2580
GGCTTTTATCG AGAATCTCCT TTCTCAAGCT AGTAAAATCG TAGTCCAACC ATTTCAAAAA	2640
AGCTAGAGAA ATGAAGAAAT TGAAAATTAT TATACATAAC CCAGTAAATG AGTAGCCATC	2700
ATATACTTGC CCTTGTCCTA AAAATGGAAG CACAAAATAG GAGACTCCTC TATAAAGAG	2760
ATTCAACCAAT ATCATTTGGA AGAGACCATA AAAGAAAAGG AGTTTTTTAG GAAGCCCTCT	2820
CAATAATAAG AAAGATAAGC CTATGCCGTA CAAGGGTTCC ATAAAAATAAG ATAGGTAAAC	2880
ATTTCTTACT ATATAGCTAA TCATCACAAA AACAAAGGCC AACAGTATCT TCAAAAGAAA	2940
GGCCTTAAAA ATCTCTCGA AAGTAAGATC AATCCATCC ACCTTAAAGA AGATGACAAT	3000
TTCTAGTCCA TTAGTAACAA GTGTATACAA CAATATCCAA GCAATGTTCA TAAATTCTCC	3060
TAGCTCAGTG TAATTTATTG ATGGCCTCAG AACTTCCCT GACCTTATAA CGGGCGATTA	3120

1151

GACAACTTCC ACCATTGGGA GAGAAGAGCA GTTTTCTTT CTTATCCAAA TGCACCACAT 3180

TGCGAGGATT GATGAGAAAA GAGCGGT 3207

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CTGAATCAAG TGTACTGCAC CAGTTCGTGC ATCAGGCATA ACAACATCTA CAGATATAAT 60

ATTGTTTTCT GAGTCCGCCT CATAAGTTAA AATCATAAAT TTTTCGATAT TCGAATTTTT 120

AGTAGCTTGT TCAATTTCTT GAATCATTTT ATCAGAACT AACTCCATCT GAATTGGAAA 180

GGAATGACTA TTTTCATCAT TTTGTAGGA AGAATGTGA TTAAGATAAA GTGTATTCAT 240

CTGAGCATAT TCAAATAAGT AGCCACTCTT ATTTTTTGT ACCAAAGGAA ATTGGTTTGT 300

AAGTCGCTT TACCCTTTA TAATTAACAA TACTTTCCCA TATTTTCTG TATTTGTTTC 360

AAATTCATAA TATCCCAAAG TCTGTCCTGC TAATTGTAAT TTATACTCAA ACAATCTGC 420

TGATGCAAAT GCAGTATCAA TATGATTAGG TCGCGTCCAT GCATAACCAT TCGACACTAT 480

CATTGTCTCT CTTTTTCTA GACGTTTCATC TACATAATCT TTTTGCCCTT TCATCAAAGT 540

ATCTACAATT TTTGTGCCT CAAGCGAATC AAAGAGATCC TGATTCAACA TAATCTCTCC 600

TCCTCCAAAT ACTTTTAAT GAATTATACC ATTTCTTAA AGAAATTACT ACAATAATTA 660

TCTTTTCTT AAAGTTCTGT GTCAGAGTAA TTTAGAAAAT TATATCTTCT ATAGTAAAAT 720

CAATTAAAAA CTGAACAAAT TTATTGGGAA ATTCAAATCG CTTTCTGAAA ATATTTTAGG 780

AACCGTAGTG TAATATTCCA GATTCAATTC ACTATAAAAC TGACCTTTCT CCTGCAAAAG 840

AAAAGGAAA GACTTCCTTT CGTGCCTTC CTCTTACTTG CTACTTGTGT GATTATTTTT 900

GGTAAGCTAC TGCTTGTCTG ATAAAATCCT GAATCGGCTC TCCTTGGTGG AGAGCTTTTA 960

CTATTTTCGA ACCGACGATA ACACCATCTG ACACCGCATT GAAGCGTTCC AGATCGGCTT 1020

GACTAGATAC ACCAAAACCT GTCAAGACTG GGATGTCGGC CACTTGATGA AGTTGCGCCA 1080

AGTGCTTGTC CAAATCTGCA CGGTAATTGC CTGATTCCC TGTCACCTCA TTGATGGCAA 1140

CGGCATAGAT GAATCCCTCC GCCCCTTCAA TCAACTCTTT CTGGCGCTCA ATTCCTGTGG 1200

TCAAGCTTAC TAAAGGAATC AAGGCGATAT CTGTATTGTC CAAAAATGGT TCTACAAAGT 1260

1152

TGGCATGTTC ATGAGGCAGG TCTGGGATAA TCAAGCCCTT CACAGCTGTA TCAGCCAGAT	1320
CTTTGACAAA GTTCTCCACA CCGTACTGAA AGAGGGGGTT GAAGTAGGTC ATGATGACCA	1380
GTGGAATCTC TGTTC AATG GTTTTCAAGG TTTCAACTAA AGCCTGGGTA GAGGTCCCGT	1440
GGGCTAAACT GCGCAAGCCA GCTTCTTCGA TAACAGGTCC ATCTGCAACA GGGTCTGAAA	1500
AGGGAATACC CACTTCAATT GCAGAGACAC CCAAATCTTC TAAAAAGTGA ATTGTTTCAG	1560
CAAGACCGTC CAAACCTTTC TCGTGGTCAC CAGCCATGAT ATAGGGAACA AAAATTCCTT	1620
TTCCAGCTGC TTTAATAGCA TTTAATTTT CTGTTAGTGT CTTAGGCATG AGCTTCTCCC	1680
TTCTTTGCTG CATCTGCTTC CAAGCGGTCC TTGACTTGAA CCACATCCTT GTCCCCACGA	1740
CCTGATAGGC AGACAATCAT AGACTTTTCT GGTCCAAGTT CTTTGGCCAA TTTCACCGCA	1800
AAGGCGATAG CATGGCTAGA TTCCAAGGCT GGGATAATCC CTTCCACACG AGACAAGAGT	1860
TGGAATCCTT CCAAGGCTTC TTCGTCTGTC ACAGGGACAT AGCTGGCAGC TTTAATATCG	1920
TGGTAGTGAG AATGCTCTGG ACCGATACCA GGATAGTCCA AACCTGCTGA GATAGAGAAG	1980
GCTTCAAGAA TTTGACCATG GGCATCTTGG AGCACATCCA TGAGGGAACC GTGAAGGACA	2040
CCTGGACGAC CCTTGGTCAA GGTAGCTGCG TGGTGCTCTG TATCCACACC AAGCCCTGCT	2100
GCTTCAGTTC CATACATAGC TACTGACTCA TCTTCTACAA AGGGATGGAA GAGCCCATA	2160
GCATTCGACC CACCACCAAC ACAGGCTACT AGGGCATCTG GCAGATCTCG ACCTGTCAAG	2220
TCACGGTACT GTTGTTTAGC CTCTCGACCG ATGACACTTT GGAAGTCACG AACGATTCT	2280
GGAAATGGAT GAGGCCCCAA GGCAGAACCA AGGATATAGT GGGTATCGTC GATATTAGCC	2340
ACCCATGAAC GAAGGGCTGC ATTGACCGCA TCCTTGAGCA CGCGCGAACC ATCTGTTACA	2400
GCCTCGACCT TGGCTCCCAA AAGCTCCATG CGGAAGACAT TGAGGGCTTG GCGTTTGACA	2460
TCTTCCTCAC CCATGTAGAT GGTACATTCC ATGTAAAGA GGGCTGCAGC AGTGCAGTT	2520
GCCACACCGT GCTGACCAGC ACCCGTTTCT GCGATAATTT TCTTTTACC CATGCGTTTG	2580
GCAAGCCAAA CTTGTCCTAA GGCATTGTTA ATCTTGTTGG CTCCTGTATG GTTAAGGTCT	2640
TCCCGTTTGA GATAAATCTT GGCTCCGCCA ATATGCTGGG TCAAGTTTTT TCGTAATAA	2700
AGAGGAGTTT CACGTCCTAC GTACTGGCGC AAAAGCTGGT TTAATTCCTC TTGGAAACTT	2760
GGGTCTGCC T GACTTTCACG GTAGGCCTTC TCCAACCTCA AACTGCTGT CATCAATGTT	2820
TCTGGGACAA AACGTCCGCC GAATTTTCCG TAAAATCCAT CTTTATTTGG TTCTGATAT	2880
GCCATGCTTT ACCCTCTCTA TAAATCTTCT AATCTTTTCA TGATCTTTT GTCCATCTGT	2940
CTCCACTCCG CTCGATACAT CTACTGCATA GGGAGTAAAG TGTGAATTG CTTTTACTAC	3000
ATTATCTTCA TTAAGGCCAC CTGCGATAAA GAAGGGCTGT GCTAGTCCAG TCGTATCCAG	3060

1153

TTGACCCCAA TCAAAGGGCT GGCCACTTCC TGCCACAGGG GCATCAAAGA GTAGATAATC	3120
TGCCTGAGAA TTGGGGACAT GCCCATTTCC ATCTACCTGC ACAGCCTGAA TACTGGCACA	3180
AGGCAAATTC TCAAATAAAT CATCTGCCAC CTGACCGTGA ACTTGAACCA AGTCCAAGCC	3240
AACCTTGTCA ATCGCTTCCA GCAGTTCTAC CCGACTTGGT GAAACAAATA CTCCAACCTT	3300
TTTCACATCT GCAGGAATAA GCTTTGCCAA CTCAGCTGCC TCTTCTAAAG TCACCTGTCT	3360
TTTACTAGGT GCAAAGACAA AACCGATATA GTCGGCTCCT GCTGAAACGG CTGTTTCCAC	3420
CGCTTCTTTG GTCGATAGTC CACAAATTTT AACCTTTGTC AATCTGCAAC TCCTTGATTC	3480
TCTGGGCCAC ATTTTCTGCC TGCATAAGAG CTGTCCCTAC CAAATTTCCG TTAAAGTATG	3540
GGGCTAGTCG TTCCGCATCC TGCCCTGTGA AAATGGCAGA TTCAGAAATG TAATAGCGAC	3600
CTTCCTCAAA GTAAGGGGCT AAATCTACAC TGGTCTGCAA GTCGACCTCA AAGGTAGTCA	3660
AGTTGCGGTT GTTGACCCCG ATAATCTCAG CACCAAGTCT GTGGGCTACC TCTAGTTCAG	3720
CTAGATTGTG AGTCTCCACT AAGACTTCCA GACCAAGCTC TGTCGCGTAG TCATACAGTT	3780
CCTTGAGGCG TTCTTCGGAC AAGGCTGCCA CAATGAGCAA GATAACTGTC GCACCTGCAT	3840
TGCGAGCGCG GATGATTTGC TTTTCATCGA TGATAAAGTC TTTGTTGAGC GTCGGAATCT	3900
CTACCTGACT GGAAATTTCC CGTAGATAAT CCAAATGCCC TTAAAGAAA ACCTCATCTG	3960
TCAACACCGA AATCATCACT GTCCTGTTT CTTCATAAGT CTGGGCCTGT TGCACAATAT	4020
CCACATCGAG ATTGATATCT CCCAACTAG GGCTAGCTTT CTTGACCTCA GCGATTACCT	4080
GCAAGCGGTC CTGATGATTC TTCAAAAATT CTGCCAAGCG ATAGGTCTGG CGCAGAGGCT	4140
GGATTTGCTC CAGCTTCATC TGCTCCACCT CACGCGCCTT CTGCTCTAAG ATTCGTGCTA	4200
AAAATTCCTG ACTCATTTT GGTACTCCTG TAACAGTCTG AGTTTTTCAA GGGCCTTGCC	4260
TCTAGCAATC ACTTGACGGG CCAAGGCAAC CCCTTCCTTG ATGCTATCAA TCTTACCATT	4320
AGCATAGAAA CCAAGACCAG CATTCAAGAC TGTCGTTTCC AAGAATGGAC TTGCTTCGTT	4380
TTTCAGAACG CTAAGCAAAA TTCTGCATT TTCTGAGCA TTCCCACCAC GAATATCTTC	4440
CATAGCATAG CCTTCCATT CCAAATCCTC TGGAGTAAAG CTGACAAGC TGATTTGCCC	4500
ATTTTCAAGA AGTGCAATCT TGGTTGTTCC GTTCAAGCCA GCTTCATCCA ACCCTTCTGG	4560
TCCAGCAACC ACGATGGCAC GTTTGCGACC CATATTTTTC AAAACCTGAG CTGTACTTTC	4620
TAGGAGTTCT GGACGACTAA TTCCAAGAAG CTGTGTTTCT AAAGCCATTG GATGAATCAG	4680
TGGACCAGTC AAGTTCATAA TCGTTGGAAT TCCAATTC AAACGAGCTG GCATGATGTA	4740
TTTCATAGCT GGGTGCATAT TTTTAGCGAA GAGAAAGACG ATTCCAGTTT TATCAAAGAC	4800

1154

CTTACCTAGT TCAGCTGGTT TGAGGTCAAG ATTGATTCCC AAGGCTTCGA GGACATCTGC	4860
GGAACCAGAT TTAGAAGATA TCGAGCGGTT ACCGTGTTTG GCCATGTGAA TACCGCCACC	4920
AGCCAAGACA AAGGCTGCAG TTGTGGAAAT ATTAATACTG AAAGACTTGT CCCACCTGT	4980
ACCACAGTTG TCCATGGCAT CATGAATCTC AGTTGGAATA TGCTGGGCAT GTCCTCTCAT	5040
GACTTGGGCA ATGGCTGTGC GTTCTTCAGG TGTTCCTCCC TTCATCTTAA GAGCTAAGAG	5100
GAGAGAAGCA ATCTGCGCTT CAGTTACACG CCCAGTTACG ATACGCTCAA TGACATCCGT	5160
CATTTCCACA CCTGATAAAT TTTCAAATTT TGCTAGTTTT TCAATAATCT CTTTCATCCT	5220
AGTTTCCTCA CTTTACAACC TCCTCGATAA AATTCCGAAT AGAAGACAAG CCGTCTGGCG	5280
TTCCAATGCT CTCTGGATGG TACTGGAAGC CATAAATCGG TAGGTTTTTA TGTGTAATCC	5340
CCATGATGGC TTGGTCATCA GTCGAACGAG CTGTCACTTC AAAGTCTTCT GGCAATTCCT	5400
CAATCAAAAT ACTGTGATAA CGCATGACCG CACGGCCATC CTCAATACCT TGATACAAAA	5460
CAGATGGCGC TTCAAAGTTG ATATTGCTCT GTTTCCTATG CATGACTTTT GGAGCCAAAC	5520
CTAGCTTACC ACCAAAGACT TCTGCAATGG CTGGTGGCC CAAACAAATC CCAAGAATCG	5580
GCTTCTTGCC TGCAAAATCA CGAATCATGT CTTCATCTT TCCAGCATCA ACTGGCCAAC	5640
CAGGACCAGG AGAAAAGACC AGACCATCTG CTTTTTCAGC TTCTTCATAC AGCTTGAAT	5700
CATCATTTCT CAGAACCTGA ACTTCTGCAA AATTCCTAAT GTATTGGGCC AAGTTATAGG	5760
TAAAAGAATC ATAGTTGTCA ATCAATAAAA TCATGGTCTT AGTTCTCAA TTCTAGTCAT	5820
AGATTTTGCT TTGTTAATGG TTTCTTGTA TTCGTTTGG GCGATAGAGT CGTAGACAA	5880
CCCTGCCCCA GCCTGCACAT AGGCTCTTTG ATTTTGTAGA ATCATGGTTC GGATGGCGAT	5940
GGCCAAATCC ATATCACCCG TCGCAGACAA GTAGCCGATT GCCCCAGCGT ATACTCCCCG	6000
TTTTTCCGTT TCCAGTTCAT AGATACGTCT CATCGCTCGA ATCTTTGGTG CTCCAGAAAC	6060
GGTTCCAGCA GGAAGCGTTG CTTTCAAGGC ATCCATGGCA GTGAGTTCTG GAAGCAAACG	6120
CCCCTTGACT ACGCTGGTCA AATGCATGAC GTAGCGGAAG AGCTCCACTT CCATATACTT	6180
AGTGACTTGG ACACTGGTCG TTTCAGAGAT GCGGCCAATA TCGTTACGCC CCAAGTCTAC	6240
CAACATTCGA TGTTCGTCTG TTTCCTTCTC ATCAGAGAGG AGGTCAGTCG CCAAGGCCTT	6300
GTCTTCTTCA TCCGTAGCCC CTCTTGGTCG CGTCCCTGCA ATCGGATTGG TTGTCACGAT	6360
GCCATTTTGT ACAGAAACCA AACTTTCTGG ACTAGCTCCG ATGATTTGAT AATCCCCAAA	6420
ATCATAGAAA TAAAGGTAAT TAGAAGGATT AGTCACGCGG AGATTTCTGT AGAAGTCAAA	6480
TGGATTTCCA GTAACCTCTG CTGAAAAACG CTGGCTGAGT ACACATTGGA ACATATCTCC	6540
GTTACGAATC AAGTCACGAG CTGTTTCTAC CATTCCTCA AACTTATGTG GAGCGATATG	6600

1155

CGGTTTGAAG TCTAACGGAG ATAGATCCAA ATCTTCAAAT TCATTTGGAG CAGGAATGCG	6660
TAATTCCTCA AGCACTTGGT TCAAGGATTT TTCCAAGGCC TCTTGACTGC GCTCACTATA	6720
AAGTGCATCC TCTATGACAT GTATCTTCTC CTTCTTGTGG TCAAAGACCA TATAGCTCTC	6780
ATAGACAAAG AAATGCATGT CTGGCGTCCC AATTGTATCC TCAGGGATTT GACCAATTTT	6840
TTCATAAAGC GAAATCATAT CGTAACCCAC AAAACCAATG GCTCCACCAC CAAAAGGTAG	6900
CTCTGAGTGG TGCTGACTCT TATGAATCAC TTCATAAAGG AAATCCAAGG GATCCCGATC	6960
AATCACTTGA CCATTTTGAT AGAGAACCCC ATTTTCAAAC TTAATCTCAA AAACCTGGATT	7020
ATAGGCTAGG ATAGAAAAAC GAGCTGTTTC CTTGTCTCTC GGAATACTCT CTAAAATAAC	7080
CTTATGTTGC CCCTTTAAGC GCATATAAGC CAAGATTGGT GATAAGACAT CTCCATGAAT	7140
GATTCGTTCC ATTGTAATTT CCCTTTCAGT TCTACTTCTA GTCCGTGGTG ACTGTATGAA	7200
AAATCCCCAC GCAAATAAC TTGCGTGAGG ACGAAATTCG CGGTGCCACC TCAATTATAG	7260
GATTTCTCCT ATCTCTCATT CCGTCTCAG ATATCTCCTG TAACAGGCTG TGCGATAAAG	7320
GGCACTCCCT TGAGAATGAT GTTTTCTTCT CTCGTTTCAG ATGAACCCAA CTTTACAGCT	7380
TTCTCTGCTT GTTTTCAGCA ACCACAAGCT CTCTGTGAGA GAAAGAACTG TAATTTTCC	7440
ATCTATTATT TTTTAGCTTC TAGTAGTCTG CAATCGCAGC TAGGTCCTTG CCTCCACGAC	7500
CAGAGACATT GATGAAGAGA TGTTCATCTC GGTACACCTT TATACTCTTC GAAAATCTCT	7560
TCAAACCGCG TCAACGTCGC CTTGCCGTAG GTATGGTTAC TGACTTCGTC AGTTCTATCT	7620
GCAACCTCAA AACAGTGTTT TGAGCTGACT TCGTCAGTTC TATCCACAAC CTCAAAACAG	7680
TGTTTTGAGC TGACTTCGTC AGTTCTATCC ACAACCTCAA AACAGTGTTT TGAGCTGACT	7740
TCGTCAGTTC TATCCACAAC CTCAAAACAG TGTTTTGAGC AGCCTGCCGC TAGTTTCCTA	7800
GTTTGCTCTT TGATTTTCAT TGAGTATTAC TAGCTTTTTT CGTATTAGTC CAGCCTTTTT	7860
GTTTGCTTTT AGTAGTAGGC ATGGAGCTGT AGATAGAACT CAAGTTCATC AAAGCGACTT	7920
AAGGCCCTAA TAAAAGATAA ACCAAACGAC GGATAGAAAA AAGCCACAC ACAGAATATA	7980
CTTCCGTGTG AGGGCGTTGG TAACGCGGTG CCACCTCAAT TATAAAGGGA CTATCCCTTT	8040
ACATCTCTGC CTTGTTTAAC AACAAAGCTGC ACTGTAAGGT GTGCGCACCG AATTTTCATT	8100
GTTTCAAATT CATTTTCAAA ATCAGCCAC TTTCCTACT TCCAACCACC TATTCACAAT	8160
CACCACAGGC TCCCTGAAGA TCAAAAATAG TTACTTTTCT GATTTGTTGA ACTTATTTTA	8220
ATACTTTGTT TTTTCTTTGT CAAGACTTTT TTACGATTTT TTTGAAAATA TCATTGGAAT	8280
ATGACCATGT CTTCCCTAGA TCGAACATGA ACATGTCCCA CTTCTTAGAA ATTGGATCCA	8340

1156					
ACTCAATAGA	AACTGAATGG	AGGCTAAACA	GAACCTATTT	TAGAACACTC	CATCTTTTCC
8400					
ACTAGGATTT	TCAAGAATTA	AACAATACTA	GAAACTCTGT	CTCCTAACAA	ATTTAGGAGA
8460					
AACTTCAACA	GATGTGACAC	TTTCCCCTTT	AATAATTGCT	AAAACACCTT	CTATCATTTT
8520					
TTTAGCCAAT	TTAACATAAT	TGGGAGCAAT	TGTAGACAAA	GCTGGAGTAT	AATACTGAGA
8580					
AATAGGAATA	TTATCAAAATC	CAATGATAGA	AATATCATCT	GGAATAAGAA	TTCTTTTCTC
8640					
ATAGCACGCA	CGAATCAAGC	CCTGAACCTT	TTCATCTCCT	GAAACAAAAA	TAATGTCCGG
8700					
ATAATTTTGG	GTAGTCAAGT	GCTGCATTGC	ATAAGAATAA	ACTGAATCAA	TTGTAGATAA
8760					
GCCATAAATG	ACTTTTAAAT	CCATAAAGTA	ATTTTATCA	TTCAGAAAAG	AACGCACACC
8820					
TCTTTCACGA	TCCTTATTAA	CATGGGATTC	TCCTCCCAT	AGCAACCACA	TATTTTTTAA
8880					
TTTTTCTTCA	GTTACAGCTT	TCATCATATC	ATAAGTAGCT	TGAAAATTAT	TATTAGATAC
8940					
ATAGACTACT	CCAGACGTTT	GAGATTCACC	GAAAACAAGA	AAAGGCATAT	GGTCTTCTT
9000					
TAAATACTGA	ATTCTGATAT	CATCTACACT	TTCATAAAAA	ACAATAACAC	CATCTACTAG
9060					
GCTACCTGTG	CTTGATATAA	TTGAATTACT	AATGTATCC	TCCTCTCAA	AGTACTCAAC
9120					
TATAGCATTA	ACACCAAATT	CTTTACACGT	CCGTAACACT	TTATCTAACA	GCGTATGAAA
9180					
CCAAATTA	GGAAAAGAGT	CGATTTTTT	TACAGAAATC	AATATATTTA	TAGCTTCTTT
9240					
TTTAGTTAAA	TTTTTTGCAT	ACGCATTTGG	AATATACGAC	AATTCCTCTA	TAACTTTTTG
9300					
AATCGCTTGA	TAAGTTTCTT	CTTTAACATT	TACTCCACCA	TTAATAAATC	GTGAAACTGT
9360					
TTTTGGAGAA	AAACCTGATA	AACGTGCAAT	ATCATAAATA	GTTACCTTTT	TCCCATTAT
9420					
ATTTTTCATT	TCAGTCCTCC	ATTACGAACA	TTCTAATATT	ACTATACAAT	ATTTAATTTT
9480					
TTTTAACAAG	AGAATTTAGT	AAATTATTTA	AGATCCACAA	ATTCACAAAA	TTAATTTTAC
9540					
AAATATTCTT	CCCCTTCAAA	AAAGTTTAAA	TTGCATTTC	CACCTTTATT	TTTAAGAATG
9600					
TTTCCAACCT	CACGACAAAT	AAATTCATAT	GAGAAAAAAC	TGCCATAAAA	TTGTAGATTA
9660					
ACTTTTTCAG	TAAAATGTGT	AGGATTTATA	AAAACATATA	ATAGCCTGTC	AATGTAACAT
9720					
TTTAACATAG	AGTTAATTTT	TTCTTTAAAG	ATAACATTG	TTATCAACTC	ATCAGGAGGT
9780					
AAATGAAAGG	CAAACACCAT	TTACACAAATA	TCATAAAAAG	AAATAAATTT	GTATACTTGT
9840					
ATCAACAAT	TATTATCAAA	ATATTCTATT	TTACCTAAAT	CAAAATTGAT	TTTATAATCT
9900					
TTCATAAAAA	CCTCTGAGCA	AAAATCTACT	CAAAAATTAG	ATGATTAAAA	CATCTAAAAA
9960					
GCAAAAGGAC	AAAAACATCT	GTCCCTTTGT	TTACTAAATT	TCAGCTAATT	TCTTCGACAT
10020					
AAATAACACC	TACAATATTA	GCAATTTCTT	CCATCAGTCG	AAGATGTTCA	AATCTACCTG
10080					
ATAATTCAG	AGTAATAAAT	GACGCTATTT	TTTTGTCCGG	AACATCAAAG	TATTCAAATC
10140					

1157

TGTCAGAATT AACATCTCCA AACGCTGTTT TTGAATCGGT CATTCTGATA CCATTTTCTG	10200
CACAATAAAC CAATACACGA TTATAGGCTT CTGTAGATTT AACCCTATA TACAATTCAA	10260
TCATTTTAGA ACGATTTTGC AGATATTTT TTAGTGGTTG GAACATGGAT ATCACACCCC	10320
AAACAGAAAT GGCTACTAAA AGAGCTCCCT CATAAGG	10357

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6867 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

CGGGACATTC TCAATCTTCT GTCTTTTGTT TTTCTCTTCT TTCTATGATA CAATGGAAAA	60
AATAAATCA AAAGGAGTTT TTTTATGACT TATCCAAATC TCTTGGACCG CTCTTTAACC	120
TATGTTAAGG TCAACACGCG CTCTGATGAA CACTCTACTA CTACTCCAAG TACACAGAGT	180
CAGGTTGACT TCGCAACAAA TGTCTTAATT CCTGAAATGA AACGTGTTGG ACTGCAAAAT	240
GTTTACTATC TACCGAATGG TTTTGCTATT GGAACCTTGC CAGCCAACGA TCCGTCTTTA	300
ACACGTAAGA TTGGTTTAT ATCGCACATG GATACTGCTG ATTTTAATGC TGAAGGAGTC	360
AATCCACAGG TAATTGAAAA CTACGATGGT GGTGTGATTG AACTAGGGAA TTCTGGTTTC	420
AAACTCGATC CAGCTGACTT CAAGAGTCTT GAAAAATATC CAGGACAAAC GCTCATCACA	480
ACAGATGGAA CAACCTTGCT AGGTGCTGAT GACAAGTCAG GAATTGCTGA AATTATGACA	540
GCCATTGAAT ATCTAATGCG TCATCCTGAA ATTAAGCACT GTGAGATTGG TGTGGGTTT	600
GGTCCAGATG AAGAAATCGG TGTGGTGCC AATAAATTG ATGCAGAAGA TTTTGATGTG	660
GATTTTGCCT ACACTGTTGA TGGTGGTCCA CTAGGTGAAC TTCAGTACGA GACTTTCTCA	720
GCCGCTGGTG CTGAATTGCA TTTCCAAGGT CGTAATGTCC ACCCTGGTAC TGCCAAAGGG	780
CAGATGGTCA ATGCCCTTCA GCTAGCAATT GATTTTCATA ATCAACTTCC AGAAAAATGAC	840
CGACCTGAGT TAACTGAAGG TTACCAAGGT TTTTACCATC TAATGGATGT GACAGGTAGT	900
GTTGAGGAGG CGCGTGCAAG CTACATCATT CGTGATTTTG AAAAAGATGC CTTTGAAGCG	960
CGTAAAGCAT CCATGCAATC TATCGCTGAT AAGATGAATG AAGAACTTGG GAGCGACCGT	1020
GTCACCTCA ACTTGACAGA CCAGTACTAC AATATGAAAG AAGTCATTGA AAAAGATATG	1080
ACTCCAATTA CCATTGCTAA AGCCGTTATG GAAGATCTAG GTATCACGCC TATTATCGAA	1140

1158

CCAATCCGGG GTGGAACAGA CGGCTCTAAG ATTTCCCTTTA TGGGAATCCC AACTCCGAAT	1200
ATCTTTGCAG GTGGCGAAAA TATGCACGGA CGTTTTGAAT ACGTTAGCCT TCAGACTATG	1260
GAACGTGCAG TTGATACCAT CATTGGCATC GTAGCTTATA AAGGCTAAAA AGACGAGGTA	1320
GCTCAGCTAC TTCGCCTTTC TTTTATTCT ACTGGTTTTT CTTGATTTCC AGTAGTTGTA	1380
GAAGATTCTG TTGTTTCATT TTCTGAAGTT GATTTCAGCAG GTTTAGAATC TCTTGTATTG	1440
CTTGTTTGT TTTGCTCGCT AGCAGTTTCA ATGTTAGATT CTGCAGTTGC GTTTGGTTGG	1500
TTCTCAGCAC TGGTGTATC ACCATTGCT TCAGCATTTT TGCTGGACT TGTTCCTTCA	1560
CTTGCGCTAG CTTTGGACTG GATTTGATGA TTCAAACTA GAATAGCTTT TGTGATTTCA	1620
AGTAAAGCTG TTTTGTCTTT ACTCTTAGCA GAAAGTTGAT CTAATAATGC ATCCACCTTA	1680
TCAAAGTCCG CATCAGATCC ATTATTACTT TCTAAATAAG AGTGAAGCGA CATGAGAATA	1740
TCGTAGAGTT TTTGATAGAG TACAAGTGC TGAGGATCTT GCTCAGCATT TTCCTTTTCT	1800
TGTTGAAGGG CGCTAGCGAT ACGAGTCAAG ACATCTTTTA CCTGACTGTT TACTTCATCC	1860
AAGTCTGCAT CAGCCTTGTT TGTGGCAGCT TTTAGATTTT CTACTTCTTC TGCCAAGGAT	1920
TGTCTGATTC CTCTTCATG GATTGTTC CAGAGTTGAT TTGCCTTGCT CAAAAGACTT	1980
TCTACTTCTT CCTTGCTATC TGTCGCAGAT TATTGGTTGC TATCTACCAT GTACTCCTAA	2040
AACAGGAGAG TTATAATCCA AGATTACAAG GCCTTACAGA AATAAGAAAT CCAGATAAGA	2100
CAATGTTTCGT CCAAGACGCT ATTCGCTTCG CACAGCAGCA CGGATTCAAT ATGCTTTAAT	2160
TTTAAAGTTT AGGTGTCAAG ACCTCTTTT AGTGTGCCCA AAATTTAGAG AAGTAATCAA	2220
TCAACTAACT TTTATTTTTT TCAAACCTTC AGTAACTGA CCTAAAGCTA ACTCAATCTG	2280
TCTTTGTAGA TGCTTCTGCT ATCAGCTAGA AGTTGATCTA CTTTGGCCAA GACTGCCTTC	2340
TCATCAAAAG TTCCAGGTTG ATAGTTGGAT TGCAGGGATG GAATCTTGTT TTTCAAAGCC	2400
GCTTCATATC CCTTAGTTTG AACCTTGATG TAGTGATTGT GGTCGCCATG AGGAATCACA	2460
AAACCTTCTG AATCTTCACT TATAATTCGA TTGGCATCAA AACCATGACC ATCTTCTTCC	2520
TCATGATGGA CATGTAGTGA CGGATTACTT AATACAGAAC TAGAAGAACT TCCTACCTCT	2580
TCCGTGTTAG AGTGTGATGG GGGATTGTTA AGAGATGACT TAGGAATATA GTGATAGTGA	2640
TCCCCATGTC TTAATATATA AGCATCACCT GTATCTCTGA CAATATCATT AGGGTTAAAG	2700
ACATATGTGG CTGCTAATTC ACCTGCCGAC AAGTCACTCT CAGGAATGAA ATGATAGTGA	2760
CCACCATGTG GTACTATAGT AGATTGAAAT AGAATATGAG CAAATTGATA AGGGGATTTT	2820
AAAGTAATTT CTAACAATGA TTTAGAACT ATGATGTGCT ATTCTAAATT CAACTCACTA	2880
TATATAACCA TCATCGGTAG TATAACGTCC CTGTAATTTT GCTACAGATA CTCTGCACT	2940

1159

AGCTCCTTTA TCGTCTTTAC CATGTTCTTG TTTTGGCGA TTGATTTTCAT CTTTGTTCG	3000
TACATTTTCT GCATGAGCTT GATCTTTAAG GTAAACATAA TACTTTCCAT CTACCTTAAT	3060
AATATATCCT CCCTTAACCT AACTGACGAT ATCTTGATCT TTCGGCTGAT AGTTGGGGGC	3120
TTTCATTAAAT AGCTCTTCAC TAAAGAGCGC ATCAAAAGGA ACTTTACCAT TATAGTAGTG	3180
ATAATGATCG CCATGAGAAG TTACATAACC TTGATCTGTA ATCTTAATAA CAATTTGTTT	3240
TGCTTGAATT CCTTCTTTT GACTAACCTA GTCTGGAGTC AAATTTTCAG TCTTCTTAGT	3300
GTCCTTATTA CTGTTTACAT ATGAAACACG ATTTTATCT GTATTGGCCT GTTAGCTATG	3360
TTGGTTCAGA GCATAAACAC ACAGACTTAA GGAAAGGATA ACAACAGATC CAGCTGCTAT	3420
ATATTTCTTT TTAATTTCA TAATTACCTC ATTTCTATAA TTATTTATAT GATGTCTTCA	3480
TTATTAAATG ATTAAATAA TTAATTAACC AATTAATTAA CTAGTAAATA TTCCACCTCT	3540
TTTTAAGTTG TATGTCAAGA AATTTTATAT ATTAATAATA AAATGAAATT CTCCCAAAGT	3600
CAGAGTTTAA TTTCTAACTT TTGAGAGAAC TTCATTTTTG ATTCAGACTT TTTCTACTGC	3660
TATTCCTTAC GCTATGAGAT CAGATAAATT CTTTTTATC ACTTCTCCAC TTGGCAATCT	3720
TAATTCATTC GTTCCATCCA TATTGAATAT AACACTATCT AAGCCTAATC CGTAACTAGC	3780
TGTAAATTTT TCTAATTTT CTTGTACAGG ATCTACTGCT GGAGCTTCCT CTAATGCTGG	3840
ATCTAACATA GGGTCACTCC CCACATTCCC TTCTGGATTC AACATTCCAT TATCCGTTGA	3900
GTTTTCTGGT TTTACAGGTT TTTCTTTGG TGCCCTCTGGT AAAGAATCTG CTGGTTTATT	3960
TTCTGTGGT TGGTCTCAA CTGTTCCAGT AGATACTTTT CCATTTTCAG ATGGTTTATT	4020
TTCAACATTT CCTTGAGGTG CTTCTCCTGT AAAATCTGCC ATATCTTTT TAATGACTTC	4080
TCCCGATGGT AAATATAATT CAATTGTTCC GTCCATATTA AACAAGACAT TTTCTAGCTT	4140
CATCCCATAA CTTTCAGCAA ATTTTGCTAC TTTTCTTGT ACAGGATCCA CTGTAGGAAC	4200
TTCTTCTAAC GTTGAATTAC TAGTACTATT CCCAGTTTCA GAAAGTTTTT CTTTTTCTAC	4260
CTTCTCACTA GTCTTTGGTT CTTCTACCTT TTCATCAAGT TTTAAGTTT CTTGTGCTTT	4320
ATTCCTTTTA AATTGTGGTA GAATACTTGG TTTATCAGTT TGATTTTCTT TTTCCAAGAT	4380
AGGTACTTCC ACAATATAAG TCGATTGATT GTCCAAATAA GCATTTGCCA TGAAGGTTAC	4440
AGGAATTTTA TTTCCGGCCG TTCTGGTTGT TCCTTGGTTT AATTTCCGAA TCGGTAATTT	4500
GATTTACCA ACTTTATAGT TATTTTCTAA ATAAGCATTT CCATGAAATT CATCAAACAC	4560
TCTGACTAAA GCATCAGTTC CTTTAGGCAC TGCAAATTGA GGGTTCACCTC TTAAATAAGT	4620
ATCCCCTGCA TGGAAAGGAT AGAAAATCGT TTGACTGGCC ATTTTGTAAG CTAAGAGGTT	4680

1160

TGGAACGTGA AATGTACCAT CATAACTTAC TTCTGGATAA TCTTTTGAAG CGATAGTATA	4740
CTTAAATGTT TGTCTGGTA AATAAGGTTG ATCTAATTCA AAGTTTGCAA TATTCCCTAC	4800
TCCTTCTCCA AATACTTTAC CAGATACTTT CTCCAATACT TTTCATCTG GTGTTATTAA	4860
TTTACTAGC ATATTGATAC CTAATTTTTT CTCCAATTCA GGCGGAAAAC TAAAAGAAAC	4920
GCGTTTTTGA CCATTGGCTA GAGTAAAGTT TTGATTATTA AACGTACTAT TTTTAAACAA	4980
ATTAACAACA TTCGTTAATT CTCTCCAGT ATAACTTTA TTCCCTTCTT TTTTAGCAAC	5040
TCCTTCTTCG GGTTTAAACA GTTCATAGTT ACTGTGAGAA TGACCAATTC CAACCGGTTT	5100
ATGTTTCATCA ATCGGATCTG CATGATGGTG ATCTCCATGC GGATAAATAA TCGCATTTTT	5160
TTCTTTATTC ACGACAATAC TTTCACGTTT GACACCATAT TGTTTCATAA TGCCAGCAAT	5220
TTTTTCTTCG ATTTTTTTAT CTAAATCTTT CATTTCTTTG GCATTACTTG GATAATCCTG	5280
TTTCATGAGAT GACAAAGAAT CTAATCCATT ATGACTAGTT TTAACCTCCT CTAAATGTTT	5340
TTGCGCAsCT TAATTGCTC TTCTGTCAAG TCCTTCTTGA AGAAATAATG ATTGTGGTCT	5400
CCGTGACTCA TGACAAAACC TGATTTCATCT TCAGCGATAA TACGATTAGC ATCAAATCCG	5460
TATCCATCTT CTCATGTTT CTCATGTGAA GTTCTGGAT TGATTGGAAG AGATGGAGAA	5520
GGTGTGCTA GACTATTGTT TGGAAGAGTC GGTGCCCCAA TTTGATTGTA TTTTGGAAATG	5580
TAATGGAAAT GATCACCATG TCTTACAATA TAAGCTGTAG CCGTTTCTTC AACGATATCT	5640
TTTGGATTAA AAATATAACC ATCAGATGCT GAAGAGAGCT CCTTACTTGT CGTTAAAGAA	5700
GAAGGATTGC TTGAAAGACT GCCTAGACTA GACACTACTT CATTAGGTTT TGCATTTGTA	5760
GAACTGTAG AACCAAGTCC ACTGATAGGC ACCATTCTGG CAATCTTTTC TTCTAAGGCA	5820
GAAAGCTTGC TGTAAGGAAT AAAGTGGTAA TGGTCGCCAT GCGGAATCGC AACTCCATTT	5880
GGTGTACGAC TGATAATCTT AGCAGGGTCA AAGACCAGGC CATCTGATTC ACTGTAACGT	5940
TGGGCGCTAG GTGAATCATA GAGTTCCTTC AAAAGACTCT GGAGATTTTC AGATTTATTT	6000
GCTGGCTTGC TAGTTGATCC TTTTGCTACA GATTGCGTGT TATTGTCACT AGCTGTTGAA	6060
GAATAGCTTA ACTGACTCGG TTGCATATTT TTTCCAGCCA GATGTGCTTT AGCTGCTGCT	6120
AATTCATAG CAGATAAATC GCTTTTGGGA ATGTAGTGAT AGTGACCTCC ATGAGGAACG	6180
ATATAAGCAT TACCCGTATC TTCGATAATA TCAGCTGGAT TAAAGACATA ACCATCATTT	6240
GTCGTATATC GTCCCTGAGA CCTTGCTACA GCAACATTAG AGTTAACCTT CTCATTATCT	6300
TTGACATGTT CTGTGTTTTG ACGATTGATT TCATCTTTAG TTCGAACATT ATCAGCATGA	6360
GCTGCATCTT TCAGGTAGAC ATAATATTTT CCATCGACCT TGATGATATA ACCACCTTG	6420
ACTTCATTGA CAATATCAGC GTCTTTAAGT TGATAGTTTG GATCCTTCAT CAAGAGTTCT	6480

1161

TCACTAAAGA GGGCATCATA AGGAACTTTC CCATTATAGT AATGATAGTG GTCACCGTGT	6540
GACGTTACAT AGCCCTGATC TGTAATTTTG ATTACAATTT GCTCAGCCTG AATTCCTTCT	6600
TTCTGGCTAA CCTGGTCTGG TGTCAAGTTT TCACTTTTCT GACTTGACTG GCTGCCATCC	6660
ACATAAGAGA CACGATTATT GTCCTTATTT TCCTGCGAAC GATGCTGGTT TAGTGCATAG	6720
GCACATAGAC TCAAGGATAC GATAACAGCT GATCCAGCTG CTATATATTT TTTACTAAAT	6780
TTTCATAAATC CCTCATTTCA ATAAATGATG AAGTTTTTTC TCAACTTCTT TTTACTTTAT	6840
AAATAGTTTT CTAAACCCGG GGTACC	6867

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

CGTTCTAAAA ATGCAGTACG TTTGATTGAG AAATCAGTTA AAGGTATGCT TCCACACAAT	60
AACTTGGGAC GCGCTCAAGG TATGAAGTTG AAAGTATTTG TTGGAGCTGA GCACACTCAC	120
GCTGCACAAC AACCAGAAGT TCTTGACATT TCAGGACTTA TCTAAGGAAA GGAACAATAA	180
AGTATGTCAC AAGCACAATA TGCAGGTACT GGACGTCGTA AAAACGCTGT TGCACGCGTT	240
GCGCTTGTTC CAGGAACTGG TAAATCACT GTTAACAAA AAGATGTTGA AGAGTACATC	300
CCACACGCTG ACCTTCGTCT TGTCATCAAC CAACCATTCG CAGTTACTTC AACTGTAGGT	360
TCATACGACG TTTTCGTTAA CGTTATAGGT GGTGGATACG CTGGTCAATC AGGAGCTATC	420
CGTCACGGTA TCGCTCGTGC CCTTCTTCAA GTAGACCCAG ACTTCCGCGA TTCATTGAAA	480
CGCGCAGGAC TTCTTACACG TGACTCACGT AAAGTTGAAC GTAAGAAACC AGGTCTTAAG	540
AAAGCTCGTA AAGCATCACA ATTTAGTAAA CGTTAATTCG AAAGAATTAC TATACTTATA	600
CAGAGCACCT TTCGGGGTGT TCTTTTTTTA TACTTTCTTA CTAAATTGGT GCAATTGACA	660
CAGTTGTTGC GACTTTAGTC GCTTACAAAT GTGGCTGCAA CCTGACATGG TCAGTTGCCT	720
CAAAACGTTA ATCAATACGA TTATATCAAC GTTTCAAAGC ACTCAAGGGT TTACCCTATG	780
GGTGCTTTTT TCTATACTTT CTAAAAAGT TTACCCTAAA ATTTGCCCTA AAATTACCTT	840
ACTTATTTTT AAGATGTTGG TAGGCAACTT GTCCAGCAGA TAATGGAACT ATGTTTGAAG	900
TATTAACATA AGTCTTAGTT GTAACGGTAT CGCTATGAGT TAATGCTTCA GAAATGGCTT	960

1162

CTAAGCTCAT TCCTGCTTTT TTAGCAAGTG TCGCTCCTG

999

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AATATTATCA CTGTTCTTGA AGGCAGAACA CAAGCTGTCA TCCGAAATCA CTTTCTTCGC	60
TACGATAGAG CCGTTCGTTG TCAAGTGAAG ATCATTACGA TGGATATGTT TAGTCCTTAC	120
TATGACTTGG CTAAACAGCT TTTTCCGTGT GCTAAAATCG TTCTAGATCG TTTCCATATT	180
ATCCAACATC TCAGCCGTGC CATGAGTCGT TTTCGTGTTC AAATTATGAA TCAGTTTGAA	240
CGAAAATCTC ATGAATACAA GGCTATCAAG CGTTACTGGA AACTCATCCA ACAGGATAGT	300
CGTAAACTCA GCGATAAAGC TTTTATTCGC CCTACTTTTC GCATGCACTT AACAAATAAA	360
GAAATTCTTG ACAAGATTTT AAGCTATTCA GAAGACTTGA AACACCACTA TCAGATCTAT	420
CAACTCTTAC TTTTTCACCT TCAGAACAAA GACCCTGAGA AATTTTTCGG ACTCATTGAG	480
GACAATCTGA AGCAGGTTCA TCCTCTTTT CAGACTGTCT TTAAACCTT TCTAAAGAAC	540
AAAGAGAAAA TCGTCAACGC CCTTCAACTA CCCTATTCAA ACGCCAAATT GGAAGCGACC	600
AATAATCTCA TCAAACCTAT CAAACGCAAT GCCTTTGGTT TTCGAACTT TGAAACTTC	660
AAAAACGGA TTTTATTCGC TCTGAACATC AAAAAAGAAA GGACGAAAT TGTCTTTCT	720
CAAGCTTAGC TTTTCTTCAA CCCACTACAG TTGACAAAGA GCCTATTTTC GCTGATTCTC	780
CACTACATTT GACTGGATT TAATTTTGA GAGAAATACA AAAGAGCTAG CTTTAGCTAG	840
CTCTTTTCCT ATGCGGAGAG AGGGACTTGA ACCCTCACGA CCTAAAGCGG TCACAGGATC	900
CTTAGTCCTG CGCGTCTGCC AATTCGCGCA TCCCGCGTC GATTACTTTA CTAGTATATC	960
AACTTTTGGG ATGCTTGTC ACACTTTTTT TCAAATTTTT TCATTTTCAC CAACCAGGT	1020
ACTCAAAAAG TTCATTTAGA TTTTCATCTA CTAACCTAGC TCCGAGTGTA TTTTGAAT	1080
GACCTAGGGC AAATTGATGA TTTTCAGGCC AGATGGAAGC AACAGCTGGT TTAACAATCT	1140
CGATGTCATA TCCTAGATTA TAGGCATCTA TAGCTGTATG TAGGACACAG ATATCCGTCA	1200
AGACACCTGT TAAGATAACG GTAGACACTC TACGCTCTCT CAAACGAATA TCTAGGTCAG	1260
TCCCTGAAAA AGCTGAGTAA TGGCGTTTAT CCATCCAAAA GACACGACTG TCTGAACCAT	1320
GCTCTTGATA AAAGATCCCC AAATCTCCAT ATAAATCCG TCCACTCGTC CCAATCAGAT	1380

1163

TATGAGGAGG AAATAACTTA CTTTCCGGAT GGAAACAATC GTTTTCTTCA TGAGCATCAA	1440
TAGTAAAGAA GATATAATCT CCTCGTTCAA AAGCTAATCG AGTTACCTTG CTGATGGCAT	1500
CCGAAATCGC CTGAGCTGGA GCACCTGCTG TTAGTTTCCC ACTATCAGCA ACAAATCTT	1560
CTGTATAATC AATCGAAATT AAAGCCTTTG TCATTAGTAA TCTCTTTTCT TCACTTCTTC	1620
AAAAATATCT GAAATCAAGA CCTTAAGATA GGTTCCTTC ATTCCAAGTG AGCGACTTTC	1680
AATAATCCCC GCAGACTCAA GTTACGAAG AGCATTGACA ATCACAGAGC GAGTGATTCC	1740
GATACGATCT GCAATCACTG ACGCAGTCAA CTTCCTTCA TTTCCATTTA ATTCCCCTAA	1800
AATTGCTGAA ACAGCACGGA GTTCGGAGTA AGAAAGGTA TTGACCGCCA TGGTGACAGC	1860
AGTACGACGA CGAATATTTT TCTCATCTTC TTCACGTTGG AAGTTAAGAA GCTGAATCCC	1920
AACAACGGTA CTGGCAATCT CAACAAGAAC CAAGTCCTCA TCTTCGAATT TTTTATCATT	1980
ACGCCAAATA ATCAAAGAAC CAAGGCGAAT CCCCAGTACA TGAATCGGTG CAATAGTCGT	2040
CAAGCCATCT GGAAATCAT CTCTACTCTC AATAGGAAA ATACTCATAT CATGCTCAAC	2100
AGGCAAGTTT GCTTCTGTTT CGTAAATCAT ATTAGCCCCT TGAACGTAGT CATCTGGGAA	2160
AATCTTAGTT TGGAAGAATT GCTACGCGA TCTGTATTG TTTTATAACG CATAAAATAG	2220
CCAAGCAGAC GTCCCTTACT ATGATAATG CAGGCATTGC AATGAATAAT ATCCGCTAAC	2280
TGACGCGTAA TAGCGTTGTA AGGGAGCTCA TCTCG	2315

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

CGATTCTTTC CATTCTTCA AATAAGAATA CTTTCTTGA CATATGTGTT ACCTTCTTCA	60
TCAAAAATTA TTTTGTAAAT GATTACATTG CAGATCGTAA CATAAAGAAA AACAGATGTC	120
AAATATTAAA CGTAAAAACA TGGTCACTAA AGAACTATAA GAGAAAAGGT AAACCTAGCG	180
ACGCGATGAA CGCTGGGTCG TTTGGTTTCG ATTGCTCTCT TCCTCTTGT TTTTCTGTTT	240
TTCTTCTTGT TTTTCTCAG CTTTCTTGGC CTCTTGTGTT GCTTTTTCCT CAGCTTCCAT	300
AATTAATTTA TCCGCCACAG TGTAGCTGTA GATTCCAGCT TCCATGTCGA CCACACTCGG	360
TTCTGACAAT TGAGGCTTAA TCTTACTGTA ATATGGCAGT TTCTTACTCA TTTCAGATAG	420

1164

AGGAACCAAG ACTTCGTCCG AATCATTTCAT GGTCAATCGA ATTAAATCGG ATGTCACCTT	480
GCTTGCGGCT AATTCCACCT TTTGGATAGC CGCCTTGAGT TCTGGGCTAA TTTGAGCAAG	540
TTCTGAGACA AAAACTTTGA TTTGTTCACT ATCATTAAAG AGAACTGATA AATAAGTTTC	600
TGGTAAACTG TTCAGACTCA CAGAACTAGT CTCGAAGCTGA CCACTGGAAA GAATAGGATA	660
ATGATTTTCA CCAGAAATAT AGTAGGCCAC AATATCATAT TCCTTGACCT TAATAGTGAA	720
CTTAGTTGGA AATTGATAGA CAAGTTGAGC TGATTCAACC CAATAGTTAG ACTTAATCTG	780
CTTTTCATAT TTTGCCTTGT CTAGCAGAAG GTTAATCGTA TAATCCGAAT CCTGAATGCC	840
TGAAGCCTGT CGAATATCAT CAGCTGTAGT TTGCACCGTT CCCTCAACAC GAATATCTTT	900
CATGGTCGCA TAAGGACTGA GCAAGTAGGC AGAGACAAAC AATAGAAGCA GACTTGGAAA	960
TAAAATCGTG AAGGCTCGCA AGATATGGAT ACCAGGAATC TTGCTTTGG CTGGTTTTTC	1020
CTTTGTAGCC TTTTGTAGCA GCTTTTATC CTGTTCTCC TTCTCTTTAG ACTCTGGTTC	1080
TTCTTTCTCT TCTTTCTCTT TGTCAGCCTC TGAGGATGCT ACTTTTCTT CAGACTCTTC	1140
CTTAGCTGAT TCTGAATCTT CCTGGTCTGT TTCACTCTCC TGGTCCTGTT TATCCTCTGA	1200
CTTCTCAGAT TCTTCTCCCA TTCGAGCTTG TCTTTCCTT TCCTTCTCCT CAGCTAGAGC	1260
CGCCTCTTCT TCAGCCTTCT TTTTGTAGATA TTCTTGGTTT CGTTTCTGCC ATTCTGATAA	1320
CTCTTTCAAT TCTTCGAGGG TTTCTTTGTC CTCATTTTTC TTATCTTTTG ACATTTACTT	1380
TCCTTATGAT AAATCTTTTT TCAACAATTG ATAAAAATCT GCTAGAGATT TCAATTCCTT	1440
AGAAGCTTTC ATCTTAGCTT GGTAATCTTC CTTGTGACTT AGTAAGTGAG AAAGCTTCTC	1500
TTCCAAACTA TCCAAGGTCA AATCGCTTTC TTGAAGGTCT TCTGCATAGC CTTTCTTAAC	1560
AAAGTAAGCT GCATTTTCAA TCTGGTCACC ACGACTAGCT TCACGACCAA GCGGCACAA	1620
GACATGCAAT TTTGCTATCG CCAAGAGCTC AAAAATCGTA TTGGCACCAC CTCGTGTCAC	1680
AACAATATCA GCCAATTCCA TCAAGGGTTG ATAGAGATCG GTCACATAGT CAACACGAAA	1740
AAGATTTTGC CTCAACTCAT TCAGACTAGA ATCTCCAGTT AGATTGATAA TATTGTAGCG	1800
CTCTGTTAGT TCTTCTTAT GGTCTGTCAC CAATTGGTTA AAGACACGAG CGCCTGCAGA	1860
ACCGCCAACA AACAATACAG TTGGCAATTT GGGATTAAAG TGGGTTTGAA TATCCACCAA	1920
TTCATCTGGT TCTGGAGTGT TTTTGTCCGA AACCTTGGTC ACCGCTCCCA CATGCTCAAC	1980
CTTAGCCAAA CTCGAAGCTT GTTCAAAGGT TGAATACATC TTAGTCGCAA ATTTATAGGC	2040
GATTTTATTG GCCAAGCCCA TAGACAGGTC AGATTCTGTA ATAAAGACAG GCACTCTGA	2100
CACACGCGCA GCGATAACAG GCGGTACTGA GACAAAGCCC CCTTTTGAAA AAAGGGTCTG	2160
TGGACGCAGT CGCAACATGA TAAAGAGCGA TTGGACAATT CCCCAACCAA CTTTGAAGAC	2220

1165

GTCCAGCATA TTTTGCCAAG AGAAATAGCG ACGCAATTTT CCAGTCGCAA TAGAATGGAA	2280
GGTGACATCC AAACCTGACT TAAGGATTTT TTGGTGTTCG ATACCACACT TGTCCTCCGAT	2340
ATAGTGGACT TCCCAACCAT CTTCGATGAA CTTGGGCATT AACAAAAGAT TGAGGGTAAC	2400
GTGTCCAACC GTCCCCCAC CTGTAAAGAC AATTTTTTTC ATATTATTCT TTTAACTCCG	2460
CTACTGTGTC GATAAAGAGG TCGCCACGTA CTTCAAAGTT AGCATACATA TCCCAGCTAG	2520
CATTGGCAGG ACTAAGAAGA ACCACATCTC CTTGAGTCGC AAGCTCATAG GCCTTGCGGG	2580
TCGCATCTGC AATATCTGTC GCCTCCACAT AAGCGACACC AGCCTTGTCT GCTGCCCGTT	2640
TGACACGTTT TGCAGATTGA CCCAGGATGA CCATCTTCTT GAGTCCAGTA ATGTCTGGCA	2700
CCAATTCGTC AAATCATTTG CCACGGTCCA AACCACCTGC AATCAAGACG ACCTTGCTGT	2760
TGTCAAATCC TGACAAGGCT TTTTGAGTAG CCAAGATATT AGTTGATTTA CTGTCGTAT	2820
AGAATTTAAC ACCCTTGATG TCATCCACAA ACTGGAGACG GTGTTTGACA CCACCGAAGG	2880
CTGAAAGAGT TTCCTTGATG GTTTGATTGT CCACATCAGC AAGCTTGGCT ACAGCAATAG	2940
TCGCAAGGGC ATTTTCCACA TTGTGGCTAC CTGGAACACC GATTTTCATTC GCTGCCATGA	3000
CTACTTCACC ACGGAAGTAG AGTTGACCAT CTTCCAGATA AGCTCCATCA ACCTTTTCAA	3060
GTGTTGAAAA TGGTACAACA GTGGCTTCTG TCTGGGAAGT CAAGTCTTTT GCCAAGTCTT	3120
GATTAAAGTT CAAGACAAGG AAATCAGCTG CTGTCATCTT GTTCTGGATA TTCCACTTGG	3180
CTGCTACATA TTCCGAAAT GACCCATGGT AGTCGATATG AGTTGGCATG AGGTTGGTAA	3240
TAACCGCAAT CTCTGGATGG AATTCTTGAA CACCCATGAG TTGGAAAGAA GAAAGTTCCA	3300
TAACAAGCGT GTCCTTATCT GATGCTATTT GAGCAACCTG ACTAGCTGGA TAGCCGATAT	3360
TCCCTGATAA AAGACCATGT TGGCCAGCAG CAGTCAAAAC TTCCCCAATC ATAGTCGTTG	3420
TGGTTGTCTT ACCGTTGAT CCTGTGATAC CAATAATCGG TGCTTCTGAA ATCAAATAAG	3480
CCAATTCCAC CTCAGTCAAG ACTGGAATTC CCTTGGCCAA AGCCTTTTCA ATCATGGGAT	3540
TGTTGTAGGG GATACCTGGA TTTTTCACCA TAAGGGCAAA CTCTTCATCC AAGAGTTCCA	3600
AAGGATGGCC ACCTGTAATG ACCTTGATCC CTTCTTCCAG CAAACTTTGG GCAGCTGGAT	3660
TGTCCTCGAA AGGTTTCCCA TCATTTACTG TCACAAATGGC ACCTAGCTTG TCCAACAAAC	3720
GAGCTGCAGA TTCACCAGAC TTGGCCAAAC CTAAACAAG GACTTTCTTA TTTTAAATT	3780
GATCTATTAC TTTCATGTCT CGAACTCCAT TTCTACTCCT ACTATTTTAC CATTTTTATG	3840
GAAATAAAAA AGCCACAAAG TGTGTTTGTG ACTCTTTCTT CTAAGTGAAT CTTACCATAT	3900
CATCTATGTG ATAAATCGGT AACTCGAATG ACCTGATCCA CTTGCTCCCA AATCAGAGGA	3960

1166

TTATGGGTCG CAATAATAAT GGTCCGATTC GGATTTTTTA AAGATTCTAG GATGGAAAGT	4020
AATTCCTCAG AGTTTTTGGG GTCTAAGGAA GCGGTTGGTT CATCTGCGAG GATCAAAGGT	4080
GGATCCTTTA AAATTATCTT CGCTAGTGCA ACACGTTGTG CTTCTCCTCC TGATAACTCA	4140
AATATAGGTT GCTTCAAATC CAAATAAGAG AGGTTTACAC GGTTTAGAGC TTGTTTCATC	4200
AAAGAGATTT TCTCTTTTC CTTCAACTTT TTACCAACTA AACCCAGATT GAGATTCTCT	4260
TTGACGGTTT GGCTTTCAAT TAAGCCAAAA TCTTGAAATA AGTATCCTAA GTAATCTCTA	4320
AAGAAAACAG AAGGCTTGAT GTCCTTAAGA GAAGTGCCAT CATAGATGAT TTGCCCTTTG	4380
TCATATGGCT CCAATCGTCC AATCATATTC AAGAGTGTG TCTTACCACA GCCACTTGTA	4440
CCGATTAAGG CATAAATTTT CCCACCTTCA AAATGAAGAT TCATATCTGA AAATAGCTGA	4500
CGGCTTCCAA ATTTTGTAGA TATATTCTTT AGTTCAATCA TCCTATTTTC CTTTCATAAT	4560
TGTCATAGAA ACACGAGATT CTTCTGCGC TTGACGGTAA AGCGTCAAAA CTGCACTAGC	4620
TAGAAAGACC AATAAAGTGA GCAAGCCAAT CACCAAGTCT CGACTGCTTA AATAAAGAG	4680
ACTAGCACCA AATACAAAAC TAGCAAATTG GCTAACCATA TACTGAGCAT GTGTTTCAAA	4740
AAATCGTAAA CCTGAAATC GTTTAATCAA GATATCTCGG CGGAATTGCT CGAAATATAG	4800
AAGATTGACA GAATAAAGA GTAACAAGGA ACTGGCTATT CCAACAATAG CTCCTAAGAT	4860
TAAAGTTGCT GTTTCAGTTT GAACTTCATT ATAACGAGTT AGATAAACAC TTCTTCCTTC	4920
TTTAAGATAG GATACTTGCT CATAAATCC AGCTTCTTTC AAGAGTTCTA GCCCACTCTC	4980
ATATCCTTTG ATAAAGAGTT GTTTTCCAGC ATTGATAGAC CAACTAGATA AGGATATAAA	5040
ACTATCACCT GTAGAAGTCG GCGTGAATAC CACTAAAATC GGATCAGTCA AATACTGAGT	5100
AGATACGGGA TTCTCACCGT TATTATAAAC AAACCGCTTT TCTCCCATTG AAAGATAACT	5160
AACGTGCGCT TTCATCTCAT AATCCAAAGG AGCACTTGCC TCCTCACCAG ATTTTCCATA	5220
ATAACTCAAT CTTTCTTCAA AAACTTTCTT AAGTTCTGCT TCTCGAGAGC GCAAATGTTC	5280
TGGGAGCAAG AGGATAAACT CACCTTTTGG GAGATGGGCT AACTTCTGTT TGGTCTCAGC	5340
ATCTACCACG ACCTTTTCCT TGTCCAAATA ACTGGGACTA ACATAGAGCG TATTAGCATC	5400
TGAACTATAG GTATCCAGTG TCTCTCCCTG TTCATTTTTT CTTGTGGAT TGGCAAAATG	5460
GAGCAGATTA TCCTTTACAT AAAGAGCTTG TTCTTCTTCG ATTGCTTCCT TGGCAAAGGC	5520
ATACCACTTG CTCTGATTTT CTGTATCTTT TCCTCTATCA CCTAAGCCAA AGGAAATCTG	5580
GTAATAGTCT GCTCTGTCCT GCCATGCTTG TTTTGAAATT TCAAGTTCTT TCAATCGTTG	5640
GTAAGACGTC AAACCTGTCT TAACAGCGTA GCCTACTGTA AAAACAGCTA CTAAGTACA	5700
CAATAGGGTT AAAGCCATCA AGCGTTTAAG GGGTAATCTT CCCTTAATAA CGGGAAGTAA	5760

1167

TGCTTTGTAA CTCAAACCTCA TTAGGTAAAG GAGCATTAGT AAAATTGAAA TCGCCAATAA	5820
AAACAACAGA TAGAAACTAA TCCCAAAACC ATAGGTGGCT AACAAGATAG GATAAAACAA	5880
ACCTTGACTA AAAAGAACGA CTCCTCCACC TAGGAAGGAA AGGAGGGCTG ATAGAAGGAG	5940
CCATTTGATA TCAGTAGATA AAGAATGCCC CATGATGGAT AAGAGAGTCT GACCAGAAAA	6000
GAGTTTATA CCTGCTGCTC TCATTTCCTT AATCCGAGTG ATAATCACTA AAGCAAAGAA	6060
AGATAAGCCA AATATTGCTA AACTAATTAA AATAAGGGGA TTTAGTAATA TTCGAAAAGC	6120
AAGAAAATAG GCGGTATCTT TTCGGTCAGC ACTTGCTTTA TAACCCAAAT CTCCTAATTT	6180
ATCGGCAAGC TTTTCTTTTCG TCAAGGAGCC TGACAAAAGG AGATAACTAT TTAGCGGANT	6240
AtACGTTTAC GACTTTCTTG GCTAGCTTCT TGGAATTCCT TTGGTAAAGT TCCCTGACCA	6300
TAAAGTGCAT AAGTAAAGTG AGTCGTCCCA TCCTTACTCG GCTCTACAAT TCTTCTAGCT	6360
ATTAACTCT GTTCTGAGTT TGCAAAATTC TCCAATTCCT GTTCAAATAC CTCACGCGTC	6420
GGTTCCTGAG TATCTTTTTT GACACGAAGT AAAGAAACGG AATCATAGCT TGCATATAAA	6480
TATTGTGGCG CACGTAAGAC AATAATCCAA GCAAGGAAGA AGCTGAGAAA AAAAGTTGAT	6540
AATAATATGA ATAGTTTCTT CATAGTAGAC TCCTTGTAAG CAAATTTCCC CCTGTAATTT	6600
CTTACAAGGG GAACGATTTA AATCAATGAA CGATTAGTCA TAATCACAGT AAAATGCTAC	6660
TTGTTCTCCC CATTTAGTCC AAATCCATGC AGG	6693

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1847 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

CCGGTCTATG TACCCACTAC TTTGGGACAA TATGGGGATC AGCTACCCAA AACTAATCGA	60
GCGTTTGGTT GACCTTGCCA AGGAAAGTTT TGACAAGCGC GACGATTTGA TATAAATGA	120
AAGAGAGGGT AGAAGCCAGA ACCATCACTG CACGGTGACT AGAGTTCTCG GACTTCAGCC	180
CTTTTAAAG GAGTAGAAAT GAAATTAACA ATCCATGAAA TTGCCCAAGT TGTGGAGCC	240
AAAAATGATA TCAGTATCTT TGAGGACACC CAGTTAGAAA AAGCTGAGTT TGATAGTCGT	300
TTGATTGGAA CTGGAGATTT ATTTGTGCCA CTTAAAGGTG CGCGTGATGG CCATGACTTT	360
ATTGAAACAG CCTTTGAAAA TGGTGCAGCA GTAACCTGT CTGAGAAAGA GGTCTCAAAT	420

1168

CATCCTTACA TTCTAGTAGA TGATGTTTTG ACAGCCTTTC AATCCTTAGC ATCCTACTAT	480
CTTGAAAAAA CGACTGTTGA TGTCTTTGCT GTTACAGGTT CAAATGGCAA GACAACGACT	540
AAGGATATGT TGGCGCATTT ACTGTCAACA AGATACAAGA CCTACAAAAC ACAAGGCAAT	600
TACAATAATG AGATTGGCCT TCCTTACACA GTTCTTCATA TGCCTGAAGG AACAGAAAAG	660
TTGGTTTTGG AGATGGGACA GGATCACTTG GCGGATATTC ATCTCTTGTC TGAATTGGCT	720
CGTCCAAAAA CAGCCATCGT GACCTTGGTT GGAGAAGCCC ATTTGGCCTT TTTCAAAGAC	780
CGTTCAGAGA TTGCTAAGGG AAAAATGCAA ATTGCAGACG GAATGGCTTC AGGTTCCTTG	840
CTTTTAGCGC CGGCTGACCC TATCGTAGAG GACTATTTGC CAACTGATAA AAAGTGGTT	900
CGTTTTGGGC AAGGGGCGA GCTGGAAAT ACTGACTTGG TTGAGCGCAA AGATAGTCTG	960
ACCTTCAAGG CCAATTTCTT AGAGCAAGCC CTTGATTTGC CAGTAACTGG CAAGTACAAT	1020
GCGACAAATG CTATGATTGC ATCCTATGTT GCCTTGCAAG AAGGAGTTTC AGAGGAGCAA	1080
ATTCGTTTGG CCTTCCAAGA TCTTGAATTG ACGCGTAACC GTACCGAGTG GAAGAAAGCA	1140
GCCAATGGAG CAGATATCCT GTCAGATGTT TACAATGCCA ATCCAACGTC TATGAACTG	1200
ATTTTAGAGA CTTTCTCTGC CATTCAGCC AATGAAGGTG GCAAGAAAAT TGCAGTGTG	1260
GCGGATATGA AGGAGCTTGG TGACCAGTCT GTTCAACTTC ATAATCAGAT GATTTTGAGC	1320
CTTCTCCAG ATGTGCTTGA TACCGTGATT TTCTATGGAG AAAATATTGC TGAATTAGCC	1380
CAATTGGCCA GTCAATGTT CCAATCGGC CACGTTTACT ACTTCAAGAA AACAGAAGAC	1440
CAGGATCAAT TTGAAGACCT AGTCAAGCAG GTCAAGGAAA GCCTTGGAGC CCATGACCAA	1500
ATCCTGCTCA AAGGCTCTAA CTCTATGAAT CTAGCCAAGT TGGTAGAAAG TTTAGAAAAT	1560
GAAGACAAAT GATTTGTCA AGTATTGCA AAGAATGATT GCCATTACAG ATACTGGCTT	1620
AACCTTTACA AAAGATCCGT TTGACCGTGA GCGCTACGAA GACTTGCGAA GTCTGTTATC	1680
TGAAATGTTG AATCAAGCAT CAGACCTGA TTCCGAAGAA GTGGCAGAAG TCTTGAAGCC	1740
AACTTCTGCT TATGCGACTC CGTTAATGGA CGTCCGTGCT TGGATTGTTG AGGATGAGAA	1800
GATTTGCTCG GTTAGGGGAC AAGGAGAGGA TAGTTGGGCT TTGCCCG	1847

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1062 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

1169

CAAGCGAAAA CATTTTTAT TCCAAATAAA CAGAGCATTT TAGGAGAACA AGAGATTTTG	60
AATGCCAAGT CGATCTTGGC CTTGCTAGAC GGTTTGGAGT CACATAGCTA TGATGTAGTC	120
TATCTCCGTC AGCCTCTTAA TCGTCTCGAA TATATCGAGT GTGCGATAGT GGGGCAATCA	180
CAATTTCTCT TTAAGGTCAG TTATGCTGAT GGTCAAAAGG CTTACCGTGT CGATCTTCCT	240
GACCTACTAA CAAAGACAGA CTGGCAGATT ATCAAGTCAT TTTTAGATGC TTTGCTTGCT	300
TATACAGGGA CTGATATTGA AGGGCTAGAT GGTTTTGATT TTGAAGCTTA TTTCCAAGCA	360
AGTATTCAAG CCTATCTAGC AGACCCTGTA GCTCGTTTGA CGATTTGCCA AGGAATTTTT	420
AATCCTATTT TCTTTAGTCG TGAGAACTTG AAAAGCTTTT TAGAGGCAGA TGGCTTGGCT	480
CAGTTTGAAG CGCGTGTGCG TCGGGTTCAA GAGACAGATG CCTACTTTGC GAGAGTTTCC	540
TTCTATCAGG ATGGAGAAGG AAAAGTGCAT GGCCTTTACC ATCTAGCTCA AGGAGTCAAG	600
ACAGTTTAC CGAGAGAACC GTTTGTTTCT GCAGCCTATA TTGAGCAATT GGTGGATAAG	660
GAACTCCAGT GGGAGATTGA CTTGGTTCAA ATCACAGGAG ATGGCTCTAA ACCAGAAGAC	720
TATGAAGCCA TTGCTCGCTT GGAATATGCA AAATCTTAG AGGTATTACC CCCATCTTTT	780
TACCACCAAC TAGACGCCAA TCAAAATAGAA GTGCAACCCA TATTAGACAA AGATTTTAAA	840
ACATTAGCAC AAGAAAAGTA AAGCAGAAGC AGGTCAATCG ACTTGCTTTT TTGACATAGA	900
AAAAATCCTG CCAAGaTGAC AGGATTGCTA CTCAATGAAA ATCAAAGAGC AACTAGGAA	960
GCTAGCCGCA GCTGTACTTG AGTACGGTAA GCGGAAGCTG ACGTGGTTTG AATTTGATTT	1020
TTGAAGAGTA TGAAGTTTAA AGAAAAGCCA AGATACGAAG AT	1062

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6846 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

TATCTAACAC CTCAAAAACA TGTTTTGawG gCTCGTCAGT cTATCTACAA CCTCAAAAAC	60
ATGTTTTgAa kGCTcGTCAG tTCTATCTAC AACCTCAAAA ACATGTTTTG AcaGCcTcGT	120
CAGTTCTATC TACAACCTCA AAAACATGTT TTGAGCTGAC TTCGTTAGTT TCATCTACAA	180
CCTCAAAAAC ATGTTTTGAG CTGACTTCGT TAGTTTCATC TACAACCTCA AAAACATGTT	240
TTGangnChT CGTCAGTTCT ATCTGCAACC TCAAAGCAGT GCTTTgagcG CTTGTCAGT	300

1170					
TCTATCTACA	ACCTCAAAAC	AGTGTGTTGC	GCAGCCTTTA	ATCAGCCGCC	360
TATGGTATTC	ATTAAGTCAA	CATCTCTGT	TTAAGAGCAC	CAAATCAGGA	420
ATTCCCTGAT	TTTTTCTATT	TACGTTTTCG	TGTTGAGCTA	CGTTCTGTCA	480
TAAGAGAACT	TCACGTTCTT	CCAACTCTTC	CTTATGCATA	ATCTTGGTCA	540
ACTAATGGCA	CCAAGGTCAT	AAAGAGGTTG	GGCAATCGTT	GTCAAGTTTG	600
GCGTGAGATT	TGTGAATCAT	CACTAGTAAT	AATTTCAAAA	TCTTCTGGCA	660
CTTATCAGCC	AAACCGTTCA	AGACTCCTGC	TGCCAACTCA	TCACCTGTCA	720
AGTTGCATTT	GATGAAATCA	AACGCTCTGC	TAAGGCGTAA	CCATCATCAT	780
AGATTCAAAT	ACCAAACCTT	CACTATAAGT	GATTCCTGCT	TTTTTCAAGG	840
GCCAACTAAA	CGAACCTTAC	CATTGATGTC	ATCCACTAGC	GGACCGCTAA	900
ACGCTCATTT	TCTTTAGCAA	GGTAACTCAC	TGCATCAATT	GTTGCTTGCT	960
ATTGACACTT	GGCAACTGGT	GCTCAACATC	GACAGTTCCT	GCGAGAACAA	1020
TGAACGCGAA	AATTCTGAGC	GAATTTTATC	TGTCAAGTGA	TACCCCATAT	1080
ATCTACCTGC	TTTGAAGA	GGGTATTGAC	AACAGAACT	TCTTTCTCGT	1140
GCTATTAGCT	AGGACAATAT	TGTACTTGTA	CATTCTTGCA	ATATCATCAA	1200
CAAACCTGAA	AAATAACCAT	TGGAATATT	TGGAATCACG	ACACCGACAG	1260
TTTACTTGCA	AGACCACGCG	CAACTGCATT	TGGACGATAA	TCCAAACGAT	1320
TAGCACTTTT	TTACGGGTAT	TCTCTTTTAC	ATTTTTATTG	CCATTGACCA	1380
CGTCGCCATG	GAAACACCTG	CTTCACGAGC	GACATCATAA	ATGGTTACTG	1440
ATTCATTCCT	TTTCCTGTCC	TTTCTATCTC	ACACATTCCT	TTACAAGTAG	1500
TGAAGCTCTA	TATCTACTTA	CAAAGTGAA	GATGTGAAAA	TTTCGTTTTC	1560
TTATTCCATT	CTATCACTAA	TTGTAAACAC	TTTCAAGTGT	TTTTTGAAGA	1620
AAATTTTATA	GAAAACTTAG	GTTTAGCTCC	TTGCTACCAC	CTTAGACTAA	1680
GGAAACTAAG	CCCTCCTAAA	GTTATAGTAA	AATGAAATAA	GAACAGGATA	1740
GACAGTCAAA	TCGATTTCTA	ACAATGTTTT	AGAAGTAGAG	GTGTACTATT	1800
TCTACTATAG	GTATTGTTCC	ATTCACTACC	GTCAATTTTA	GCACATAGTC	1860
TATTATATCA	TCATAACCAA	CCAGATTCTT	TCGCGATATT	AGCTGCCTCT	1920
CTGCATCTAG	TTTCGAAAGA	ATATTGGTGA	CATAGTTTCG	GACTGTTCCG	1980
AAAGTTTGTC	TGCAATTTCT	TGGTTAGAGA	AGCCCTGAGC	AATTCCTTTT	2040
TTTCTTGCTC	CGTTAATGGA	TTGGGATGCA	TCATCACCAC	TTCCATCAAT	2100

1171

ACTCCTTGCG TCCTTCGAGG ACGGTGTGCA AGGTTTGCAT GAGGTCTGCA ATGTTTCTTT	2160
CTTTTAATAC ATAAGCATCT ACTCCAGCCT TGACCGCACG TTCAAAATAC CCAGGACGCT	2220
TGAAGGTCGT CACCACAACC ACCTTTGTTT CAAGCTTTTC TGCTCGTATC CACTCCAAGA	2280
CTTCAAGACC TGTCTTAACA GGCATTTCTA CGTCAAGGAT GCGGATATCT ACAGACTCCT	2340
TTTCTAATAG TTGGATTGCT TCTTGCCCAT TCTTGGCTTG AAAGACAGAC TCTACATCCG	2400
GTTGAAGCAT GAGCAACTGG CACATGGCAT CTCGCAACAT ACTTTGATCT TCTGCGACTA	2460
ATACTTTCAT CTACTTCTC TCCTTATAAA GTAGTCGAAC CTGCACCTCA GTTGGATGTT	2520
TCTGACTGAT TACACTTACT TCTCCTGAAA ATGGAAAAAC ACGATTTCGG ACTGTATGGA	2580
GCTCATCCCC GCTTATAGAG GCAAAGCCAC AGCCATCATC TCTCACTGTT AGAATGAGTT	2640
CTTCTCTGT CCGTTCTAAT TTCAAGTAGA CTTTAGACGC TTTAGCATGT TTGATGATAT	2700
TGGTCACTAA TTCAAGCAAA ATCATGGAAG CCGTTGACTC CAATTCCTGA GTTAAGCTAG	2760
ACTTGCCAA GTGATTCTCA ACTTGAACCT CAATCCAGC AATTTCTAAC ATCTTTTCA	2820
CAGTCTCTAG TTCGGATGTC AAAGTTCTAG ACTTAAGATT TTCCACAATG GTTCGCACTT	2880
CATTCATGGA TCCTTGCTGA TCTGGTGAAT TTCTTTTAA TCCTTTTCCA CCTGTGGATA	2940
AGCCTCCATC TGAAATAACT GCAAGGCTAA ATCTGTCTTG ACACTCAGCA TAGCAAAGGT	3000
ATGTCCCAGA CTATCATGCA AATCCTGACC GATACGACTA CGTTCATTTT CAGCAAGCAA	3060
TAGATTATC TGAGCATTTT GCTTGACCTG AGCTTCTTTC AAATCCTCGA CAATACGAAT	3120
CCGAACCAAT CCAAAAGTCA TTAAATCGAC AAAAGTAAGA ATTACAAGTA GATAGAATAG	3180
AAACTCAACT TCGATTCTCT GAAAAATCAA CAGTTGCCCC ACAACAAGGA CTTGAGCAAG	3240
AAGAAAAGTC CAGACATGTA AAGACTTTAA ACTACGTACG CTGAAATGAT AACTTAAGAG	3300
ATTGGATAGG AAAAAGAAAA ACCAGATATA ATTAACAGCA ACAAAGGCAG TATTCCCAAC	3360
TACATAAGTC AGCATGAGGC CCCAATATAG CCAAGATAGG CGCTGGCTCT TAGTTGTTAA	3420
AACACCCAAA TATGCCACTA CAAATAGAAT ATCAATCAAT AAATGCCAGG CAGAAAGCCA	3480
CCCAGTCACT ACAGACAGGA TGGGGAAAAT CATAAAAATT AAAGTATCC AAAACATATA	3540
ATGTATTCTT TTCAGTCTTT CAAGCATTA GCATTCTCCT TATGACCTTG AAGGTAAATG	3600
GTCAAACCAA ACAAACCTAC TGAAAAACA AGTAAATAAA CTGTGGCTGA TAGATTGATG	3660
CCACCCCTCAT TTAAGAAGGT CTTGAGCAAC TCCATCAACT GATAGGTCGG GAGACACTTA	3720
CCTACTACTT GCATCCAGTC TGGAAATAAA GAGATAGGCA TCCAGAGTCC ACCTAAAACA	3780
GCCAACCCTA GATAAAGAAG ATTGCCCACG ACAGACATCA ACTGACTAGT TGGTAAGAGA	3840

1172		
GTCAAGGTCA AACCAAGCGC TACGAAGGCA ATACTTCCTA CTATCAGCAA AAGTGCAGCC	3900	
CCAATCCAAT TTCCAAGAGA CATGTCCACA CCTCTTACAA AATGCCCAAC TGAGAAAACC	3960	
ACCAAGATTG AAACCAAATA ATCAACCAGC ATACTTGTTA TCTTTGATAG ATAATATTCT	4020	
ACCATATTTA CAGGGCTATG ACGCAATGTT TTCTGCCAGT TGTGTATCTT GTCGGTATGT	4080	
AAAACAAC TGGAATGAGAA GATAGCTGTT GACATCATGG AAAATGCAGT CATGGAGATA	4140	
AGATAATCAC GCATAAAAT CGCGAGTTCA CCTGGTGTGT CCTGATAGAT ACCAGAAAAA	4200	
AATAAATAGA AAGCCGTCGG CATCCCTACT GACAATAGAT AATAGATCAA TTGTCGTTTG	4260	
GTCAATAAAA ATTCTATCTT ACTAAGTGCT AGCCATCGTT TCATCTTAGT TATCTCCCTT	4320	
CTGCGTTTCT TCAAAGATTG TATCCAACAA ACTACGATTA TTAACCTCAA TTTCTTGTAT	4380	
GCCACATCCT GCTTGAAC TAAGTTCCCA AAAAGCATCT GCTTCGCGTG TGACTACTTG	4440	
TAGAGCATCC TGTTTGTG ACCAGTTTTC AACCAAGTTA GACTGCTCAA TGACTTCCTT	4500	
GTATGCCAGA GGAAGGATAA AATGCTTTTC AATTCCTCA CTACGCATAG CTAGAGGCGT	4560	
CGTATCACGA ATCAACTCTC CCTTATTTAA AACCAAAATC CGGTCAGCCG TATGCTCTAC	4620	
CTCTTCAATA TAATGAGACG AATAGAGAAT CGTGACTCCT TCGCTTTTA GGTCCCGAAC	4680	
GATTTCCCAA AAGCGTTGAC GAGTTGAAGT ATCCATGGCA GCAGTTGGTT CATCTAAAAA	4740	
GACAAGCTTT GGTGCGCCAA TCAAGGTCAA GACAAAAGAG AAGAGACGCT TTTGCCCCC	4800	
TGACAATTTT TCTGCGAATT GCTCTTTTG TTGCTGGTCA AACTGCAATA GTTGATCGAT	4860	
TTCCTGATCG CTCAAGGAAT TTGGATAGAT ACGTTGAAAG AAAGCAATCA ACTCTTGAC	4920	
CTTTAATTTT TGAACGATGA CATTTTCTTG AGGCAGATAA CCTCTAATAT AGTCTAACTG	4980	
AGAACTCGTC ACTGACAAGC CTTGGATGGA TACTTGACCG CTGTGACCA GTTTATCTCC	5040	
AAGCAGACAG TCCAAGAGTG TGGTCTTCCC AGCACCATTG GGCCCAATCA AGGCGACGCA	5100	
TTCACCTTCA GCTACCTCAA AGGAAATACC CTTCAAAATA GCCTTGCCCT TGATGTTTTT	5160	
ATTTAGGCTT TCTACCTTAA TCATATTCAT GATATTCTCC TTTCAACCAC TCCATTCTCA	5220	
TAAGGAAAAC GACGAAAATC ATAAATCCAA ACCCCAAAGC ACCACGAATG AATTGGCGAA	5280	
GCAAGGTTTG GTCAAACCAA CCTGTAAACA TTTCCACTAA CCATACCAAG AGTGACAGGC	5340	
CGATAAAGAA ATAGATGATC CCTCTCTTCA TTCCTCAAGC TCCTTTTTC CATCTCCGAC	5400	
TAATTTCAAA CCTTCTCTAA CAAGCCAAGA CATCATTTCA AAGCCAGCAA AGAGCTCCCA	5460	
AGGAAAATGA TAGAACTCT CATCCAATCC CGAAAACATG AGTTAGGTCA TAACTCCTGC	5520	
TACTACTAAA CTCACTGCGA TAATCATTTT ATTTCTCATC TCTTCTTCT CCATTTTATA	5580	
CTACAATTAT AGTCTTTTGA ATCAGAGGA GACAGAAGCT TCTGTCACTA GAAAATATGA	5640	

1173

CAAATGTCAT AAAAAATTCT GTTCAAAACA AGCAAGATAC ACTATACAAT AAAACACAAT	5700
TAGAAAAATC TAAGGCAACT TCCTCAAAAG AGATATCAAA CCCAATTCAC ACCATAATGT	5760
AAACTAATAC TTATTTAAAA TCAAAAAGAG TAGAAATTTT TATCAGACAA ACACATATAT	5820
AGTGTATTGA ATCTATAACA GTAGGCCTTA AATACTAAAA TATTTCTATA AATTAATTTA	5880
ACTTTCCTGA TAGAGCTGTT CATATCTTAT TTCAATTCTC TAAATTATAC GTTGAACAAA	5940
ACCCCTCTAT TTCTTCTTA AAGATTTATA AGAGTTATAA AATCTGTTAA ATTTCAATGT	6000
GTATACCTAA ACTACGGTAT TTATTGAAAA GACTGGAGAC AAAAAGTATA CGCTGCCAAA	6060
ATGAATTACT GAAAATCAAA AAAGAGAGAA CCAAACTGAT TCCCTCTTAA TGTATATAAT	6120
ATCTAGTTTT AAAAATACAC ACTCACATAT CTCTGTAATG AATCGGGAAG ACAGGATTCTG	6180
AACCTGCGAC ACCTTGGTCC CAAACCAAGC ACTCTACCAA GCTGAGCTAC TTCCCGAGTT	6240
AAATAGAAAA ATGCACCCTA GAGGAGTCGA ACCTCTAACC GCCTGATTCTG TAGTCAGGTA	6300
CTCTATCCAG TTGAGCTAAG GGTGCTCCAT ATTATGCCGA GGACCGGAAT CGAACCGGTA	6360
CGATCGTTAC CAATCGCAGG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC	6420
CTCTCTAAGC GAACGACGGG ATTCGAACCC GCGACCCCCA CCTTGGCAAG GTGGTGTCTT	6480
ACCACTGAAC TACGTTGCGA CTGTTTTCTT CTATCTAAAA ATGCCGGCTA CATGACTTGA	6540
ACACGCGACC CTCTGATTAC AAATCAGATG CTCTACCAAC TGAGCTAAGC CGGCTCATTT	6600
GTTATATCTT AATGCGGGTT AAGGGACTTG AACCCCCACG CCGTTAAGCG CCAGATCCTA	6660
AATCTGGTGC GTCTGCCAAT TCCGCCAAAC CCGCATATAT GACCCGTA CTGGCTCGAAC	6720
CAGTGACCCA TTGATTAAAA GTCAATTGCT CTACCAACTG AGCTAACGAG TCTAAAATAA	6780
CTTGCGTTAC CTTAAACGGT CCCGACGGGA ATCGAACCCG CGATCTCGCC GTGACAAGGC	6840
GACGTG	6846

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GAATTCATTT TAAATAAAGA TACGGGAGAG GTAAGTGAAT TAAAACCTCA TAGGGTAACT	60
GTGACCATTC AAAATGGAAA AGAAATGAGT TCAACGATAG TGTCGGAAGA AGATTTTATT	120

1174

TTACCTGTTT ATAAGGGTGA ATTAGAAAAA GGATACCAAT TTGATGGTTG GGAAATTTCT	180
GGTTTCGAAG GTAAAAAGA CGCTGGCTAT GTTATTAATC TATCAAAAGA TACCTTTATA	240
AAACCTGTAT TCAAGAAAAA AGAGGAGAAA AAGGAGGAAG AAAATAAACC TACTTTTGAT	300
GTATCGAAAA AGAAAGATAA CCCACAAGTA AACCATAGTC AATTAAATGA AAGTCACAGA	360
AAAGAGGATT TACAAAGAGA AGAGCATTCA CAAAAATCTG ATTCAACTAA GGATGTTACA	420
GCTACAGTTC TTGATAAAAA CAATATCAGT AGTAAATCAA CTAATAACAA TCCTAATAAG	480
TTGCCAAAAA CTGGAACAGC AAGCGGAGCC CAGACACTAT TAGCTGCCGG AATAATGTTT	540
ATAGTAGGAA TTTTCTTGG ATTGAAGAAA AAAATCAAG ATTAAGATAA AAGCTATAGA	600
AAAAATGGT TTATGTACTG AGATTAGATA GTGAGGTGAT GACATAGTTT TGTGAAAATA	660
GCCATTTATA ACTCAATTAT TTAGTTTACT TTACTTTACT AGTGATACTA TTTGGAGTTA	720
TTAATGGACT TAGTTTATAT AACTAATGAA TTGATTGAAA GGGTTAGTAT TGACAATATT	780
GGTCATATTG ACTAGAAAAT AGAGTCTATC AAAATTTAAA GGCTAATAGA GGTGATGAGA	840
CAATTTCGGC TCTTTGTCAA CTGTAGTGGG TTGAAGTCAG CTAAGCTCGA GAAAGGACAA	900
ATTTTGTCTT TTCTTTTGTG ATATTCAGAG CGATAAAAAT CCGTTTTTTG AAGTTTTCAA	960
AGTTTCGAAA ACCAAAGGCA TTGCGCTTGA TAAGTTTGAT GAGATTATTG GTCGCTTCCA	1020
GTTTGGCATT AGAATAGTGT AGTTGAAGGG CATTGACAAT CTTCTCTTTA TCTTTGAGGA	1080
AGGTTTTAGA GGATGAACTT GATTCAGATT GTCCTCAATG AGTCCGAAAA ATTTGTCAGG	1140
CTCCTTATTC TGAAAGTGAA AAAGCAAGAG TTGATAGAGA TTATAGTGGT GTTCAAGTC	1200
TTCTGAATAG CTCAAAAGTT TATCTATAGT AGATTGAAAC TAGAATAGTA CACCTCTGCT	1260
TCTAAAACAT TGTTAGAAAT CGATTGACT GTCCTGAATG ATTTGTCCTG TTATTATTTT	1320
ATTTTACTAT AAATCCACGT TTACGAATCT CTTCCACAC TTGTTCAATG GGGTTCATCT	1380
CTGGTGTGTA TGGAGGAATA AATGCAAAAC CAATATTAGT CGGAATCTTT AAGGTACTTG	1440
ATTTATGCCA TATAGCATTG TCCATAACGA GTAAAAGATA ATCATCTGGA TAAGCTTGTG	1500
AAAGCTCCTA TTCCTAAAGC CCCTTTATAA CCTCTTGCGA GAGAGACTAT TGA CTGAGCC	1560
CTTACTTCAT GCGGATGAAA CTTCTTATCG GGTCTAGAG AGTCATAGCC ATCTGACCTA	1620
CTATTGGACC TTTTGTCTG GGAAAGTTGA GAATCAAGCA ATCACGCTGT ACCATCATGA	1680
TCAGAGTCGG AGTGGTTCGG TAGTACAAGA ATTCCTAGGA GATTATTCTG GCTATGTTCA	1740
TTGTGATATG TTGCGGCAGT AACTTAGGAC TTTAGTCCTC TAGTTCTGCC TATGCGATAG	1800
CAGTCCAAGG TTTAGGAGCA AGGCGACGCT AAGCTTGGTA AACTGCGAAC CGCTAGAAGC	1860
TTATCGTCAA CTGGAAGAAG CTGAACTTGT TGGATGTTGG GCGCATGTGA GAAGGAAATT	1920

1175

TTTTGAAGCG ACCCCCAAGC AAGCAGATAA ATCATCCTTA GGAGCTAAAG GTTTAGCTTA	1980
TTGTGATCAG TTATTTTCCT TGGAAAKAGA CTGGGAGGCT TTGCCAGCTG ATGAACGACT	2040
ACAGAAACGT CAAGAACATC TCCAGCCCCT AATGGAAGAC TTCTTTGCTT GGTGCCGCCG	2100
TCAGTCAGTT TTAGCAGGTT CAAAACTAGG AAGGGCAATT GAATACAGCC TCAAGTATGA	2160
AGAAACCTTT AAGACTATTT TGAAAGACGG ACATCTGGTC CTTTCCAATA ATCTAGCTGA	2220
ACGCGCCATT AAATCATTGG TTATGGGACG GAGTAAAAGA GTCCAGTGGA CTCTTTTAGC	2280
CTGAGCTCAG TTTAAAAAAG CGAGGGTGGT TATTTTCTCA AAGTTTGAAG GGAGCTAAAG	2340
CAAGAGCTAT TGTTATGAGC TTGTTGGAAA CAGCTAAACG TCATCAATTA TAGTGCGTTG	2400
AATCTATAAC AGTACGCATC GACTGCTAAA ACATTTCTAT AAATCAATTT TCCTTTCTTA	2460
ATCGATTTGT TCATATCTTA TTTCAATCCA TTATAAATAG CGAGAAATAT CTATCCTATC	2520
TTCTAGAATG TCTTCCAAAC GAGGAACTC TCGTAAACAA AGAGGTTTGA GAGGTTTATT	2580
TACCATGGAC TAAAGTTGTA CAAGAAAAGT GCAAATAAGA AATCTCCAGA TTAGGAACTA	2640
TCCGTGAGTT CACTAATCTG GAGATTTTTC AATAGATTCG TTATTGGGCG GTTACCATAT	2700
GATCACTACT TCGTCAGTCT TATCTACAAC CTCAAAACAG TGTMTTGAGC AACCTGCGAC	2760
TAGCTTCCTA GTTTACTCTT TGATTTTCAT TGAATATTAG AACAGAAAAA ATGCTTGGAG	2820
TATTTGTTTG TGTGTTTATT TTTATATAAC AAACATAAAA CAAAATAAAA ATATAAAAAA	2880
AGAGACAAAA AAGAACAGAA AGTAATTGAC A	2911

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6854 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GAAAAAAGT CTTGACAGAA AGCGCTATCA ATGATAGAAT GAATTCAGAT AAAAAGATTT	60
ATTTTAAAAA CAAAAATGAA ACGTTTCAAA AAAAGAAATA AAGAGACAGC GCCAAGCGCT	120
ATCTTTTCTA GAAAAAATG AAACGTTTCA AAAAAGGAGG TTGCTATGAA TAGCAAAGCG	180
AAGCAAGTTT CTCTTTGGGA AAGAATCAAG AAACAAAAAC TCTTGTATT GATGACTGTC	240
CCCGGTTTAG TTTTAACCTT TATCTTTAAA TACATCCCTA TGTATGGGGT TTTAATCGCA	300
TTTAAAGATT ACAATCCTTT AAAAGGAATT TTAGGGAGTG ATTGGATTGG TTTTCTGAG	360

1176

TTTACAAAAT TCATATCCTC TCCCAACTTT GGTATCTTGT TAGCCAACAC ATTAAAATTA	420
AGTATCTATG GTTTATTGCT TGGCTTTTTA CCACCAATCA TTCTCGCGAT TATGCTCAAT	480
CAACTCTTGA GTGAAAAAGT CAAAAACGA ATTCAGCTCA TTTTATACGC ACCAACTTT	540
ATCTCAGTCG TTGTTATTGT CGGTATGATT TTCCTCTTCT TTTCAGTGGG AGGACCAATC	600
AACAATTTTC TTTCTATGTT TGAATGAAG GCTGACTTCT TGACAAATCC AGACTTCTTT	660
AGACCTTTAT ACATCTTTAG TGGTATCTGG CAAGGAATGG GCTGGGCTTC AACGCTCTAC	720
ACGGCAACAT TGGTAAATGT AGATCCAGCC TTAGTAGAAG CAGCCCGACT GGATGGAGCC	780
AATATCTTCC AACGAATCTG GCACATTGAT ATTCAGCTC TTAAGCCTAT TATGGTTATC	840
CAATTTGTTT TAGCTGCAGG TGAATATATG AATGTCGGAT ATGAAAAAGC ATTCTTGATG	900
CAGACATCGT TAAATTTGCC AACTTCTGAA ATTATCTCGA CATATGTCTA TAAAGTTGGT	960
CTTGTATCAG GAGACTATTC TTAACAACA GCGGTTGGTT TGTTTAATGC AGTGATTAAC	1020
GTAGTATTGC TTGTTGCAGT TAACCAAATC GTTAAACGCA TGAATAATGG TGAAGGAATT	1080
TAAGGAGGAA AGTATGAAAA ATTCGATTAT GGATACAAAA TTGATAGAC GTATCTTACT	1140
CTTAAATAAA ATCATTATTG TCTTTATCGT TTTGATGACT TTGCTTCCTT TACTTTATAT	1200
CGTCGTAGCA TCCTTTATGG ATCCTAAGGT TCTGGTTAGT AGAGGGATTA GCTTTAATCC	1260
AGCCGATTGG ACTGTAGAAG GTTACCAGCG TGTATTCTAGT GACCAATCTA TTCTAAGAGG	1320
TTTTATCAAT TCTCTACTAT ACTCTTTTGG ATTTGCAGCT TTAACAGTCT TGCTATCTGT	1380
GTTTACAGCT TATCCTCTTT CTAAGAAAGA CTTGGTTGGA CGTCGTTGGA TTAACACTT	1440
CTTGATTGTA ACTATGTTCT TTGGTGGTGG TTTAGTCCCA ACTTACTTGC TCGTAAAAGA	1500
ATTGGGAATG CTCAATACTC CATGGGCTAT CATGTTTCCA GGTGCTGTGA ACGTTTGGAA	1560
TATTATCTTT GCTAGGGCCT ATTTCCAAGG ATTGCCCTGAA GAATTAGTTG AAGCTGCTGT	1620
CATTGATGGT GCAAATGATT TACAGATTTT CTTCAAATC ATGCTTCCTC TTGCAAAACC	1680
AATTATGTTT GTTCTCTTCC TTTATGCTTT TGTAGGACAG TGGAATCAT ACTTTGATGC	1740
AATGATTTAT ATCAAGGATC CAACTTGGA ACCATTGCAA CTTGTACTTC GTAAAATCT	1800
CATTAGAGC CAACCAGGTC AAGACATGAT TGGAGCACAA GCGGCTATGA ATGAAATGAA	1860
ACGTTTAGCT GAATTGATTA AATACGCAAC TATTGTCATT TCCAGCTTGC CATTGATTGT	1920
TATGTATCCA TTCTTCCAAA AATACTTTGA TAAAGGAATT ATGGCTGGTT CACTTAAAGG	1980
ATAAAAAAAG AAAAAATAAA AGGAGTTTTC TCATGAAATT CAAAACATTC TCAAAATCAG	2040
CAGTTTGTGT GACAGCTAGT TTAGCAGTAC TTGCAGCCTG TGGCTCAAAA AATACAGCTT	2100
CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCTCGT TCAAGAAAAG AAAACATTGA	2160

1177

AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC AAATGAAAAG TTAATTTTGC	2220
AACGTTTGGA GAAGGAACT GCGGTCATA TTGACTGGAC CAACTACCAA TCCGACTTGT	2280
CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC AGATGCTATC CACAACGACG	2340
GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG TGTATTATT CCAGTTGAAG	2400
ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAAATTT GGATGAGAAA CCAGAGTACA	2460
AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT TCCATGGATT GAAGAGCTTG	2520
GAGATGGTAA AGAGTCTATT CACAGTGTC ACGATATGGC TTGGATTAAAC AAAGATTGGC	2580
TTAAGAACT TGGTCTTGAA ATGCCAAAA CTACTGATGA TTTGATTAAA GTCCTAGAAG	2640
CTTTCAAAA CGGGATCCA AATGGAAATG GAGAGGCTGA TGAAATCCA TTTTCATTTA	2700
TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC TGCATTTGGT ATAGGGGATA	2760
ACGATGATCA TTAGTAGTA GGAAATGATG GCAAAGTTGA CTTACAGCA GATAACGATA	2820
ACTATAAAGA AGGTGTCAA TTTATCCGTC AATGCAAGA AAAAGGCCTG ATTGATAAAG	2880
AAGCTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAG TCATGATCAG AAATTTGGTG	2940
TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA CGAAAGTTAT GATGTTTTAC	3000
CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG TACAAACGGT ATGGGATTTG	3060
CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT AGAATTGACA GCTAAATGGA	3120
TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATA CTGGGGAAC TACGGAGATG	3180
ACAAACAACA AAACATCTT GAATTGGATC AAGCGTCAA TAGTCTAAAA CACTTACCAC	3240
TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA AGTAGGAGGA CCACTAGCTA	3300
TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA TGATGCCAAA TGGCGTTTGG	3360
ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT CAATAACTAT CCAAGAGTCT	3420
TTATGACACA GGAAGATTG GACAAGATTG CCCATATCGA AGCAGATATG AATGACTATA	3480
TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT TGATACTGAG TGGGATGATT	3540
ACAAGAAAGA ACTTGAAAA TACGGACTTT CTGATTACCT CGCTATTAAA CAAAAACT	3600
ACGACCAATA CCAAGCAAAC AAAAAGTAGA GGTTGATTAT GGGAGATAAG AAATACACAG	3660
TAGAAAAAGC CAATCGTTTT ATAGCAGAAA ATAAACATCT CGTTAATACT CAATATAAGC	3720
CTGAAGAACA TTTTTCAGCT GAGATTGGT GGATCAATGA TCCAAATGGA TTTGCTATT	3780
TTCTGGGAGA ATACCATCTC TTTTATCAAT TCTATCCATA TGATAGTGTT TGGGGGCTA	3840
TGCACTGGGG ACATGCTAAA AGTAAGGACT TGGTGACTTG GGAGCACTTG CCAGTGGCAC	3900

1178

TTGCTCCTGA CCAAGATTAT GACCGAAATG GTTGTCTCTC AGGCTCTGCC ATTGTCAAGG	3960
ATGATCGCCT CTGGCTCATG TACACTGGAC ATATCGAAGA AGAAACCGGT GTCCGCCAAG	4020
TGCAAAATAT GGTATTTTCA GATGACGGGA TTCACCTTGA AAAGATTTC CAAATCCAG	4080
TTGCAACTGG ATCAGACTTA CCAGATGAGT TGATTGCTGC TGATTTCGGT GATCCAAAAC	4140
TCTTTGAAAA AGATGGACGC TATTACTCCG TAGTAGCTGC CAAACACAAG GATAATGTGG	4200
GCTGTATCGT TCTACTAGGG TCCGATAACC TAGTAGAATG GCAGTTCGAA TCCATCTTTT	4260
TAAAAGGGGG AGAACACCAA GGTTTTATGT GGAATGCCG AGATTACTTC GAGTTAGATG	4320
GGAAAGATTG CCTTATTATG TCACCCATGC GTTATCAGCG TGAGGGAGAC TCATATCATA	4380
ACATCAACTC ATCGCTTTTG TTCACGGGTA AGGTAGATTG GAGAGAAAAA CGTTTATCC	4440
CAGAATCAGT TCAAGAAATT GATCATGGCC AAGACTTCTA TCGCCTCAA ACATTGTTGG	4500
ACGATCAAAA TCGTCGTATC CTGATTGCTT GGATGCAGAC ATGGGGGCGT ACCCTTCCAA	4560
CCCATGACCA AGAACACAAG TGGGCATGTG CCATGACTCT ACCTAGAATT CTAAGATTGG	4620
AAGATGGCAA ACTAAGACAA TTCCCTGTTA AAAAAGGCCA ATATCAAATC CAAATAGATA	4680
AAGATTGTCA TTACCACTTA GGAAATGATA TAGATTATCT TGAATTTGGT TATGACAGTA	4740
ATGCGCAGCA AGTTTACATT GATCGTAGCC ATCTTATTCA AAAAATCTA GGTGAAGAAG	4800
AACAGGACAC TAGTCGACGG TATGTAGATA TTGAAGCTAA AGAATTGGAA GTTGTCTAG	4860
ATAAAAATTC CATCGAGATT TTTGTCAATC AAGGTGAAGC AAGCTTGACT GCAACTTATT	4920
ACTTAACGGT GCCAGCTGAG CTATCACGAA TTGATTAAAA ATTAAGTTAT TTCTCCTAAA	4980
GAAAAAGTTC TCTTTCTAAA ATAGTGGAAG GAGGACTTTT TGTGTTTTGG GTATATAAGC	5040
TTAGTTTATG GTATTGTAA AATTGGTGT GGATTATGAT TTAAGCTAGT TTTCTAAAGA	5100
ATTTGAAAAA AATTTTATTT AAGCAAAAAA ACCTTGGTTC CAAGGCTTTT CCTGTGTAT	5160
TTAGATGCCC CCTACAGGGA TTGTAGGAGA TATGTTGCTT AGATGTTCTT GATTTTCTGG	5220
TGTTTTGTAA CGTTTAAATG AGTTTTTTGA GTTTGTTGGT GGGGCGTTGC CCGGCAATTG	5280
CCCGACTTAT TGCTTGAAAA AGAATTTAAA ATATAGTATA GTTAATTATA GATTAACT	5340
TGCTTGAGG AACTGATGAA GAACAATGAA AGATTAGGTA TTAAATTAAG TAGAGATAGC	5400
GTTTTAGGAT TGAGGGAAGT TAGAAGGCTT TATTTAGGCA GTTCAGATAT CCCAGTTTCT	5460
GATGGCTATG TGATTGAAGT TGCTTATAAC CAGATATCAC ATGAGATTGA TATTATTGAT	5520
TGGGTAGAGT TGAACAAGTC AAAAATTAAG ATAAGTGAAA TTAGTGAAAG CGTGGATATA	5580
GATGCCACTA GCTTGAGAAC AACTTTGACT TTAGACACAT TAGTATATGA AGGTATGAGA	5640
GATATACAGT TAAAGTTGAG AGAGCTTACA AAGGGGAGAG TATTCTTTTC ATTTGTAGTG	5700

1179

AAGTTAGTTT TGTTCGCTC TATTTTAAAG AAAAAAGATT TACTAGAAAA ATTTCAAGAA	5760
AAGTGTTAAT CAAGTATTGA CACTTTATCT GGATTTCGGT ATAATATGCT TAGAAAGGAA	5820
TCTTTCTAAA TTTTTCGT CCTTATGTGT TAATCAAAGA CGAATACAAA AACATATTTT	5880
TTTACTCTAA AAAGTGTTAA TCAATGATGT ATTTGTTAGA GAGGTAGATA AATGGAATTG	5940
AGAGCACCAC CAGTTATAAT AGTATAAAC GTATAATAA AATATTTTAA CTTGAATTAT	6000
AGAAAAGGAG AAACAAATCA TGAACAAAA ACAACCGATT GTTCTAGAA CGAAACAACA	6060
TACATTTGAA GAGCTTATTC AAGACAAAA GTTAGAAAGA TTGGCTAAGT TGTGCCCCGA	6120
TTTGTTGGA AGGTATGGTT TTAGTGCTAG CTGTGCGTCT TCATTTGCGA ACTTGATTAA	6180
AGAAGCGTAT GGGGGTAAAA ATCTAAACGT AGTTTATGCG AGTCGGATGT TGGCTCTCTG	6240
GAATATTGCT TGCAGTTGTT ATCATAAGGC TGATGGGTAT TCTTTAGCAG ATGCGCTTTT	6300
TAGTGATAAA AAAATTTGTC TAGATTCTTA CTATTACCAC AAGAATACCT CTAATACCAT	6360
AAGTAGTGAT GTGATAAAG ATGTTTACGA TAATTATAAT AATTATATGG TTTAACTCG	6420
AGAAGCGACA CCTGAATACA TTTATGTTGT ACAAACGAA ATGCCAAAAG ATTCAGATTT	6480
ATATTTTAT ATTAGAGAAG TTCTGGGATT ATCGTTTAGT ACCATGCATT ATGCATTTTT	6540
AGTCAAGGTT CTGTCAGGAG CGCTTGCTAG AAAATATAAG CCATATCGAA ATTGAATTAT	6600
TTAAATTTAT ACTCTTCGAA AATCAAATTC AAACCAAGTC AGCTTCGCCT TGCTGTACTC	6660
AAGTGCTGTC TGTGGCTAGC TTCTTAGTTT GCTTTTGTAT TTTCATTGAG TATTACTCTT	6720
ATGGTAGTTA TTTATGGCAT AATAATATTG ATTTGGGAGT TATAGCGAAA ATTTTAGGTT	6780
CTATAATATT TGTAGTGGGT AAACCACTAT AGATATTATG GAGCCTATTT ATTGTAGAAA	6840
AAAGTCCCAT ATGA	6854

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3895 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

TCCTTGCTAA GTTTATACTC AATGAAAATC AAAGAACAAA CTAGGAAGCT AGCCACAGGT	60
TGCTCAAAGC ACCGCTTTGA GGTTCAGAT AAAACTGACA CGGTTTGAAG AGATTTTCGA	120
AGAGTATTAA TTTACATAAA TAGCCAGTGT TTGATAGGGT TTGAGTAGAA TTTTCTCAGA	180

1180		
CACTTCTGCA TCTTCATAGT TTGATATCAA AATCTGTCCA TTTTGGTAGA CTGCTGGCAA	240	
GTCGATTTcA CTTCTTTAGC ATAAAAGTTA TTGAGCACTA GTAACCTTTG ATCCTCAAAC	300	
TGGCGTTCAA AAGCGTAGAC TTGTTTGCTA TCTTCAAAGG CTGGTTTGTA ACTTCCTTCT	360	
GAAATGATTG GCATTCCTT ACGCATCGAA TCAAGTCTTG ATAGAAGGTA AAAATCGGAC	420	
CCTGGATTTC ATTTTCTACA TTGATGTATT TATAGGATTT ACCAGCTTTC AACCAAGGAG	480	
TGCCTGTGTA AAATCCTGCA TTTTCCGAAG CATCCCACTG CATGGGAATG CGTGAATTAT	540	
CACGCGACTT AGCTTGAATA ATCTGGAAGG CTCTTGCTG ACTCTTTCCT TCTTCTAAGA	600	
GCATCTGATA GGCATTAAGC GATTCGACAT CCACATAATC AGCCATAGAA TCATAGTCTG	660	
GGTCAATCAT CCCGATTTC TCACCCATGT AGATATAAGG TGTCCACGT GACAGGTGAA	720	
TGCTGGCTGC TAGCATGGTG GCTCCTTCCT TGCGGAAGTT TTGAATATCG ACAAACGGT	780	
TCAAGGCACG TGTTGATCG TGATTATTCC AAAAGAGGGC ACTCCAACCG TCTTTATCAC	840	
TCATTTCTT ACCCCAATA TGGTAAAGAC TCTTCACTC TTCAAATCA AAGGGAGCCA	900	
AGGTCCACTT TTGTCCATCC TTATAGTCCA CCTTGAGGTG ATGAAAATTA AAGGTCATGG	960	
ATAATTCCTG ACGATCAGGC GACGAATAGA GGACACAGTT TTCCATGGTG GTAGAAGACA	1020	
TTTCCCCAAC TGTCATAAAG CTATCGTCGG ATCCAAAAGT GGCTTGTTTC ATCATACGCA	1080	
AATAGTTATG AACGATGGGT TTGTCTGTAT AAGCTGGCTT CCCTTCATTT TCAGGACAGT	1140	
CCACTGAAAC CTCGTCTTA CCGATCAAAT TGATCACATC AAATCGGAAA CCTTTGACAC	1200	
CCTTGTCGCG CCAGAAATTA ACAACCTGA AAAGCTCCTT ACGGACATTG GAATTGCGCC	1260	
AGTTAAGGTC AGCCTGGGTC TCATCAAATA GGTGAAGATA GTATTTCCCA GTATCCCCGA	1320	
AAGGCGTCCA TGCAGAACCA CCAAACCTAG ACTGCCAATC TGTGGTTGG TCTTGGATGA	1380	
AGAAAAAGTC TTGATAATAC TTATACCAG CTAGGGCTTT CTGAAACCAT TCATGCTCTG	1440	
TCGAACAATG ATTAAGTACC ATGTCCAGCA TAAAGTCAAT CTTGTGCTCT TTACCGACAC	1500	
ACACCATTTT CTCAAAATCA GCCATATCAC CAAAAGAGG ATCCACTGCC ATATAATCTG	1560	
AAATATCGTA ACCATTATCC CGTTGAGGGC TTGGATAGAA TGGATTGAGC CAGACCATAT	1620	
CCACACCTAG TTTGGCTAAA TAGGGAATTT TTTCGATAAT CCCACGAAA TCCCCAATAC	1680	
CGTTTTAGT GGTGTCTTTG TAAGATTTTG GATAGATTG ATAGACTACT TTTCTTTTAT	1740	
CAAGTGTCTAT CTGTTCTCC TTTTCTGATA AAAGGGAGGA AGCAGTCTTC CGTCCCTATT	1800	
TGTGCTATTT CAATTATACT CAATGAAAAT CAAAGAACAA ACTAGGAAGC TAGCCACAGG	1860	
TTGCTCAAAA CACTATTTTG AGGTTGCAGA TAGAGCTGAC GTGGTTTGAA GAGATTTTCG	1920	
AAGAGTATTA GATTCGTGTA GCGACCATGA GAGATGCTCC AGCTTGATC GTTGTGCGAT	1980	

1181

AAGTTCCGGG AATAGTCGCT GTATAAGCAT CTGGTTGGT GATGATAACA GGAGTTTCTG	2040
TCACCAGACC TGCAGCCTTA ATGACATCCA TATCAAAACG AATCAGTTGC TGACCAACTG	2100
TAACGTGATC TCCTTGGA CTACAAGACTTT CAAAACCTTT GCCATCAAGA CCTACTGTAT	2160
CCATACCGAT GTGGATGAGC AATTCAACTC CCTCGTCAGA GACAATGCCG ATGGCATGCT	2220
TGGTAGGGAA AAGAACCGTC ACTGTCCCAT TAACTGGAGA GGTCAACTCA CCTTGGCTTG	2280
GTTCAATGAC TAGACCTTGC CCCATGACAC CTGATGCAAA AATAGGATCC GTCGCTTGAC	2340
TCAATTCTTT CACTTGGCCA GTTAGTGGGC TGATAATTTT TACCGAAGTA AGTTCTACTG	2400
GTTTCATGGT CACAAATTCT GCTTCTTCTT GAGCAACGAA TTCTGCCTGC AAGTTCGTAT	2460
CGCCCTCTGT TTTTGTAAAG AGACCAGCCT TGCAGAAGAA GAAAGTCAAG AGCATTGGAA	2520
CAACAATCGC AACTAGCATA GTTCCTGCAA ATGGCAGCAT GTATTGAGGT TGAATAGAGA	2580
GAATACCTGG CAAACCACCG ATACCAATAG AAGCCGAGT TACATTAAAA GTAACGGATA	2640
ACATGCCTGC AAGGGCTGAA CCAGTCATCC CAGCAACAAA TGGATAAATA TATTTTACGT	2700
TAACCCCAAA AAGAGCTGGT TCTGTAACAC CGAGATAGGC TGAAATGGTT GCAGGAAGTG	2760
AAACCTGAGC CTCACGCTCA TCATGGCGAT GCATGAAATA ATAGGCAAAC ACGGCTGAGC	2820
CTTGAGCAAT ATTAGAAAGA GCAATCATTG GCCATAGGGC AGTGCCACCA GCATCCGCAA	2880
TCAATTGTGT ATCAATGGCA TTGGTCATAT GGTGCAGACC TGTGATGACA AATGGAGCGT	2940
AGAGGGCGCC AAAAATTGCA CCGAAGAGCC ATTTAACTGG ACCAGTTAAA CCTGCCAAGA	3000
CAACTGATGA AAGTCCTTGT CCAATTGTCC AACCGATTGG TCCCAAAACA GTATGAGCCA	3060
AAATCAAGGC TGAATCAAT GACAAGAAAG GTACAAAAT CATAGAAATG ACTTCTGGGA	3120
TATGCTTGTG CCAGAAGATT TCAAGATAAG ACAGACTCAA ACCTGCAAGC AAGGCTGGGA	3180
TAACTTGGGC TTGGTAACCG ATACGATTAA CAGTAAAATA GCCAAAATTC CAAACCCAGT	3240
TTGCCGCGAT ATCAGCTGCT GCGGTTGAAG CAACCGCATA GGCATTGAGC AACTGAGGCG	3300
ATACCAAACA GATTCCGAGA ACAATCCCA AAATTGGCT GGTTCCTATC TTACGAGAAA	3360
CAGACCAAGT AATCCCTACT GGTAAGAACT GGAAGATAGC TTCACCAGGC AACCAGAGGA	3420
AGTGATTGAC ACCTGCCCAA AACTGAGAGG ATTCTGTGAT GGTCTTGCCA TCCAACATCG	3480
ACCAATGGAC ACCTTCCAAG ACATTACGGA AACCAGGAT CAATCCTCCG ACTATCAAGG	3540
CTGAATAAT CGGAGTAAAA ATCTCCGCCA GAGTGGTCAT AACACCTTG ACCACGTTTT	3600
GATTACTCTT AGCTGCAGAC TTGGCTGCTT CTTTGGAAAC ACCCTCAATA CCTGAAACGG	3660
CTGTAAAATC ATTATAAAAG ATGGGCACGT CATTTCCAAT GATTACCTGA AATTGACCTG	3720

1182

CATTGTGAAA GGTTCCTTTA ACAGCTGGAA TTGACTCGAT AGCTTTAACA TTAGCCTTCT	3780
TATCATCTCC TAAAACAAAC CGCATCCGTG TCGCACAGTG AGTTACGGCA GTCACATTTT	3840
CTTTGCCTCC GATTGCCTGA AGCAGATCTT TGGCTTCTTG TTCAAATTTT CCCGG	3895

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGGATCGCCG CTCCAGCTAC TAAGTCTCGT GCAGTGCCGA TTTATCAAAC AACATTTT	60
GTTTTTGATG ACACGTAGGA AGGTGCCGAT CTGTTTGCCT TGAGGAAACC AGGGAACATT	120
TATACTCGTA TCACCAATCC TACAACAGCT GCCCTTGAAG GTGGTGTTGA AGCGCTAgcA	180
ACAGCATCAG GTATGACTGC AGTGACTTAT ACGATTTTGG CGATTGCCCA TGCTGGTGAC	240
CATGTAGTGG CTGCTTCGAC TATTTACGGT GGAACCTTCA ATCTTTTGAA AGAACCCCTT	300
CCTCGTTATG GTATCACAAC AACCTTTTTC GATATTGATA ATTTGGAGGA AGTAGAAGCA	360
GCTATCAAAG ACAATACCAA GCTTGTCTTG ATTGAAACCT TGGGTAACCC CTTGATTAAT	420
ATTCCAGACC TGGAAAAACT GGCAGAGATT GCTCATAAAC ATCAAATCCC ACTTGTGTCA	480
GACAATACTT TTGCAACACC TTATTTGATT AACGTCTTCT CTCATGGCGT TGACATTGCC	540
ATTCACTCTG TGAATAAGTT TATCGGTGGG CATGGTACAA CTATTGGAGG AATAATTGTC	600
GATAGTGGTC GTTTTGACTG GACGGCTTCA GGGAAATTC CTCAATTTGT TGACGAGGGT	660
CCAAGCTGCC ACAATTTGAG CTATACTCGT GATGTGGGTG CAGCAGCCTT TATTATAGCT	720
GTTCGAGTTC AATTGCTTCG TGATACAGGT GCAGCCTTGT CACCATTCOA TGCTTTCCTC	780
TTGCTACAAA GACTTGAAAC CTCTTCACTT CGTGTGGAAC GCCATGTACA AAATGCTGAG	840
ACAATGTGTG ATTTTCTTGT CAACCATCCT AAGGTAGAAA AGGTAAATTA TCCAAAACCT	900
GCAGATAGTC CTTATCATGC CTTGGCTGAG AAATACTTGC CAAAAGGTGT CGGTTCAATC	960
TTTACCTTCC ACGTCAAAGG TGGCGAGGAA GAAGCACGCA AGGTCATTGA TAATTTAGAA	1020
ATCTTTTCTG ACCTTGCAAA CGCGGCAGAT GCTAAATCGC TTGTTGTCCA TCCAGCAACA	1080
ACCACTCACG GTCAATTGTC AGAAAAAGAC CTAGAAGCAG CAGGTGTCAC ACCAAAATAA	1140
ATTCGTTTGT CAATCGGTCT TGAAAAATGA GAAGATTGTA TTGAAGACTT GCGCTTGGCC	1200
TTGGAAGAAA TTAAAGTAA AAGAAGATAA AACTGCGCT TCGACTCACT GTTTTGTATT	1260

1183

TTCCCTCAGG CATGATATAA TGGTTACAGA AGTCTAGAAA GAGGAACGAT ATGAACGAAA	1320
TCAAATGTCC CAACTGTGGG GAAGTCTTTA CAGTAAATGA GAGTCAGTAT GCCGAACTCT	1380
TGTCCCAAGT GAGAACGGCA GAGTTTGATA AGGAACTACA CGATAGGATG AAGCAGGAAC	1440
TGGCCTTGGC TGAGCAAAAG GCCATGAATG AGCAACAGAC TAAACTGGCT CAGAAGGATC	1500
AAGAAATTGC GCAATTACAG AGTCAGATCC AAAACTTTGA TACAGAAAAA GAATTGGCCA	1560
AGAAAGAGGT TGAACAGACA AGCCATGAGG CTCTCTTGGC TAAGGACAAG GAAGTACAGC	1620
TCTTAGAAAA TCAGTTGGCT ACCTTGCGTT TGGAGCATGA AAATCAACTA CAAAAGACCC	1680
TTTCTGACCT AGAAAAAGAA CGGGATCAGG TTA AAAACCA ACTACTTTTG CAGGAAAAGG	1740
AAAATGAATT ATCTTTGGCT TCTGTTAAGC AAAACTACGA AGCCCAGCTC AAGGCAGCTA	1800
GTGAACAAGT CGAGTTTAT AAGAATTTTA AGGCTCAACA ATCTACAAA GCGATTGGGG	1860
AAAGCCTAGA ACAGTATGCA GAGAGTGACT TTAACAAGGT TCGTAGTTTC GCCTTTCCAA	1920
ATGCTTACTT TGAGAAGGAT AACAGGTCT CTTCGCGTGG GTCTAAAGGG GACTTTATCT	1980
TCCGTGAGTG TGATGAAAAT GGAGTTGAAA TCATTCTCTAT CATGTTTGAG ATGAAAAACG	2040
AAGCGGACGG AACAGAGAAG AAGCACAGA ATGCAGATTT TTACAAGGAA TTGGACAAGG	2100
ACCGTCGGGA GAAGAACTGT GAGTATGCCG TTTTGGTGAC CATGCTTGAG GCTGATAATG	2160
ACTACTTTAA CACAGGGATT GTTGACGTCA GTCACGAGTA TGAAAAAATG TATGTTGTTT	2220
GTCTTCAATT CTTTATCCAA TTGATTGGTC TCTTACGTAA TGCGGCGCTA AATTCCCTAA	2280
AATACAAGCA GGAGTTGGCC TTGGTTCGCG AGCAAAATAT TGACATTACG CATTTTGAGG	2340
AAGATTTGGA TGCCTTTAAG CTAGCTTTTG CTAAGAACTA TAATTCAGCT TCGACTAACT	2400
TTGGAAAAGC TATTGATGAA ATCGACAAGG CCATCAAACG CATGGAAGAG GTTAAGAAAT	2460
TCCTGACCAC ATCTGAAAAC CAACTCCGTT TAGCTAACAA CAAATTGGAA GATGTCTCTG	2520
TTAAAAAATT GACCCGGAAT AATCCAACAA TGAAAGCGAA GTTCGAAGCA CTGAAGGGGG	2580
AGTAGAAAAGC AAAAATGAAC GGTATTATTA ACTTAAAAA GGAAGCAGGA ATGACCTCGC	2640
ATGATGCGGT TTTTAAACTG CGTAAGATTT TGGGAACCAA GAAAATTGGT CATGGTGGAA	2700
CCTTGATCC GGATGTGGTG GGTGTTTTCG CGATTGCGGT TGGCAAGGCG ACACGCATGG	2760
TCGAGTTTAT GCAGACGAG GGTAAGATCT ATGAGGGGGA AATCACTCTG GGCTATTCCA	2820
CGAAGACTGA GGATGCTAGT GGGGAAGTGG TCGCAGAAAC CCCTGTTTTC TCTCTCTGG	2880
ATGAAAAGCT TGTGATGAA GCGATTGCTA GCTTGACTGG GCCTATTACT CAGATTCCCC	2940
CTATGTATTC GGCAGTTAAG GTTAATGGTC GCAAGCTCTA TGAGTATGCG CGTGCTGGTC	3000

1184

AGGAAGTGGA GCGTCCAGAA CGTCAGGTGA CCATTTATCA ATTTGAGCGA ACAAGTCCGA	3060
TTTCTTATGA TGGCCAACTT GCCCGATTCA CTTTTCGTGT AAAATGCAGT AAAGGGACGT	3120
ACATCCGTAC TTTGTCTAGT GATTGCGGTG AAAAGCTTGG TTATGCGGCT CATATGTCCC	3180
ATTTGACTCG TACTAGTCTG GCTGGCTTAC AATTAGAAGA CGCTCTTGCC TTGGAGGAAA	3240
TTGCTGAAAA AGTAGAGGCT GGGCAATTAG ATTTTCTCCA TCCTTTAGAG ATTGGGACAG	3300
GTGACCTTGT CAAAGTTTTC CTAAGTCCAG AAGAGGCTAC AGAAGTTCGC TTTGGTCTGT	3360
TTATTGAGCT AGACCAAACG GACAAAGAAC TGGCTGCCTT TGAAGATGAT AAATTGTTAG	3420
CCATTCTAGA AAAACGGGGC AATCTCTATA AGCCAAGGAA GGTTTTTAGC TAGATCGTTT	3480
AGGAATAAAA ATCGGGTGAT AGATAACAAT TGCTTGATAA AACCCCATAC TAATAGTAGA	3540
ATGGTTTTTG GAATTATAAT ATTCCAATTG TTGCGAGTTG TAGGTACTCA AATAATCTAT	3600
ATAGAAATTT AGAGGTGTGA AATGAAGCAA TTTAAAATTC TTTCAGATAA ATATTTAGAG	3660
TCCATTACAG GTTCTGATGG GAACTTAGGC CCAGGATTG GTGTGATAAT TCCATGATGC	3720
GAAATGAGTT TCGAGAAAGG GTGGAGCAAC TTCTTCAACA AAAAGAAATA AATGAAAATA	3780
GTGAGTTGAG TCACCTGTTT CGTCTTGCTA TACAAAATTT AGACAGAAAT GAAAAATACC	3840
AATCGGTCAT GGCCAATTTG AGTCAAGGGT TGTCACTTTA CCTCATGACG CATCATTACC	3900
AGGCACCTAA GTCTGTCATT GATTTTGTTT TATGGA	3936

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

CATCCAGCAA CTGCTCCTCT GAGCGTTTCA AAATTGATGT AATTTTCTA GTTTTCTA	60
ATAAATGTGC CATTTTTCAC CTCGAATTTA ATCGCTATCA TTATAACATA AAAACGTCTC	120
TTTTTCAATA ATTATCTGAA AATTCCTTAT TGAATTGCAT TGAATTACAA TTTAATTAAA	180
AACCAGAATA TTTTAAATTA AATTGTTCCCT TTTCTATTGA CAAGTTGCCT ATTTTGTGT	240
ATCATAATAT TATAAAAGAT AATATAATAA TTTTATTGT CTTTTCACAT TCGGTCTCCT	300
TATATAAAAA AGCGATTCAT TTTGAACCGC TTTTCTTAT TTATCGCCTT TGTACGAAT	360
AACAAAGCCT GTTTGCTTTT CGCTTAAAGT ATTGCGTGGT TTTTATTAT CCTTACGGTA	420
ACGTTTTTCC TTATCAAAAC GATCGTTGCC ACGACTTCCT TTTTGAACCT CATCACGGCG	480

1185

ACCATTGCCA CGGCGATCAC GCTCTCGACG GTCGTCCCCA CGACGGCCTC CACGACCTCC	540
CTTAGCTTTA CCACCGAAAC CATTACCTGA TGGTTTAAAC GGTAGTGGTT TTTACAGTGC	600
AATCTCCACT TCTGGAAGGC TATCTGGGTC TTGGACTGTC AGACTCAAGA TATACATTGC	660
CAATCTTCTT GGAGTAAACT CAGCAGCCAA TTTGCGAGCA TCCTTACCAA ATTTCTCAAA	720
GTTGGCACGA ATGGTTTCAT CTGCAAAATC ACGTTCGATT TTCTTGAGAG CTACCTGTTT	780
TTTTGATTGG AAGGATTCTT CTACACTTGC AGGTTTGAGA CCTTTCATGC GTTCTTAGT	840
CAAGTTTTC AATGATTGAA GGTAAACCAT TTCGTTTGGA GCAACAAAAG TAATAGATTG	900
ACCTGACTTA CCAGCACGAC CTGTACGACC GATACGGTGA ACATAACTCT CAGGATCTTG	960
TGGAATATCG TAGTTGTAGA CATGGGTAC ACCTGAAATA TCCAAACCCAC GCGCTGCAAC	1020
GTCTGTCGCA ACCAAAACAT CAAGATTGCC ATTTTAAAG TCACGAAGGA CACGAAGACG	1080
TTTGTTTTGG TCTAGGTCGC CATGAATTCC TTCTGCACGG AAGCCACGAA TTTTCAAACC	1140
ACGAGTCAAT TCATCCACAC GCGGTTTGGT ACGACCAAAT ACAATAGCGA GTTCTGGTTG	1200
TGCCACATCC ATGAGACGAG TCATGGTGTC AAATTTTCT TGTTCCTTAA CACGGATATA	1260
GTA CTGGTCA ACCAATTCTG TTGTCAATTC CTTAGCCGCA ATCTTGACAT GTTCAGGGGC	1320
TTTCATAAAC TGAACACCGA TACGTTTGAT GGCATCTGGC ATAGTTGCTG AGAAAAGCAA	1380
AGTTTGACGG TTCTCAGGTA CACGGGAAAT AATGGCTTCG ATGTCTTCAA GGAAGCCCAT	1440
GTAAAGCATT TCATCCGCTT CGTCAAGGAT AAGGGTTTCA ATGTCTTGTA ATTTCAAGGC	1500
CTTGCGTTTA ATCAAGTCCA AGAGGCGACC TGGAGTTCCC ACCACAATAT GGGCACCAGA	1560
TTTAAGAGCC TTAATTTGTT TTTCAATGCT TGATCCGCCA TATACTGAAC GGA CTTTGAC	1620
TCCCTTACTA CGACCAAAGC GGAAGAGTTC TTCTTGACTT TGGACAGCTA GTTCACGAGT	1680
TGGAGCGATG ACCAAGGCTT GGATAGTCGC TTCTTCTGTA CGGATTTTTT CAAGGGTAGG	1740
CAAGCCAAAG GCTGCAGTTT TTCCTGTACC AGTCTGAGCT TGACCGATAA CATCCTTGCC	1800
TTCAAGGGCC AAAGGAATAG TTTGTTCTTG GATAGGACTA GCTTCTACAA AACCAGCTTT	1860
TTCAATTTCT GCTAGCAAAT CAGCAGACAA GTTTAATTCA TTAAATTTCA CGTTATTCTT	1920
CTTTCTAAAG GTGGTGCGAA GCCACCCTAT AGGGCTTAGT TTATACTTTT CTTTTTATGA	1980
CGTATTTTCA TATACTAGA TATAAAATCG TGTGCTTCT TTTCCACAAA AGAAAAGTAC	2040
TGTTTTCTTT GCAACCTATC TAGTATAACA CAAGACCAGA GCAAAAGATA GCCCATTTT	2100
TACAGAAAAT CATGTAAGCG CTTTTTGACT TTCTTTTTTG ATTGAACGAC CTAGATAATA	2160
AGACAAAGCC AAGGCGATAC TGTATAAAAT GAGAAAAACG AACAAGGTTT GTGTGTACGA	2220

1186

ATGAGCCATT TTATAAGTCT CTGCTAATAA AATAGGTCCC GCTAAACCAG CCATTGCCCA	2280
AGCTGTTAAA ATATAACCAT GCAGAGCGGC CAATTCCCTTG GTTCCAAAAA TATCACTGAG	2340
ATAAGCTGGA ATCAAAGAAA AACCAGCTCC ATAGCAAGTC ATCAAAATAG ACATAGCAAC	2400
TACAAATAAA ACGGAATCTG TAAAGAGCCA AAGTGAGAGA GAAAAGAAAA GATTGACAAG	2460
CAGTAATATA CTAAAGGTTA GAGGGCGACC GATATAGTCA GACAAACTCG CCCAGAGCAA	2520
GCGACCAAAT CCATTGAAAA TCCCCAAAC ACCCACCATT ACTGCTGCAT GACTTGTTAGA	2580
CAAGCCAGCC ATCTCCTGTG CCATTGGCGA TGCCCGTGAA ATTAAGCCTA AACCACAAGC	2640
TATGTTGATA AAGAAAATAA TCCAAAGCAT ATAAAACCGA TTGCTTTTTA GAGCCTGATT	2700
TGCAGCCATT CCTTGCGTCA AAGAGGCTGT TTTTCTTTC CCTGAAGAAG ATAAAATTGC	2760
AAGCTCTTGC TCATTGGAC GCTTAATGAA TTGTGAAGCT AGGAGCATGA TAATAAGTA	2820
ACTTGCTCCT AAAATATAAA AAGTTTCTAC AAGCCCTACC CTGCGATGA GGTGTTGCGC	2880
TATGGGACTA GTCAATAAAG AAGCAAAACC AAACCCATA ATCGCTAAAC CTGTTGCGAG	2940
ACCACGTTTA TCAGGAAACC ATTTTATAAT CGTCGACACA GGGTAATAT AGCCTGCTCC	3000
CAAACCAAGC CCACCTAAAA TGCCATAAGC GAGATACAAC AACCACAGCT CTGACGGTCT	3060
ATTGCAAATC CTGTTAAGAT ATTTCCACCT GCGTATAGAA AAGCAGATAG ACTTCCCATG	3120
ACTTTCGGAC CAAATTTTTC TACCAAACGC CCCATAATG CAGCCGATAA GCCCAAACAA	3180
AAGATTGCTA GACTAAAGGC GAAGGCAACA GAAGCCTGAT CCCATCCCGT	3230

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5096 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CCTATGAAGA CTGTCCCAAC TGGGTGTCCT TCTAGGCTAT CTGGTCCTGC CACTCCAGTC	60
AAACTAATTC CAAAATCAGA CTGGGTCTTG CTTCGTGCCT GCTCAGCCAT CTTCTGAGCT	120
GTAAATTCAG ACACCACACC ATGTTCTTCC AAATTCTTGG CAGGAATATC CAACATCCTT	180
GATTTTTCCT CCAAGCTATA GGTCACAAAA CCACCCTTAA ATATACTTGA AACTCCAGAA	240
AAATTCGCCA CGGTAGCTTG GAAAAGACCT GCCGTCAAAC TCTCTGCAGC CGCGATGGTT	300
TTCCCTTGCC TTTTCAGTTC TTCTACCACA ATGCTGGCTA AACTAGTTTC TTCCCATAA	360
CCATAGCAAA AGTCTCGTAA AGAAATTCCT TCGAAAGTCT GGCAGTCCAA GATTTGATTT	420

1187

TCCAAGATAT CCAGCGCTTG ATTCGCCTCT TCTTGA CTGC TAGCCTTTGT TGACAGACGT	480
AGAGTGACTT CTCCTGTCTT GGCATAAGGG GCCAAGGTAG GATCGATCTG ATTATCAATT	540
AAATCAGCCA AAATCGTAAC CAACTGGCTC TCGCCAATCC CAAAGAAACG AAGAACTCGG	600
GAATACAGCT TGCTCCCTGT CATCAACTTG GGTAGAAGTT GGTTTAAGAC CATGGGTTTC	660
AATTCACCTG GCGGACCTGG AAGGACGACA TAGGTCACTC CGTCTACTTC TAATTTTCCT	720
CCAACAGCCA GTCTGTCTT GTTTGGCAGT GGAATCGCTC CTTCTACAAT TTGAGCTTGT	780
CTTTCGTTAT TCGGTGTTTC GGCATAGTCT GGTGCGAGGG TAAAAAGAT ATCCAACCTC	840
TCCTGAGCCT GAGGATCAAA GACTAATGCT TTCCCTAAAA ATTTAGCTAG GGTTCGTTTG	900
GTTAGGTCGT CCTCAGTTGG CCCCAAACCG CCTGTCAAAA TCACCAGACT GCTACGTTGA	960
CTGGCAATCT CAAGCAAAGA CAAGAGACGA ACTTCATTGT CTCCTACAGC CGTCTGAAAA	1020
TATACATCTA CCCCAATCTC AGCTAGTTTT TCCGACAAAA ACTGGGCATT GGTGTTGACA	1080
ATCTGCCCTG TCAAAATCTC TGTTCACACA GCAATGATTT CTGCTTTCAT GTTTCCTCCT	1140
ACCTATCTAT TCGTATTTTT TTGAAAAAT CGCAGGAATT TTCCTACGAT TGATTTTTTT	1200
ATTTGTATCA AAAGTTAATT ATCTTCATCA CCAACAGGTG CTCTGCCAAA TAAATCTTCA	1260
AATAAAACCG CATTGGTTTC AAGCTGAGTA ACTTCTTCTT GTCCCAAAGA ACGTCGGAGT	1320
AGATTTTGCA TTTCCAACAT ATGTGCTCTC GAAACAATCT GGTAAAGAAC ACCTTGAAGT	1380
ATCTCTCCTT CACCCTGCAA CTGCTGAGTT TCAATGGTTT TAAATGAATC TTTATAGCCT	1440
AGCAAGTTAG GGATACTTTT TGCAGACAAA TCAATATTGG TCTGCATATT GTCAC TCAAA	1500
GCTTTTAGAA TCTCTTGATA ATGACCAATG CTATT TAAAC TGAGAGCTTT TTCCATGACT	1560
TTTTGAATAA CTTACGTTG ACGTTTTTGA CGACCATAAT CCCCCTCAGG ATCTTGGTAA	1620
CGCATTCGTG CATAGACTAG GGCTTCTTCT CCCCCAATAT GTTGCTCCCC AACACCGATA	1680
GAAATAGTAT TAAATCTTC TTGGTCACTG ATAGAAATTG GGAAACCTAG GATATTATTG	1740
ACTGTAATAC CTCCTACTGC ATCCACTAGT TTTTGCAATC CTCTCATATT GACCATCACA	1800
TAGCGATCAA TATGGATATT CATCATTTTT TGAATGGTTT CTATAGCAAG CTCTGCTCCA	1860
CCATCTGCAT ATGCTGAGTT CAGTTTCGCT TCATGAGCCT GACCATTCCC TGATTCAATG	1920
CGCGTCAGAA TATCCCGCTC TAAACTCATC ATTGTTGTTT TTTTCGTTT AGGATTCACT	1980
GTCATCAAGA TCATGCTATC ACTTCTACCG ACCCAAGTTT CAGTTCGTTT AACATTTCCG	2040
GTGTCCACTC CCATTAACAG AATGGTTAGA GGTTCACTCG CTTCAATAAC CTTGGTTTCT	2100
TCACCGATTT TTTTATAGGT TTTAGCTAAG GTTTCTGTCC CTGTTGATA AATAGTATAA	2160

1188

GCAAAAACAC	CTACTCCTAC	TACAGTTACA	GAAAGTAAAG	CTAGCACCAT	TCCAATAATT	2220
TTTTTAACCA	TATTTCTACT	AACCTATCAG	TTTACCCATC	AAGTAAACAT	CGATAAATTT	2280
CCCTTCTTCT	ATATATGCCC	CACGCTCTTG	GCTACCTTCA	ATGACAAAGC	CATGCTTTTG	2340
ATAAAGATGG	ACTGCTGCTT	GATTACGAGT	TTGGACAGTC	AGTTGGAGAC	GACGCAGAAT	2400
GCCACTTGCT	TGTGCCCCACT	CTATCGCTTC	TTCTAGCAAC	AAACTTCCCA	AGCCATTATT	2460
C CAATATCTT	TTTCCAATCA	CAATGAAGAG	ATCTCCAATA	TGACGGACTC	TCTTACGCTG	2520
ATCAGCTGTA	ATATTTACAA	TACCAGCAAT	TTTGCCATTT	AAGAATGCAA	GTAAGGTTAT	2580
CTGATTGTCC	GAAGTAGCTT	GCTTGTGAG	GAATATTTCC	ATCTCCTCAC	TAGTCAAGAG	2640
AATACCATCT	CCGTCTAGGC	TGGTAAAGTC	TGTCTCCAAA	CTCACACGAT	TTAAAAAGGC	2700
CACTAATTCA	GCTGCATCTT	TGGGCTCTGC	TTCCCTAATG	AGCAATTCAT	ACTCCATATT	2760
GAAGCTCCTC	TAACAATTTT	TCAGCACGCA	AACCCTTTGC	CTGAAAATTT	AAACGGCGTC	2820
CATCTGCTTC	TTTLAGAATT	TCCAATTCTA	AATAAGCATC	TGGCAAGGCA	TCTCCTAAGA	2880
GATTTCCCCA	CTCAATAACA	GTCACGCCGC	CACCAAAGAT	AAACTCATCC	AAGTCGATAG	2940
AATCAGCATC	TCCTTCAATA	CGATAAACAT	CTAGGTGATA	AAGTGGAAGT	CGACCTTCAT	3000
ACTCTCTCAC	GATAGTATAG	GTGGGACTTT	TAATCATTTG	AGAAATCTGT	AATCCTTTTG	3060
CAAGTCCTTT	AGTAAAGGTC	GTTTTACCTG	CACCCAGTTC	TCCAGTTAAG	ATTAAAACAT	3120
CATTCTTTGC	TAATAGATGG	CCCAAACGCT	CCCCTAAGGC	TTGCAACTCT	TCTTCATTTT	3180
TTGTGTACAT	ACTCTTATTA	TACCAAAAAC	TTTTCTTTTG	TGTCTATTTT	CCTACTAAAC	3240
TTATCATCAT	AACATCCATA	AAAAACAGGC	TTTCTCTAAA	AGAAAATGAG	CGTAACAATG	3300
ACCAATACAA	GATCTCGGAA	AATATGACCA	TAAAAGGAAA	CTTCCTTCTT	AACCGAATTT	3360
GGGACAAGAT	AGGCTGCAAA	AAACAAGCCC	AGTCCAATAT	AAATCAGAAG	TGAGACAATG	3420
GTCATTGGAT	TTCTTAAGAA	AAGAAGTGT	GCTAAAATAG	TCACCAACAC	TGTCTTTTTT	3480
CTGTCCAGCA	TAGCAAGAAA	ATCGCGCACG	TATTTTTTCA	AGGGTAAAAA	AATCAGCAAA	3540
TCTAGCCCAA	ATAGGAAAAA	GAAGGATGGC	AATAAAAAGT	CAACTAATTC	TTGCTGCAGC	3600
GTATTTTTGA	TGAACAAGTT	ATCTGACAAA	ACAAGAACAG	CTCCTAACAA	ATTAAATTAAG	3660
AGTAACATAC	TGTAAAAAAG	CTTCACCGAC	TTCTTACTGG	CTAGGACACT	ATGGACTTCT	3720
TGCTTACGGG	TATAAAGATA	ATTTACTCCA	GCACAGATTC	CTGAAACGAA	AACCATGCTT	3780
CCGATGAAAA	AAGCTGTACT	TTGTTTAAAG	GACAAGATGC	ATTCCCTCCA	TAGGAAACAG	3840
CTACTCAAAC	TGATTTGAAT	TAAAGCTAAC	AAAAATAAGA	TTCTCATTGA	TTTCATCTTC	3900
TCTCTCCCTT	CCTACCAATC	ATTATACTAG	GAGAAAAGAG	AGAACTGTTT	CTAATCTTCT	3960

1189

CAAATGTCTC TTTAAGACGC TAAACAAACA CTAGAGACTA ATACTCAATG AAAATCAAAG 4020
 ATCAAAC TAGCTAGCC ACAGGTTGCT CAAAACAGTG TTTTGAGATT GCAGATAGAG 4080
 CTGACGTGAT TTGAAGAGAT TTTCAAGAA TATAAATTTG AAATCATGAA AATCCGTCAA 4140
 ACGGGTGGTT GTTTGTCTC GCACCTCACG GAGCGAGACG GACTCAGAGT CACATAATTA 4200
 TAAGGCTGAT AGTATTAATC TAACTATCAG CTTmCAGGTT ATTTAACGTT TCAGAAAAAC 4260
 TATAATGTCA AGATTAAC TAACAGTATCT AGTTCCTTCA AATAATTTTC TATCTTCATC 4320
 AACATTAAAG GATGTTTATA AATCTTACAT AACTCTCTTG CTTCTATATA ATAATTTTGT 4380
 ACTTGTTCTC TGTCTAGAAA TTTGGCTCCA GCATTTCTTA CAAGAATAAG TAGAGGAGCC 4440
 AATTGGTAGC TTGTCTGTCT TTGTTTACAG AGTTCAATCG TTTCAAGAGC TTCTTGGATG 4500
 GCTTCATTAT ATTTTCTCTT TGATACTAGG TAGTGAGCGT AGTTGTAACG AACTCTGATG 4560
 TAGCCAAATA AAAACTCTTG ATGGTCCAAA TTTTTGTCT GATACAACTC TATTAAATGA 4620
 GAGTAGTTTG CCTCATATTC TTGTTACAG CCCACTAAGG AATAGAAATT AGATAGAGTA 4680
 TTCAACGCCT TTAATAAAT CAGAGTATTT GAAGAGACTT TTAATAATAT ATTTTCCAAT 4740
 GACGAAATG CCTCACACTT ACTGTCATAT TGATAGAAGT CAATTATAGA TTAAATCCAT 4800
 TCAAGGTAAG TTCGGTCTTC TAATGTTAGA AAAGTGCTTC GTTCTACTTC TATTTTATAA 4860
 AGATATTCTA AATCGTCATA ATTTCTGTCA TCTAATAGGC GAGCAGATAG ATGTTTGAAA 4920
 TTAGAGAGGT TAGACTTAAC TTCGATTTGT TCATTGAAA AGTAATCCAA AGGGACTTCA 4980
 AGTCGTTGAG AGAGTTTGAA TAACAAGTCT GCGGAGGGAA TAAATGACC TCTTTCAATT 5040
 TTAATAATCT GGCTTTGTTC ACAAATTCCT TCTGCAAGAG TTTGTTGGGA GAGTCT 5096

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ACAAGATAAA AATAAAGGAT TACAATGGG AATATAAAGT AAACCGGTAA ACCTAAAAAG 60
 AAAGGAGAAA AGATGAAAAT TGTACTTGTA GGGCATGGAC ATTTTGCTAC AGGGATTAT 120
 AGTTCTTTAC AATFGATGCG AGGTAATCAA GAAAAATGTTG AGGCGATTGA CTTTGTGGAA 180
 GGAATGTCAG CAGATGAACT CAAGCAAAAA ATCTTACTTG CAATTTCAAA TGAAGAAGAA 240

1190

GTTTTAATCC TAAGTGATCT CTGGGAGGA TCGCCATTCA AGGTTTCTTC TACCATAATG	300
GGAGAAAATC CAGCCAAGAC AATGAATGTT CTCTCGGGTT TGAACCTAGC CATGTTAATG	360
GAAGCAGTCT TTGCTAGAAT GGCTCATAGC TTTGATGAGG TTGTTAATAA ATCAGTAGTG	420
GCGGCCCAGG GCGGAGTCGT AAATGGTAAA GAATGTGTTT CAACGGATGC AGAGGAAGAG	480
GAAGAAGATT TCGAATCGGG TATTTAAAGG GTAAAAGAAT GATAAAAAAG GTTACGATTG	540
AAAAAATAAA ATCGCCTGAG CGCTTCTTAG AAGTACCACT TCTGACGAAA GAAGAAGTCG	600
GCCAGGCAAT CGATAAGGTT ATTCGGCAGT TAGAACTCAA CCTTGACTAT TTCAAGGAAG	660
ATTTCCCAGC GCCAGCTACC TTTGATAATG TCTATCCAAT CATGGATAAC ACGGAATGGA	720
CCAATGGTTT CTGGACAGGA GAACTGTGGT TGGCTTATGA ATACAGTCAA CAGGATGCAT	780
TTAAAAACAT CGCTCATAAA AATGTTCTTT CTTTCCTGGA TCGTGTCAAT AAGAGAGTAG	840
AATTGGATCA CCATGATCTC GGCTTCTTGT ACACACCGTC TTGTATGGCT GAATATAAGA	900
TAAATGGAGA TGGAGAGGCT AGAGAAGCAA CCTTGAAAGC TGCAGATAAG TTGATTGAAC	960
GCTATCAAGA AAAAGGTGGT TTTATTCAAG CTTGGGGAGA CTTGGGCAAG AAAGAGCATT	1020
ACCGTTTGAT TATCGACTGC TTGCTCAATA TCCAACCTTT ATTCTTTGCT TATCAAGAAA	1080
CAGGCGATCA AAAATACTAC GATATTGCAG AAAGCCATTT CTATGCTTCA GCTAATAATG	1140
TAATCCGTGA TGACGCTTCG TCCTTCCACA CCTTCTATTT TGATCCTGAG ACAGGTCAAC	1200
CCTTTAAAGG TGTAACGAGA CAAGGGTATA GTGATGATTC ATGCTGGGCA CGTGGTCAAT	1260
CATGGGGAGT CTATGGTATT CCTTTGACTT ATCGTCACTT AAAAGACGAG TCCTGCTTTG	1320
ACTTGTTTAA GGGTGTGACC AATTATTCTT TGAATCGTCT GCCAAAAGAT CATGTGTCCT	1380
ATTGGGATTT GATTTTAAAT GATGGTAGTG ATCAATCAG AGATTCTTCA GCAACAGCTA	1440
TCGCCGTCTG TGGGATTCAT GAAATGCTAA AACATCTCCC AGAGGTGGAT GCTGACAAAG	1500
ATATTTATAA ACATGCTATG CATGCCATGC TTCGTTCCCTT GATCGAACAT TATGCAAATG	1560
ATCAATTTAC CCCTGGTGGG ACAAGTCTCC TCCACGGTGT GTACTCATGG CATTCAGGTA	1620
AAGGAGTGGA TGAAGGCAAT ATCTGGGGTG ACTACTATTA CCTAGAAGCC CTTATCCGTT	1680
TCTACAAAGA CTGGAACCTA TATTGGTAGG AGGAGAAATA TGACAATGCC AAATATTATT	1740
ATGACCCGTA TCGATGAACG GTTGATTCAT GGACAAGGAC AACTTTGGGT AAAATACCTA	1800
GGTTGTAATA CGGTCATTGT TGCCAATGAC GAAGTAAGCA CGGACAAGAT GCAACAACT	1860
CTGATGAAAA CAGTTGTGCC AGACTCAGTT GCCATGCGTT TCTTCCCTTT GCAAAAGGTG	1920
ATTGATATCA TTCACAAGGC TAATCCTGCT CAAACGATCT TTATCGTTGT AAAGGATGTG	1980
AAGGACGCTT TAACCTTGGT AGAAGGTGGT GTCACTATCA AAGAAATCAA TATTGGGAAC	2040

1191

ATTCACAATG CCCCTGGTAA AGAGCAAGTG ACACGCTCCA TCTTCCTGGG TGAAGAGGAC	2100
AAGGCGGCCC TCAAGGAATT GAGCCAACT CATCAAGTAA CATTTAATAC GAAAACAACT	2160
CCAACAGGAA ATGATGGAGC TGTTCAGTC AACATTATGG ACTATATTTA ACAGAGGAGA	2220
TCGTTATGTC GATTAATGTA TTTCAAGCGA TTTTAATTGG ATTATGGACA GCTTTCTGTT	2280
TTAGTGGAAT GCTGTAGGA ATTTACACCA ATAGATGTAT TGTTCGTCA TTTGGTGTCTG	2340
GAATTATCT AGGTGATCTG TCATGCTCTT GCAATGGGAG CCAATGGTGA ATTGG	2395

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CCTTCTTTAG AGGTTAATTT TGCAAAATCG TCGATTGTTA TATAAGGATT ATTATAGAGA	60
CTGTTTCGCAA AGAATCTCTG ATATGTTTTT GAATCTTTTG AATACAAAAC TATCTCTCTA	120
ATAGCATTGC CATCTGTTC ATCAATTGGT AAACATACCG TAACTAGAAA AAGAATTATA	180
TTCAAAATAA AAAATTCTGA TCGGTACGGC ACAAATCCCA AAAGTGCTAA TATTGCGACA	240
ATTAGGTTAG CTCCACCTCC CCCAAAGAAG TAGAACACCA AATTCCTATC ACTATTTTTT	300
TCATTAGTAA TGTTTCTATT ACTCATTGA CAATAACCGA ATGCTAATAA CACTGGAAT	360
TTGAAATATA TTTTTTTTCT GAAATAGAAG AAAAAGGGAG TAGCAAGCAT CTCTAGTTTA	420
TAAGATAAAC ATCTTCCCAC TAAAAAATGA CCTAGTTCAT GTAATGTAAT TGATATTAAC	480
GAAATTAAAA TCAATCGAAA ATAATAGATT AATGAATCAT TTGGAAAAAT TATCAATAAT	540
AGGAACAATA ACGGAATCAA ACATAAATAT ATGACAGAGT TATTTAATAT TTTCAACATA	600
ATACCATTC TCTAACTAT TAGCTTCAAA AAGGCGTTTT TTCTCCCAAT ACATCTTCTC	660
AAAATGTTTC GAATCATAAT TTTCTAAAAT TAATTTTATG TCTGGTAAGC TCTTTCTTGA	720
TAATCCGTTG TTTTGTACTT AATTTTCCCT TCAAGTACAT CTTCAATTTT ATAAGTTGCC	780
TCCATCAACT GAGCCTCTGC AATATCTTTG AGTGAATTGG TAATTGAAAC TTGGTGTAAT	840
ATCTGTCCTs CCATATATGA AAATATATCT CTAAGATATT CTGACACATT ATCAGAGCCG	900
TTACTCTCAG CAACATCTAA TGTTACAACA AACTTTCCAG CTAATCGAAA AAGATGGCTC	960
CACCCCCCAA TCCTTTCAAT AAAGTTTTTT GTGTCCACAG ATACGTTTTG TAAATATACA	1020

1192						
GGAGAAGAGA	TAATTATAAT	ATCAGACTCT	AATAACTCTT	TTTTTATAAC	ACCTCCATCA	1080
TCAGCATTAC	TTTGCCATATC	AATTCCCTTTC	TAAACAAC	CTTCTGAATC	AGAATTAGAT	1140
ATTTCTAGCT	CTGAATTGAA	AGGTGTCCTG	AAAGATATAT	CAACATTATT	TCTACTAGAA	1200
ATGATACTTG	AAAGTCTCTT	AGTATACTCT	AAAGTCTTAG	AGTTATGATT	TCGCACTCCT	1260
GCATATATAA	ATATTTTATT	CATTTTAATT	CATCCTCTCA	ATTTGAATTT	AGTAGATTTT	1320
TCAAGATAGT	ATGGTACAAA	AACAGACTTT	TGTTGACTCA	CATTATTACA	TATGTTTTGT	1380
ATTAAACCAA	AATCAATACT	ATTTTTGGAG	TAATTTTGAT	TTTAGTTTAA	AATCATTTCT	1440
ATAACAGTAG	CATATACCTC	AAGCCGTTTA	GCAATTAGAA	TAGAACTTTT	CTTTATTATA	1500
TTATTATCTC	AACGAAAAGC	TACACTATTA	AAAATATTTT	ATAGAATTAC	ATATTAAACT	1560
AGTCAATCTT	GGTATTTTTA	TATTGCTTAA	TGAGTGGACA	CCTCTATTTT	AGAAACAAAA	1620
CTATAAATTA	AGCTAGATTT	CAAGTAATGA	GGGGATAACT	ATCTTTTGT	CATTCTGATT	1680
CAGTGCGATA	TACCTTAAAA	AAGTATAAGC	AATACCAGTC	ACACCTGTAT	ACAAAGAAAA	1740
ATCTGGGAAA	TTGCTTGTTT	GGACGATACG	ATACTCTCCT	TCTTTTGATT	TATTCATTAC	1800
AACACTACAC	AATAAAGACT	CCAATCCAT	ACTAGTATCC	ATTTCTTTCA	TGTAGTCGAT	1860
GTAAAAATTT	ATTATGGCCA	TACTTCCATG	GCAAAATGTA	TCATTATCTA	AACTAGCTAC	1920
AATTCCCTCT	GGAACACTTT	GGGGATGATT	AACTAATGTC	CCAAATCTC	CACTACACCA	1980
CTTCAAAGAA	TGAATTTTGA	TTTTCTCCCT	AGGAACTAGT	TGTAAAATTA	ATTCTTTATA	2040
TTTTTTAAGT	CTTGTCACCT	TATAAATATT	TTTAAATGTA	AAAATTACAC	CTGATAGTCC	2100
ATGGCCAAAA	CTATATCCAA	AATTACTATT	ATCTCTCTCG	CTTACATCAT	TATATAGCGT	2160
ATCACCTAAA	CTTAATACTA	GCCTTAGAAC	ACGTTCCCTC	TCTATTCCTC	TCCTATAATA	2220
TCTTACCAGT	GTATTAATTA	AAGGTAGAAG	ACCATTAAATA	TAGTCAGACT	TGTTTGAAAC	2280
ACTTGCAAAA	TCAGTCTTTT	CAAGCTCAGT	TAAAACACTC	TTTATATAAT	TTAAGCATGC	2340
GAGAGTATTT	GTATCGTAAT	CCTCTATAAT	GGATAGAACA	ATGAAATATC	CTATATCCCC	2400
AGTTAAACCA	AATGTGGTCT	TAGATAAAGA	AACAGATGGC	GGAATTGCAG	ATAACATTTT	2460
ATTGTACAGT	TGAGTATATG	ATGATTTATC	TTTCAATAAT	TTTACATAGT	ACATAAACAG	2520
TAATATTCCA	GCTCTACCCC	TATACATATC	ATTmCCCCTT	TGTTCAAGAC	ACCATTTAGA	2580
ACCTTTAAAA	TTAACAGGTA	TACTCCAAAT	TGGATATTTC	TCATAAATAT	TATTAATAAC	2640
CAAAGAGTCT	GCAATATTTT	CTACTTCATT	ATGCAGAATA	GTAACATAAC	TTTCATTTGG	2700
GAGTTTTTTT	CTATTAGATA	AGTTTAATTT	ATATCCTTTT	TTTCGCTGAT	CAAAGCTTGG	2760
AAAATAAATT	TCAATGATAT	CAAGTTGCTT	TTCTAAATTT	TCCAAATTAT	TATTAGGTAA	2820

1193

ATATTTTCATA AAATAGTCAT ATCCAGAAAA TTGATGTAGG GAAATAAAAT GATTTCCAAA	2880
ATCATCGTAG ATTTTCATTGA TATTTGTATC TGTATAAAAA ATCGGAATAT CTAATAACCT	2940
CATTTGTTCA CATTCGCTTG CTACAATACC TTGATTAGAA AACTTATTGC TCCAGAGATT	3000
TTCCAATGCT TTTTCTCTAT CTAACATTTT TCATAAAAA TCAGGATGAT ATAAAAAGA	3060
TAGTACTGAA GCATAGCTAT TTGTGTCTCT AAAAAGTACC CTTGTCTTTA AACCATACAA	3120
GTTTGCTTTT AATAGCATTT TAAATCTTTC TGTTTTATTT AACTCTTCAA ATATCAGATA	3180
AAAATCCCTA AAACCTTTTT TGAAATCTTT TATATACTTA TCAAATTCTA TATCACCATC	3240
CCGAACAGGC AGGTTTTTCC CACCTTCAA ATCAATTTTC CCAATATCAA ACTTTACCTT	3300
ATCAGTATTT AAATTAATTA AACTTGACC AGGGATCCTC TA	3342

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GAGAAAAGAA TGTTAAAGAA AAATGATATT GTAGAAGTTG AAATTGTTGA TTTGACCCAT	60
GAAGGGGCAG GAGTTGCCAA GGTAGATGGT TTGGTCTTTT TTGTAGAGAA TGCTTTACCG	120
AGTGAAAAAA TTCTCATGCG TGTCCTCAAG GTCAATAAAA AGATTGGCTT TGGAAAAGTT	180
GAAAAATACC TTGTCCAGTC ACCACACCGT AATCAAGATC TAGATTTGGC TTACCTGCGT	240
TCAGGAATCG CGGATTTAGG ACACCTTTCT TATCCAGAAC AGCTCAAGTT TAAAACCAAG	300
CAAGTCAAGG ACAGTCTCTA CAAGATTGCT GGAATTGCAG ATGTAGAAGT TGCTGAAACG	360
CTTGGTATGG AACATCCAGT CAAGTATCGC AATAAGGCGC AGGTGCCCCG TCGTCGAGTG	420
AATGGTGTCT TGGAAACAGG ATTTTTCCTG AAGAATTCGC ATAACCTCAT GCCCCTGAA	480
GATTTCTTTA TCCAGGATCC TGTCATTGAC CAAGTCGTAG TAGCTCTTCG AGACCTGCTC	540
CGTCGTTTTG ATTTAAAACC TTATGACGAA AAGGAACAGT CTGGATTGAT TCGGAATCTT	600
GTGGTGCGTC GTGGTCACTA TTCAGGACAA ATCATGGTCG TTTTGGTGAC AACTCGTCCA	660
AAAGTTTTTC GTGTTGACCA ATTGATTGAA CAAGTTATCA AGCAGTTCCT AGAGATTGTG	720
TCTGTCATGC AAAATATCAA CGACCAGAAT ACCAATGCGA TTTTGGTAA GGAGTGGCGC	780
ACTCTTTATG GTCAAGACTA TATTACGGAC CAGATGTTGG GAAATGACTT CCAAATCGCT	840

1194

GGCCCAGCCT TTTACCAAGT CAATACTGAA ATGGCGGAGA AACTCTATCA AACAGCCATT	900
GACTTTGCAG AGTTAAAAA AGATGATGTG ATTATTGATG CCTATTCTGG TATTGGAACC	960
ATTGGTTTAT CAGTCGCCAA GCATGTCAAA GAAGTCTACG GTGTTGAACT GATTCCAGAA	1020
GCAGTAGAGA ATAGCCAGAA GAATGCTTCT TTGAACAAGA TTAATAATGC CCACTATGTC	1080
TGTGACACGG CTGAAAATGC CATGAAGAAA TGGCTCAAGG AAGGTATTCA ACCAACC GTT	1140
ATCTTGGTTG ATCCTCCACG CAAGGGCTTG ACAGAAAGCT TTATCAAAGC AAGCGCCCAA	1200
ACAGGAGCCG ATCGCATCGC CTATATCTCC TGCAATGTCG CAACCATGGC GCGTGATATT	1260
AAACTATACC AAGAGTTGGG ATATGAATTG AAGAAAGTCC AGCCGGTGGA TCTATTTCTT	1320
CAACGCATC ACGTCGAGAC GGTAGCACTT TTGTCCAAAC TCGATGTCGA TAAGCACATA	1380
AGTGTGAAA TTGAGCTGGA TGAGATGGAT TTGACAAGTG CGGAGAGCAA AGCAACATAT	1440
GCTCAAATCA AAGAATATGT TTGGAATAAA TTTGAATTAA AAGTTTCGAC ATTATATATT	1500
GCACAGATAA AAAAGAAATG TGAATAGAA TTACGAGAAC ATTACAACA GTCTAAAAAG	1560
GATAACAAA TTATCCACA GTGTACACCT GAAAAAGAAG AAGCCATCAT GGATGCTTTG	1620
AGACACTTCA AAATGATTTA ATAGAAAAGA ATGACAGTAT ATGACTTTCT GCATTTATTA	1680
CATTCTACT TGGTATAGGA ACAGCTATTA TTCCTTTCTT GCAAGGTATC AATTAGAAAA	1740
TAGGCTCAAT ATAAAGATTG ATAGGATCAT TTTTATATTT AAAGGAGCGT TGAAATGATT	1800
GATAAAGGCA ACAAAAAATT TTAGGATAAA TTTGCTAAGT TGTATGCCTC TTTTATGAAA	1860
AAAGATAAAG AGGTTTATGA TAAAGTTTGT GAATATCTTA GTCCTCATTT GAATAAAGAT	1920
ATGGAGGTGC TTGAACTTGC TTGTTGGTTT CGTGTCTATA CAGTTATAGA GGCAAAAGT	1980
TATGTAAATA TAAGGAGTTC AAGACTTCTA CCAAAGTTTA AACTCAAAA AATAAATAGT	2040
TGGTGTGCTG CTTACAATAT CCATTTTAAT AATGGATATT GTAAGCAGCA CCCCcAtGAA	2100
TTTAAAGATT CTTTAAAGAG TCTTATTTTG TGATGAAAAT TTAATATGTA AATCTCAGAC	2160
GATAGAAATT AAAAATCTA TCGTCTTTT TATACTCAA ATTAGGAGGT AAAAATGGTA	2220
AGGATAAGAG GTCCCACTTA AAACAATTTA TGGCAAAATA AGGACGGAAT AACACAACAA	2280
ATTCTCTAAA ACAAATCACT AAATCAATGT AAGATTGAAT GAAATCAATA TTTATGCTAT	2340
AATTAAATAA ATTTAATGAA GAAAAAAGA GGGATATTAT GGCACCTAAC TATAAACCAT	2400
TATGGATACA GTTAGCAAAA AAAGGACTAA AGAAAACAGA TGTAAATAGCT ATGGCAGGAC	2460
TTACAACAAA TGTATGGCA CAAATGGGAA AGGATAAACC AATTACATT AAGAATTTAG	2520
AAAGAATATG TAAGGCTTTA TCTTGCACTC CTAATGATAT TATTAGTTTT GAAGATAATT	2580
TTAGTGACGA GGAATAGAAA ATGACTTTAA GGACAGAAGA TCAAGTTAGG GATTATGCAA	2640

1195

GAGAAGTATA GGCTTTAATG AAGTTGAAGA AAACATCAAT CAAGGTACTG GTCAAATAAC	2700
TACTTTTAAAT CAATTAGGCT TCAAGGGATA TTCAAATAAG CCAGATGGTT GGTATTTACC	2760
TAAAAATATG AATGATGTAG CAATAATCCT TGAAACAAAA TCAGAAGAAA GAGATATTAG	2820
CAACAAATTT TTTATTGATG AGTTAATGAA AAATATAGAC ATAATTTAAC TAAAAATAAA	2880
AACTAGATCC TTTTTTGAAA AAATTATATT ATTAAATTTG TAACTGTATC TATTGACAAT	2940
GATAATTATT ATCGATACAA TAGACTTGAA ATATGTTTAA GGAGTTTTTA TGAAAaCAAA	3000
TTTTTTCTAA TmGCTATTTT AGCTATGTGT ATAGTTTTTA GCGCTTGTC TTCTAATTCT	3060
GTTAAAAATG AAGAAAATAC TTCTAAAGAG CATGCGCCTG ATAAAATAGT TTTAGATCAT	3120
GCTTTCGGTC AAACATATT AGATAAAAAA CCTGAAAGAG TTGCAACTAT TGCTTGGGA	3180
AATCATGATG TAGCATTAGC TTTAGGAATA GTTCCTGTTG GATTTTCAA AGCAAATTAC	3240
GGTGTAAGTG CTGATAAAGG AGTTTACCA TGGACAGAAG AAAAAATCAA AGAACTAAAT	3300
GGTAAAGCTA ACCTATTTGA CGATTTGGAT GGACTTAACT TTGAAGCAAT ATCAAATCTT	3360
AAACCAGATG TTATCTTAGC AGGTTATTCT GGTATAACTA AAGAAGATTA TGACACTCTA	3420
TCAAAAATTG CTCCTGTAGC AGCATACAAA TCTG	3454

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CGGGAGTATA CTTAATATAA TTATAGTCTA AAAATGACTA TCAGAAAAGA GGTAAATTTA	60
GATGAATAAG AAAAAATGA TTTTAACAAG TCTAGCCAGC GTCGCTATCT TAGGGGCTGG	120
TTTTGTTACG TCTCAGCCTA CTTTGTGAAG AGCAGAAGAA TCTCCACAAG TTGTCGAAAA	180
ATCTTCATTA GAGAAGAAAT ATGAGGAAGC AAAAGCAAAA GCTGATACTG CCAAGAAAGA	240
TTACGAAACG GCTAAAAAGA AAGCAGAAGA CGCTCAGAAA AAGTATGAAG ATGATCAGAA	300
GAGAACTGAG GAGAAAGCTC GAAAGAAGC AGAAGCATCT CAAAAATTGA ATGATGTGGC	360
GCTTGTTGTT CAAAATGCAT ATAAAGAGTA CCGAGAAGTT CAAAATCAAC GTAGTAAATA	420
TAAATCTGAC GCTGAATATC AGAAAAAATT AACAGAGGTC GACTCTAAAA TAGAGAAGGC	480
TAGGAAAGAG CAACAGGACT TGCAAAATAA ATTTAATGAA GTAAGAGCAG TTGTAGTTCC	540

1196

TGAACCAAAT	GCGTTGGCTG	AGACTAAGAA	AAAAGCAGAA	GAAGCTAAAG	CAGAAGAAAA	600
AGTAGCTAAG	AGAAAATATG	ATTATGCAAC	TCTAAAGGTA	GCACTAGCGA	AGAAAGAAGT	660
AGAGGCTAAG	GAACCTGAAA	TTGAAAAACT	TCAATATGAA	ATTTCTACTT	TGGAACAAGA	720
AGTTGCTACT	GCTCAACATC	AAGTAGATAA	TTTGAAAAAA	CTTCTTGCTG	GTGCGGATCC	780
TGATGATGGC	ACAGAAGTTA	TAGAAGCTAA	ATTAATAAAA	GGAGAAGCTG	AGCTAAACGC	840
TAAACAAGCT	GAGTTAGCAA	AAAAACAAAC	AGAAGCTGAA	AACTTCTTGG	ACAGCCTTGA	900
TCCTGAAGGT	AAGACTCAGG	ATGAATTAGA	TAAAGAAGCA	GAAGAAGCTG	AGTTGGATAA	960
AAAAGCTGAT	GAACCTCAAA	ATAAAGTTGC	TGATTTAGAA	AAAGAAATTA	GTAACCTTGA	1020
AATATTACTT	GGAGGGGCTG	ATCCTGAAGA	TGATACTGCT	GCTCTTCAAA	ATAAATTAGC	1080
TGCTAAAAAA	GCTGAGTTAG	CAAAAAACA	AACAGAAGCT	GAAAACTTC	TTGACAGCCT	1140
TGATCCTGAA	GGTAAGACTC	AGGATGAATT	AGATAAAGAA	GCAGAAGAAG	CTGAGTTGGA	1200
TAAAAAAGCT	GATGAACTTC	AAAATAAAGT	TGCTGATTTA	GAAAAAGAAA	TTAGTAACCT	1260
TGAAATATTA	CTTGAGGGG	CTGATTCTGA	AGATGATACT	GCTGCTCTTC	AAAATAAATT	1320
AGCTACTAAA	AAAGCTGAAT	TGAAAAAAC	TCAAAAAGAA	TTAGATGCAG	CTCTTAATGA	1380
GTTAGGCCCT	GATGGAGATG	AAGAAGAAAC	TCCAGCGCCG	GCTCCTCAAC	CAGAGCAACC	1440
AGCTCCTGCA	CCAAAACCAG	AGCAACCAGC	TCCAGCTCCA	AAACCAGAGC	AACCAGCTCC	1500
TGCACCAAAA	CCAGAGCAAC	CAGCTCCAGC	TCCAAAACCA	GAGCAACCAG	CTCCAGCTCC	1560
AAAACCAGAG	CAACCAGCTA	AGCCGGAGAA	ACCAGCTGAA	GAGCCTACTC	AACCAGAAAA	1620
ACCAGCCACT	CCAAAAACAG	GCTGGAAACA	AGAAAACGGT	ATGTGGTATT	TCTACAATAC	1680
TGATGGTTCA	ATGGCAATAG	GTTGGCTCCA	AAACAACGGT	TCATGGTACT	ACCTAAACGC	1740
TAACGGCGCT	ATGGCAACAG	GTTGGGTGAA	AGATGGAGAT	ACCTGGTACT	ATCTTGAAGC	1800
ATCAGGTGCT	ATGAAAGCAA	GCCAATGGTT	CAAAGTATCA	GATAAATGGT	ACTATGTCAA	1860
CAGCAATGGC	GCTATGGCGA	CAGGCTGGCT	CCAATACAAT	GGCTCATGGT	ACTACCTCAA	1920
CGCTAATGGT	GATATGGCGA	CAGGATGGCT	CCAATACAAC	GGTTCATGGT	ATTACCTCAA	1980
CGCTAATGGT	GATATGGCGA	CAGGATGGCT	TAAAGTCAAC	GGTTCATGGT	ACTACCTAAA	2040
CGCTAACGGT	GCTATGGCTA	CAGGTTGGGC	TAAAGTCAAC	GGTTCATGGT	ACTACCTAAA	2100
CGCTAACGGT	TCAATGGCAA	CAGGTTGGGT	GAAAGATGGA	GATACCTGGT	ACTATCTTGA	2160
AGCATCAGGT	GCTATGAAAG	CAAGCCAATG	GTTCAAAGTA	TCAGATAAAT	GGTACTATGT	2220
CAATGGCTTA	GGTGGCCCTG	CAGTCAACAC	AACTGTAGAT	GGCTATAAAG	TCAATGCCAA	2280
TGGTGAATGG	GTTTAAGCCG	ATTAAATTAA	ATCATGTTAA	GAACATTTGA	CATTTTAATT	2340

1197

TTGAAACAAA GATAAGGTTC GATTGAATAG ATTTATGTTC GTATTCTTTA GGTACCTATC	2400
TTATGATTTT AGGAAATGTC ATTAACAAAA CGACTCATTT TCTCTAACCT GAAAAATAGA	2460
TTAGAGAAAA TGGGTGTTTT TATCTATTAT AGTTATTTGA ATGAAGmTAA GAAGAAGGTA	2520
TACTCACATC ATTCACATAA TCTGTATATT GACTATAAGT TTTAAAAAAC AATTTTAAAG	2580
CTCTTCCTTG TCTTCTCTAA CCAAGCGTGT TATAATGAAT ACTGCTCAAG CGACCTTCAA	2640
TCGTGAAGCA CACACGACCT TCAATCGTGA ATAAACGAAT AGATGGGAGA CTTACCATGA	2700
GTGATAACTC TAAACACGT GTTGTCTGG GGTGAGTGG TGGTGTGAT TCGTCGGTGA	2760
CGGCTCTTTT GCTCAAGGAG CAGGGCTACG ATGTGATCGG TATCTTCATG AAGAACTGGG	2820
ATGACACAGA TGAACACGGC GTCTGTACGG CGACCGAAGA TTACAAGGAT GTGGTTCGGG	2880
TGGCAGACCA GATTGGCATT CCCTACTACT CTGTCAATTT TGAACAAAGAG TACTGGGACC	2940
GCGTTTTTGA GTATTTCTTA GCGGAATACC GTGCAGGGCG CACGCCAAAT CCGGACGTTA	3000
TGTGCAACAA GGAAATCAAG TTCAAGGCCT TTTTGGACTA TGCCATAACC TTGGGGGCAG	3060
ACTATGTAGC GACTGGGCAT TATGCTCGAG TGGCGCGTGA TGAGGATGGT ACCGTTTACA	3120
TGCTTCGTGG CGTGGACAAT GGCAAGGATC AGACCTATTT CCTCAGCCAA CTTTCGCAAG	3180
AACAACCTCA AAAAACCATG TTCCCACTAG GACATTTGGA AAAGCCTGAA GTACGCAGAC	3240
TAGCAGAAGA AGCAGGCCTT TCGACTGCTA AGAAGAAAGA CTCGACAGGG ATTTGCTTTA	3300
TCGGAGAAAA GAACTTTAAA AACTTTCTCA GCAACTACCT GCCAGCTCAG CCTGGTCGCA	3360
TGATGACTGT GGATGGTCGC GATATGGGCG AGCATGCAGG TCTTATGTAC TATACAATCG	3420
GTCAGCGTGG CGGACTCGGT ATCGGTGGGC AACACGGCGG TGACAATGCC CCTTGGTTTCG	3480
TTGTTCGAAA AGATCTAAGC AAGAATATTC TCTATGTAGG ACAAGGATTC TACCATGATT	3540
CGCTCATGTC AACTAGCCTA GAAGCCAGTC AAGTCCACTT TACTCGTGAA ATGCCAGAAG	3600
AGTTTACGCT AGAATGTACG GCTAAATTCC GTTACCGTCA GCCTGACTCT AAGGTGACCG	3660
TTTCATGTCAA AGGAGAAAAG ACAGAGGTCA TCTTTGCGGA ACCACAACGC GCGATTACAC	3720
CAGGACAGGC AGTGTCTTT TACGATGGCG GG	3752

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TATTTATATT TTTTATCTC TGGCATACTT TGATACCTTT TTAGACTTAA AGTCTTTAAT	60
AGTGCCTTTC CACCTCTTTT TATCTATAAA GATTCTCCTA CATCATAATT CATTPTTTTA	120
TTTAAACCTT TCTGTCTAG TTTGTCTTTA TCTTCTTCAT ACCATTTTAA GATTGTCACA	180
TAGTGGTTTT GATAGGCTT ACCACTGCTT TCCATGTATC TGGATAGTTT ATTTATCATT	240
ATATCTGTGT GTGAGTTTAA TTTTCTTTT AGATTTTTAT ATTCTTCTTT GCTTAACCTT	300
ACATTTTTGA ATTCTCCATA AAAAATGGGG GTGGACTTTT TATCTATCTC TCCCTCTCTC	360
TCTTTATCTA TCTCTATATC TTTCCATGTA ATTCCAATCT GGAGTACCTC TACTGTCTAT	420
CGGTAATTTA ATTTTGATAT CTGGCAATAC TGTGCTAGAT ATTTGATCTT TATATPCAGT	480
ATTTTTTAAA GCTTGCCTAA TAATTGAAGT TAAATAGAAT GCTACTTCTT TATTCAATTC	540
TTTATTTTTT AATTTTAAAC AATGAATTTT CATATCTAGG CTGCTTTTAT ATTTATGATA	600
AAAGACTGCT CCTAAAAATG AAACAGATAT AAAATTTTCA AAACTCTAT AATTTTATC	660
ATCTATATCT TCGTAGTAAC CTAAGATACC ATTGTCAATA TTTGTAGCAC TAATCTAGG	720
AGTTTTTCCA TCGAGTAAAT ATCTTTTGG AATAGATGAG CCTGTTGGTA CTTAACTCGA	780
TTTCCCTTTT TTTTCGGTAA TAAATATTC TTTTATTTT GTTGTCTGAT ATTTTCCTA	840
CCTGTCCTTT GTAGGATGAG TATTTCTAG ATTTTCyTGA ATAACTTTTT ACTTGAAGTT	900
TTAGCTTTTG AACTAGTCGT TGTACTTTCT TTTTGTATAT TATCAGTCCT GATCTTTTTA	960
ATATTGCTGT TATCTCTAT ATCCTATTTT TCATTCATGA TATCTTTTA CTAATTTTAT	1020
CTTAAATCTT GTGCTGTATT TGCCATTAAA AAAGTACCT CCTTTAGTTA GTTTTTTGGC	1080
CTAACTTTTG AGGGTCAGTT CAAAATTTGC GACTTTTAAA TGAATTCCAA TATTCAATTA	1140
TTAAGAGTTA ACATGGTGCT TGCCAATAGG AATCATTAGA GGCGAATTGG AAATAGGGTC	1200
ACGTATAATT TTTGCTTCAA GATTAAAGAT ATCTTTAACT AGTTTATCAT TTAGTATATC	1260
TTCAGGCTTT CCTCTGCAA CAAGTTTACC TTCTTTAATT GCAAATAGGT AATCAGCGTA	1320
TCTTGCTGTT AGATTTATAT CGTGCAAAAT CATGCAAAAT GTTGTCTTAT ATTTTGGTT	1380
TAGATCAGTC AAGAGGTCTA ATAGTTCTAT TTGATATGAG ATATCCAAGT AAGTAGTTGG	1440
CTCATCTAAA AGTAGGATAC TTGTATCTTG GGCTAGGGCT AGAGCTATCC ATACTCTTG	1500
CCTTTGACCC CCAGAAAGTT CTTCAACTAG GTTATTTGCT AGATCTTCAA CATTGGCCTT	1560
AACCATTGAT CTGTTTATTA TTTCAAGGTC ATCTTTTCCA AGACTCTTAA AAGGCTTTCT	1620
GTAGGGGAAA CGACCACGGC TTACAAGATC AGCTACTGTT ATTGATTCAG GGATTATTGG	1680
AGATTGAGGT AATATAGCTA TGTGTTTTGC TAAATCTTTT TCTTTATAAG AATTAATTGA	1740

1199

TTTATTATCA AGCAATACTT CTCCCTCTAA TGGCTTTATA AGTCGAGACA AGGTTTAAAT	1800
GAGTGTGAT TTCCACAAC CATTTGACCC AATAATAACT GATATTTTTT CTTCAGGTAT	1860
TTTTATATTT ATATTTTCCA AGATTATTTT TTCATCATAA CCGCAGGTAA GATTATTTGA	1920
CCACAGACCT TTCATTATAT ATTCCCTCCTG TTCATTTTTA TTAGTAAGTA TATTAAGTAT	1980
GGTGAACCTA ACAAGCCAGT TACAACACCT ACTGGATATC TAGCTGGTAA AATATTTTGA	2040
GAGAATATGT CTGATAACAA AACTAGTAAA ATTCCAACCA ATCCAGCTAA TATTGGGCTT	2100
CTTTCTTGC CAATATTTAA GGCTATGGGA CCAGCTAAAA AAGATATACA AGCTATTGGT	2160
CCTGTAATTG AAGTAGAAAA AGCAGTTAAA GATACAGCGC AAAAAATTAA AACAGCCTT	2220
GAAAGCTCGG GATTTGCTCC AAGTCCGATT GCTATTTCTT CACCAAGTTC AATAATTTCT	2280
AGTCTTTTAT TAAAAAATAA AACTAATATA GTAGCAATAA TACTTACTAT TAGAACAAGA	2340
GGTATGTCAT CTAACTTTGT AAAAGATAAA GAGCCACTGA GCCATCTCAT AACTTCTTGT	2400
AATTCATATC TTGCTACTTT CAACAATAAA AATGAGGTGC CTGCTCTTGT GACAGCTTGA	2460
AAACCAATAC CTAATATTAT CAGTCTTGCT GCTGAAAAAC CATCTTTTTT AGCTAGTAAA	2520
AATAATATTA AAGATGATGT TAGTCCACAA GTTATTGAAA TAATTCAGT AGTTAAACTA	2580
TTTGTTTTTA ATACCAATAT GCAAAAGACC GCTGCAATAG ATGAAGAACT TGTGACACCG	2640
ATTATATCAG GACTTGCAAG AGGATTTCTT AACATAGTTT GAAAGATAAA TCCTGCCAAT	2700
CCAAAAGACC AGCCAGCTAT AATTCCTGCT AATAATTTTG GTAATCTAAT TTCCATAATC	2760
GAAAACTAG CTCCAGGAAC AGTTTCACTA TTAAAGACTT TAATCAAAGT TGAAAAAGAA	2820
TAACTTTCAT CTCCGATAAG TAAATGAAA AATGATAGAC TGATTATTAT TAATAAAAAT	2880
AGTGAGGAAA ATAGTGTTAT TCTATTTTTT CTTTTTTGAA TACCTATAAT TAAATTTTGC	2940
ATTAGTTATT AACCCCTCTA TTTTTCATAG TTACATAAAT AAGTACTGGA CCCCCGATTA	3000
TTGCAGTAAT TATCCCTACT TCAATTTTAC CTGGTTTACC TAACATACGG CCGATTATAT	3060
CACATATAAG CAAGAGCTCT GCACCTATAA AAGATGAAGA AATGGTCATT GTGCGTATAT	3120
CTTTGCTTAT AAATAAGCCA CAAAAGTGAG GAACTATAAG ACCTACGAAG CCAATAGGTC	3180
CACCAATTGC AGTAATACTT GAACATAAAA GCACACTTGC AATTATTGCA AGTGATCTTA	3240
TCCTATTAAAC ATTAACTCCA AGACCAACAG CCATTTTCATC ACCCATAGCT AAAGCGTTTA	3300
AATCTGATGA AATAAATATA GCTATCAAGT GACCTAAAAT TATAAAAGGT AGTAGTGTAG	3360
ATATAGAAGA TAATGTAGCT GCTCCAAGGC TACCTATTTG CCAAAATCTA AATTTGTCTA	3420
AGACGTTATT ATTCGGTAAA ATTA AAAAAC TTACAAAACCT GCTTAAAGCC ATACTAACAC	3480

1200

AAGTTCCTGA TAAGGCAAGT TTTATAGGGG TAAGGCCTGC TTTTCCGTTA CAGCAATCGC	3540
GTATACAAAA ATTGCACTTA CTAAGCCACC AATGATTGCG	3580

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

CCAAATTGCT CCACAATTAT TATGGAGTCG TCGTTTGGCA GATGGGCGTG ATATGTGTGC	60
TCAAGAATGG TTGACAGGCA AGATATTGAC CCCCTATGAT ATGAATCGTA AGCAAATCGT	120
CAATATTTTA ACCCGTCTTC ATCGCTCAGC TCCGTTGATG ACACAATTGA GTCGTTTGGG	180
CTATGCCATG GAAACACCTG TAGATTACT ACAGTCTTGG CAGGAAACGG CTCCAGATGC	240
TTTGCCTAAA AATCATTTTA TCAGTGAAGT GATGGCTGAT TTACGTCAGA CTATTCCAGG	300
ATTTAGAGAG GACCATGCGA CCATTGTCCA TGGAGATGTA CGACATAGTA ATTGGATTGA	360
GACAGATAGT GGCTTGATTT ATTTAGTAGA TTGGGATTCG GTTCGCTTGA CCGATCGCAT	420
GTTTGATGTG GCCCATATGC TCTGCCATTA TATTTACAGAA CATCAGTGGA AGGAATGGTT	480
GACCTACTAC GGTTACAAGT ACAATCAAAC GGTATTAAGT AAATTGTATT GGTATGGTCA	540
ATTGCTCTTAT TTGAGTCAGA TTTCCAAGTA TTATATGAAC CAAGATTAG AAAATGTCAA	600
TCGGGAGATT CATGGTTTGC GTCATTTCCG AGACAAGTAT GGAAAGAGAA GATGAGAGTT	660
AGAAATCGTA AAGGGGCAAC AGAATTACTA GAGGCAAAATC CCCAGTATGT GGTCCCTCAAT	720
CCCTTGGAAG CCAAGGCAAA ATGGCGGGAC TTGTTTGGCA ATGATAATCC CATTGATGTG	780
GAAGTTGGAA GTGGAAAGGG TGCCTTTGTT TCAGGTATGG CCAAGCAAAA CCCTGACATC	840
AACTATATCG GGATTGATAT TCAAAAGTCT GTTTTGAGCT ACGCTTTGGA CAAGGTGCTT	900
GAAGTTGGAG TGCCTAACAT CAAGCTCTTG TGGGTAGATG GTTCTGACTT AACTGACTAC	960
TTTGAAGACG GTGAGATTGA TCGCTTGAT CTGAACTTTT CAGATCCATG GCCGAAAAAA	1020
CGCCATGAAA AGCGTCGTTT GACCTACAAG ACCTTCTTGG ATACCTTCAA ACGTATCTTG	1080
CCTGAAAATG GAGAAATTCA TTTCAAGACG GATAACCGTG GCTTGTTTGA GTACAGTTTA	1140
GTGAGCTTTT CTCAATATGG CATGAACTC AATGGTGTCT GGTAGATTT GCATGCCAGT	1200
GATTTTGAAG GCAATGTCAT GACAGAATAC GAGCAAAAAT TCTCAAACAA GGGGCAAGTT	1260
ATCTACCGAG TTGAGGCAGA ATTTTAAGAG ATAACCTAAA ATTAGGCTGT ACAAGTGCTT	1320

1201

TTGCTTTACA TAAGTTGGCA AACGTGCTAT ACTGATAGTA AGAATATGAA AAGTGAGGCG	1380
GGGAAATATC TTCGCCTCTT GCTTATGAGG AGGTGGACGC AATCGCAACA ATCGTAGAAT	1440
TAGTCAGAGA AGTTGTAGAA CCTGTCATAG AAGCTCCTTT TGAACTCGTG GATATCGAGT	1500
ATGGAAAGAT TGGCAGTGAC ATGATCTCA GTATTTTGT AGATAAACCC GAAGAATTAC	1560
CTTGAACGAC ACGGCAGACT TGACAGAAAT TATCAGTCCT GTCCTAGACA CCATCAAGCC	1620
AGATCCCTTC CCAGAACAAT ATTTCTAGA AATTACCACT CCAGGTTTGG AACGTCCTTT	1680
GAAAACCAAG GATGCCGTCG CTGGAGCGGT TGGAAAATAC ATCCATGTCG GGCTCTACCA	1740
AGCCATCGAT AAGCAAAGG TCTTTGAAG AACCTTGTG GCCTTCGAAG AGGACGAGTT	1800
GAATATGGAA TATATGGACA AGACGCGTAA GAAAACCGTC CAAATTCCAT ACAGTTTAGT	1860
ATCAAAAGCA CGTTTAGCAG TTAAATTATA GAAAAGAAA GGATAGCTTT TGAGGATTCA	1920
AAAGTGAAGA AACATGAGT AAAGAAATGC TAGAGGCCTT CCGCATTTTG GAAGAAGACA	1980
AGGGAATCAA AAAAGAAGAT ATCATCGACG CAGTAGTAGA GTCGCTTCGT TCCGCTTATC	2040
GCAGACGCTA TGCTCAGTCA GACAGCGTAG CTATTGACTT CAACGAAAA ACAGGTGACT	2100
TTACAGTTTA TACTGTCCGT GAAGTTGTG ATGAAGTATT TGATAGCCGT TTGGAATCA	2160
GCTTGAAAGA TGCTCTGCC ATTAATTCAG CTTATGAACT TGGAGACAAA ATCAAGTTTG	2220
AAGAAGCACC AGCTGAGTTT GGTCTGTAG CAGCCCAATC TGCCAAACAA ACCATCATGG	2280
AAAAATGCG CAAGCAAACA CGTGCCATCA CTTACAATAC TTACAAAGAA CATGAGCAAG	2340
AAATCATGTC TGGTACAGTA GAACGCTTG ACAACGCTT TATCTATGTC AACCTTGTA	2400
GCATCGAAGC CCAATTGTCA AAACAAGACC AAATTCCTGG AGAAGTTTTT GCTTCTCATG	2460
ATCGTATCGA AGTTTATGTT TACAAGGTG AAGACAACCC TCGTGGTGTG AACGTCTTTG	2520
TTAGCCGTAG TCATCCAGAA ATGATCAAAC GTTTAATGGA GCAAGAAAT CCAGAAGTTT	2580
ATGATGGAAC TGTGAAATC ATGAGCGTGG CTCGTGAAGC AGGTGACCGT ACGAAGGTTG	2640
CTGTTCGTAG CCACAATCCA AACGTGGATG CTATCGGTAC AATCGTTGGA CGTGGTGGTG	2700
CTAATATCAA GAAGATTACT AGCAAATCC ACCCAGCTCG TTACGATGCT AAAAATGACC	2760
GCATGGTACC AATCGAAGAA AATATCGATG TTATCGAGTG GGTAGCAGAT CCAGCTGAAT	2820
TTATCTACAA TGCCATCGCT CCTGCTGAGG TTGACCAAGT TATCTTTGAT GAAAACGACA	2880
GCAAACGTGC CTTGGTGGTT GTTCCAGATA ACAAGCTTTC TCTTGCCATT GGTCTGCTG	2940
GACAAAACGT GCGCTTGGCG GCTCACTGA CTGGTTACCG TATCGATATC AAGTCTGCTA	3000
GCGAATTTGA AGCCATGGAA GACGCTGCTT CAGTAGAGTT GGAAGTAGAA AACGATACTG	3060

1202

TAGAAGAATA AAAGCTGCTA GAGGAGGGAA AGATGAAAAC AAGAAAAATC CCTTTGCGCA	3120
AGTCTGTGTGT GTCTAACGAA GTGATTGATA AGCGTGATTT GCTCCGCATT GTCAAGAACA	3180
AGGAAGGACA AGTCTTTATT GATcCTACGG GCAAGGCCAA TGGCCGCGGC GCTTATATCA	3240
AACTAGACAA TGCAGAAGCC CTAGAGGCGA AAAAGAAGAA GGTCTTTAAC CGCAGCTTTA	3300
GCATGGAAGT GGAAGAAAGC TTTTATGACG AGTTGATCGC TTATGTGGAT CACAAAGTGA	3360
AAAGAAGAGA GTTGGGACTT GAATAAGCAA AAGATAAGTA ATCTCTTGGG GCTTGCTCAG	3420
CGAGCAGGGC GCATCATATC GGGTGAAGAA TTGGTGGTCA AGGCCATTCA AGACGGCAAG	3480
GCCAAGTTGG TCTTTCTAGC TCATGATGCT GGACCCAATC TGACCAAGAA GATTCAAGAT	3540
AAAAGTCATT ATTATCAAGT AGAAATTGTA ACCGTGTTTT CAACACTGGA ATTAAGCATA	3600
GCAGTCGGGA AATCGAGAAA GGTTTTGGCT GTAACAGATG CTGGATTTAC AAAGAAAATG	3660
AGGTCTCTTA TGGAAATAGAA GAGGAGGACA TGATTTGTCT AAGAAAAGAT TGTACGAAAT	3720
CGCAAAAGAA CTTGGAAAAG AAAGTAAAGA AGTTGTAGCG CGTGCAAAAG AGTTGGGCTT	3780
GGATGTGAAA AGCCACTCAT CAAGTGTGGA AGAAGCTGTC GCTGCAAAAA TTGCTGCCAG	3840
CTTTAAGCCT GCAGCTGCTC CGAAAGTAGA AGCAAAACCT GCAGCCCCAA AAGTAAGTGC	3900
AGAAAAGAAA GCCGAAAAAT CTGAGCCAGC TAAACCAGCT GTAGCTAAGG AAGAGGCAAA	3960
ACCTGCAGCC CCAAAGCAA GTGCAGAAAA GAAAGCCGAA AAGTCTGAAC CAGTAAAACC	4020
AGCTGTAGCC AAGGAAGAGG CAAAACCAGC TGAGCCAGTC ACTCCGAAAA CAGAAAAAGT	4080
AGCGGCTAAA CCGCAAAGTC GTAATTTCAA GGCTGAGCGT GAAGCACGTG CTAAAGAGCA	4140
GGCAGAGCGA CGCAAGCAAA ATAAGGGCAA TAACCGTGAC CAACAACAAA ACGGAAACCG	4200
TCAGAAAAAC GACGGCCGTA ATGGTGGAAA ACAAGGTCAA AGCAACCGCG ACAATCGTCG	4260
CTTTAATGAC CAAGCTAAGA AGCAGCAAGG TCAGCAAAAA CGTAGAAATG AGCGCCGTCA	4320
GCAAGAGGAT AAACGTTCAA ATCAAGCGGC TCCACGTATT GACTTTAAAG CCCGTGCAGC	4380
AGCCCTAAAA GCAGAGCAAA ATGCAGAGTA CGCTCGTTCA AGTGAGGAAC GCTTCAAGCA	4440
GTATCAGGCT GCTAAAGAAG CCTTGGCTCA AGCTAACAAA CGCAAGGAAC CAGAGGAAAT	4500
CTTTGAAGAA GCGGCTAAGT TAGCTGAACA AGCACAGCAA GTTCAAGCAG TGGTTGAAGT	4560
CGTCCCTGAG AAAAAAGAAC CTGCAGTGGA TACACGTCGT AAAAAACAAG CTCGACCAGA	4620
CAAAAATCGT GACGATTATG ATCATGAAGA AGATGGTCCT AGAAAACAAC AAAAGAATCG	4680
AAGTAGTCAA AATCAAGTGA GAAATCAAAA GAATAGTAAC TGAATAACA AAAAAAGAA	4740
CAAAAAGGC AATAACAAGA ACAACGTAA TCAGACTCCA AAACCTGTTA CGGAGCGTAA	4800
ATTCCATGAA TTGCCAACAG AATTTGAATA TACAGATGGT ATGACCGTTG CGGAAATCGC	4860

1203

AAAACGTATC AAACGTGAAC CAGCTGAAAT TGTAAAGAAA CTTTTCATGA TGGGTGTCAT	4920
GGCCACACAA AACCAATCCT TGGATGGGGA AACAATTGAA CTCCTCATGG TGGATTACGG	4980
TATCGAAGCC AAACAAAAGG TTGAAGTGGA TAATGCTGAC ATCGAACGTT TCTTTGTCGA	5040
AGATGGTTAT CTCAATGAAG ATGAATTGGT TGAGCGTCCA CCAGTTGTTA CTATCATGGG	5100
ACACGTTGAC CACGGTAAAA CAACCCTTTT GGATACTCTT CGTAACTCAC GTGTTGCGAC	5160
AGGTGAAGCA GGTGGTATTA CTCAGCATAT CGGTGCCTAC CAAATCGTGG AAAATGGTAA	5220
GAAGATTACC TTCCTTGATA CACCAGGACA CGCGGCCTTT ACATCAATGC GTGCGCGTGG	5280
TGCTTCTGTT ACCGATATTA CGATCTTGGT CGTAGCGGCA GATGACGGGG TTATGCCTCA	5340
GACTATTGAA GCCATCAACC ACTCAAAAGC AGCTAACGTT CCAATCATCG TAGCTATTAA	5400
CAAGATTGAT AAACCAGGTG CTAACCCAGA ACGCGTTATC GGTGAATTGG CAGAGCATGG	5460
TGTGATGTCA ACTGCTTGGG GTGGAGATTC TGAATTGTGT GAAATTTTCGG CTAAATTCAA	5520
CCAAAATATC GAAGAATTGT TGGAAACAGT CCTTCTTGTG GCTGAAATCC AAGAACTCAA	5580
AGCAGACCCA ACAGTTCGTG CGATCGGTAC GGTATATCGAA GCGCGCTTGG ATAAAGGAAA	5640
AGGTGCGGTC GCAACCCTTC TTGTACAACA AGGTACCTTG AATGTTCAAG ACCCAATCGT	5700
TGTCGGAAAT ACcTTTCGGTC GTGTCCGTGC TATGACCAAC GACCTTGGTC GTCGTGTTAA	5760
AGTTGCTGGA CCATCAACAC CAGTCTCTAT CACAGGTTTG AACGAAGCAC CGATGGCGGG	5820
TGACCACTTT GCCGTTTACG AGGATGAAAA ATCTGCGCGT GCAGCAGGTG AAGAGCGTGC	5880
CAAACGTGCC CTCATGAAAC AACGTCAAGC TACCCAACGT GTTAGCCTTG AAAACCTCTT	5940
TGATACCCTT AAAGCTGGGG AACTCAAATC TGTTAATGTT ATCATCAAGG CTGATGTACA	6000
AGGTTCTGTT GAAGCCCTTT CTGCCTCACT TCAAAAGATT GACGTGGAAG GTGTCAAAGT	6060
GACTATCGTC CACTCAGCGG TCGGTGCTAT CAACGAATCA GACGTGACCC TTGCCGAAGC	6120
TTCAAATGCC TTTATCGTTG GTTCAACGT ACGCCCTACA CCACAAGCTC GTCAACAAGC	6180
AGAAGCTGAC GATGTGGAAG TCCGTCTTCA CAGCATTATC TACAAGGTTA TCGAAGAGAT	6240
GGAAGAAGCT ATGAAAGGGA TGCTTGATCC AGAATTTGAA GAAAAAGTTA TTGGTGAAGC	6300
GGTTATCCGT GAAACCTTCA AGGTGTCTAA AGTGGGAAC ATCGGTGGAT TTATGGTTAT	6360
CAACGGTAAG GTTGCCCGTG ACTCTAAAGT CCGTGTTATC CGTGATGGTG TCCTTATCTA	6420
TGATGGTGAA CTCGCAAGCT TGAAACACTA TAAAGACGAC GTGAAAGAAG TGACAAACGG	6480
TCGTGAAGGT GGATTGATGA TCGACGCTA CAATGATATT AAGATGGATG ATGTGATTGA	6540
GGCGTATGTC ATGGAAGAAA TCAAGAGATA AGATTTTTTG CTCCTTTCTT AGGTGGTGAG	6600

1204

GGACGCAAGC AAACCGATGG TTTCATTGCT TATTTTGTAG CCTAGGGTCT CAAAAATCCC	6660
CTGTGATGGG ACTGATAAAT CAGTTCCATC ACTTTCACCA CGGCGAAAGA AGCAGATGAC	6720
TTCAAATTGA ACTTCGTTTC AATTTAAGT GAAATCAAG AAGTTTAAAA TAGCTAGGTC	6780
TGCTGGCCTA GCTTTTGGTT CAAAGTAGAG AAAGGAATAT CATGGCAAAT CATTTCCGTA	6840
CAGATCGTGT GGGCATGGAA ATCAAGCGTG AAGTCAATGA GATTTTGCAA AAGAAAGTCC	6900
GTGATCCACG TGTCCAAGGT GTGACCATCA TAGATGTTCA GATGCTGGGT GACTTGCTCTG	6960
TTGCCAAGGT TTATTACACC ATTTTGAGTA ACCTTGCTTC GGATAACCAA AAAGCCCAAA	7020
TCGGGCTTGA AAAAGCAACT GGTACCATCA AACGTGAAC TGGTCGCAAT TTGAAATTGT	7080
ACAAAATCCC AGATTTGACC TTCGTCAAAG ACGAGTCCAT CGAGTATGGA AACAAGATTG	7140
ACGAGATGCT ACGCAATCTG GATAAGAACT AAAGAAGAGG GGTGCCCCCT CTTTTTGGT	7200
GGAGGAAAAT AGGTGAATT TGAAATGGAA AAATATTCTT TTATAATAGA TTGAAACTAG	7260
AATAGTACGC CTCTACTTCT AAAATATTGT TAGAAATCGA TTTGACTGTC CTGATCGATT	7320
TGTCCTGPTC TTGTTTCATT TTAATATAAA AAAGGATTTC TGTATTTTTT AATGTTATCT	7380
AATTAGAAAA TGCTTTTTTT GTAGGAAATA TAATATGATA AGGTGCAAAA AAGAAATAAG	7440
GAGTTGTAT ATGGCTGAAC AAGACTTAGC TATGCAAGTA TTGCAACAAG TGGTGAAACT	7500
ACCTGTTGTT AAGGTGATC GTTCGAAATT TTTAGTGGAT AAGTTTCCA AAGAATTGGA	7560
TCCAAAAGAT ATTCCTACCT TATTGGAACA AGGTCCAACG ACTCTTCTAT CTCAAGAAAT	7620
ATTAGATCGT GTAGCTAATG CTTGTATTCTG GGACAATGTA TTATTAGCGA GTGGGACTTC	7680
TGTTTTGGCA GGATTACCTG GAGGGCTTGC TATGGCAATT ACCATTCCAG CTGATGTGGC	7740
TCAATTTTAT GCTTCTCTC TGAAATTGGC TCAAGAATTA GGTATATTT ATGGTTATGA	7800
GGATCTTTGG GCTTCACGAG AGGAGTTGAG TGAAGATGCT CAAAATACCC TCTTGCTTTA	7860
TCTAGGCGTA ATGTTAGGGG TGAATGGAAC CGCTGCTTTG CTACGTGTTG GTAGTATAAC	7920
AATTGCCAAA CAGGTAATGA AAATAGTGCC TAATAAAGCT TTAACAAAGA CGCTTTGGTA	7980
CCCTATTTTG AAAAAAGTCT TAAAAATATT TGGTGTGAAT CTTACCAAGG GAGGGTTGGC	8040
CAAAGGAATG GGGAAATTTA TTCCTATCTT GGGTGGTATC ATTTTCAGGTG GTTTAACCTT	8100
TGCAACTATG AAACCAATGG GGGAAAGCTT GCAGAAAGAA TTATCCAAGC TAGTCAACTA	8160
TAGTGAAGTT CAATATCAAG AAGATGTTGA AACAAATCCGA AAAGAGGCTG AAATCATCAA	8220
AGGAGAGTAA TATGAATCCT ATCAAAGCTT TTGCTAAAAT TTATGGTAAT TACTTTTGA	8280
CCGTGCAAGG TGTAAGAGTG ATGAAAACGA TAAAGAAAGC TGACCATGTC GTTGTGGTC	8340
TGGGGAAACT TTTTATTGCC GACAAGTTAA TGGATACGGC TCGGTGGCTC ATTAAGCCAG	8400

1205

AGGAGAGAGA ATGAAATTTT TTTGGTCTTC TTGCTATTCT TTTTATCAAA CCGATTATTG	8460
GGATTGTGAA ATTCTTTTGG ATGATCATCT CTTTTCAGT CCAATTGCTG TTTTACAAGA	8520
TAGTGTPTAA GATATTGGAT TGGCTCTTTA AACTTATCTA GATGGTAATC CAAGTTGCAG	8580
AGAACTAGCA GGAACCTCCAC TGCTAGTTTT TTATTCTCTT TCCATATGGT ATAATATAAG	8640
CAGTAAAATC ATTTTATACT CTTGCGAAAAT CTCTTCAAAC CACGTCAGCT TCACCTTGCA	8700
GTATATATGT TACTGACTTC GTCAGTTCTA TCCACAACCT CAAAACGGTG TTTTGAGCTG	8760
ACTTCGTCAG TTCTATCTAC AACCTCAAAA CACTGTTTTG AGCAACCTGC GGCTAGCTTC	8820
CTAGTTTGCT CTTTGATTTT CATTGAGTAT TAGAACATAC AATGGAGGTC GTCATGGACA	8880
ATATCATCGA TGTGTCAATT CCTGTTGCAG AAGTGGTGA CAAGCATCCA GAAGTCTTGG	8940
AAATTCTAGT GGAGTTGGGT TTAAACCCC TTGCCAATCC CTTAATGCGC AATACAGTTG	9000
GTCGTAAAGT ATCACTTAAA CAGGGTTCTA AGCTAGCAGG AACTCCTATG GACAAGATTG	9060
TACGCACACT GGAAGCGAAT GGCTACGAAG TGATTGGATT AGACTAATGA CAGATGAACG	9120
GATTTCATATC CTACGGGATA TTTTGTTAGA ATTGACACAAT GGCGCCTCTC CTGAGTCGGT	9180
TCAAGATCGC TTTGATGCGA CCTTTACGGG CGTGTGAGCC ATCGAGATTT CCCTTATGGA	9240
GCACGAGCTG ATGAACTCGG ATTCGGGCGT CACTTTTGAA GATGTTATGG AACTCTGTGA	9300
TGTCCATGCC AATCTTTTAA AAAATGCTAT CAAAGGTGTC GAAGTTTCAG ATACTGAGCA	9360
TCCAGGTCAC CCAGTTCGTG TCTTCAAAGA AGAAAATCTG GCTCTCCGTG CGGCCTTGAT	9420
TCGCATTCGT AGATTGTTAG ATACCTATGA GTCTATGGAA GACGAGGAAA TGCTGGCGGA	9480
GATGCGTAAG GGTTTGGTGC GTCAGATGGG ACTTGTGGGT CAATTGACA TCCATTACCA	9540
ACGTAAGGAA GAACTCTTCT TTCCTATCAT GGAGCGCTAT GGACACGATT CACCTCCCAA	9600
AGTTATGTGG GGAGTGGATG ATCAGATTAG GGAACCTTT CAAACAGCTC TAACGACAGC	9660
CAAGTCACTA CCAGAAGTGT CAATTAGCAG TGTAAAGGAA GCTTTTGAAG CTTTTCGAC	9720
AGAGTTTGAA AGTATGATTT TCAAGGAAGA GTCCATCCTC CTCATGATTC TCCTTGAGTC	9780
TTTTACTCAG GATGACTGGC TTCAGATTGC GGAGGAGAGC GATGCCTATG GCTATGCCAT	9840
CATCCGTCCG TCAGAGAAAT GGGTGCCAGA ACGACAGAGC TTTATTGAGG AAAAGATTGC	9900
AGAGGAGCCT GTACAGCTAG ATACGGCAGA AGGTCAAGTT CAACAAGTCA TAGATACGCC	9960
AGAAGGCCAT TTTACCATTA CCTTTACCCC TAAGGAAAAG GAAGCTGTGC TGGACGCCA	10020
TAGTCAACAG GCTTTTGGTA ATGGCTATCT TTCAGTCGAG CAGGCCAATC TCATCCTCAA	10080
TCATCTCCCT ATGGAGATTA CCTTTGTCAA TAAAGAAGAT ATTTTCCAGT ATTACAATGA	10140

1206

CAATACGCCA GCTGATGAGA TGATTTTCAA ACGGACGCCG TCCCAAGTCG GCGCAATGT	10200
CGAACTCTGC CATCCGCCTA AGTACTTGGA CAAGGTCAAA ACTATCATGA AGGGGCTTCG	10260
TGAGGGAAGC AAAGACAAGT ATGAAATGTG GTTCAAGTCT GAGTCGCGAG GTAAGTTTGT	10320
CCACATCACC TATGCTGCAG TACACGATGA AGACGGAGAA TTCCAAGGAG TGTGAGTA	10380
TGTTCAAGAT ATCCAGCCCT ACCGTGAGAT TGATACGGAC TATTTTCGTG GATTAGAATA	10440
AGGAGAAAAA ATGAGTTACG AACAAGAATT TATGAAGGAA TTTGAAGCTT GGGTCAATAC	10500
CCAAATCATG ATTAACGACA TGGCGCACAA GGAAAGCCAA AAAGTTTACG AAGAAGACCA	10560
GGACGAGCGT GCCAAAGATG CCATGATTCTG CTACGAGAGT CGCTTGATG CTTATCAGTT	10620
CTTGCTTGGT AAGTTTGAAA ACTTCAAAGT AGGCAAGGGA TTCCATGATT TGCCAGAAGG	10680
CTTGTTTGGT GAGCGAAATT ATTAAACGAG AAAGATTCTT GATTTTTCAC TAAAATCTTG	10740
ATAGAATGTT TATGTTAAAT CCTTGTCAGA GCAGGGATT TTTATTGAAA GGATTTTATC	10800
ATGTCAAAGA AACTCAATCG TAAAAACAA TTACGAAATG GCCTCCGTCG CGCAGGTGCC	10860
TTTCAAGTA CGGTGACTAA GGTGTAGAT GAGACAAAAA AAGTCGTGAA GCGTCAGAA	10920
CAGTCAGCAA GCGCAGCTGG TAAGGCTGTT TCTAAAAAAG TTGAACAAGC AGTAGAAGCT	10980
ACCAAAGAGC AAGCTCAAAA AGTAGCTAAT TCTGTAGAAG ATTTTGCAGC AAATTGGGT	11040
GGACTTCCAC TTGATCGTGC CAAGACTTTC TATGATGAAG GAATCAAGTC TGCTTCAGAT	11100
TTCAAAAACCT GGACTGAAAA AGAACTCCTT GCCTTGAAAG GAATCGGCCC AGCTACCATC	11160
AAGAAATGTA AAGAAATGG CATCAAGTTC AAGTAATTTT TCTTGAGCCT TGCATTTCCG	11220
AAAAATCTT GCTACAATAG AGCCATTAGA GGTGTTTGA ATCCCACATT TTACAGAAAG	11280
TGGCGGCGCT GAGAAGTCCA CAAATGTGTC AAAACTGGTT GCTAATGGAT GAAAAATTGA	11340
AATAAAAGTG TCTTTTGCT TTAAAGACGA GAGTTGCG	11378

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CCGCGAGCCA CGCGAATTT GCTGCGGTA TTCATCAGTC AGGATCTATG ATCTTTGGTG	60
AACAAGAAAA GGTTCAGTT GTGACCTTA TGCCAAATGA AGGTCCTGAT GATCTATACG	120
CTAAGTTTAA TAACGCTGTT GCTGCATTTG ACGCAGAAGA TGAGGTTCTA GTTTTGGCTG	180

1207

ACCTTTGGAG TGGTTCTCCA TTTAACCAAG CTAGTCGCGT GATGGGAGAA AATCCTGAGC	240
GTAAGTTTGC CATCATCACA GGACTTAACT TACCGATGTT GATTCAAGCC TACACAGAGC	300
GCCTCATGGA CGCTGCTGCA GGTGTAGAAA AAGTCGCTGC TAATATCATT AAAGAAGCCA	360
AAGATGGCAT CAAAGCTCTT CCAGAAGAGC TAAATCCAGT CGAAGAAGTT GCAAGCGCTG	420
CAGCTGCTCC AGTTGCCCAA ACTGCTATCC CAGAAGGAAC TGTATATCGGA GACGGTAAAT	480
TGAAAATCAA TCTTGCCCGT CTTGACACAC GTCTACTTCA CGGTCAGGTT GCAACTGCTT	540
GGACTCCAGA TTCAAAAGCA AATCGTATCA TCGTTGCTTC AGATAACGTG GCTAAAGACG	600
ACCTTCGTAA AGAATTGATT AAACAAGCAG CTCCAGGTAA TGTCAAGGCT AACGTGGTTC	660
CAATTCAAAA ACTGATTGAG ATTTCAAAAG ACCCACGTTT TGGAGAAACA CATGCCCTTA	720
TCTTGTTTGA AACACCTCAA GATGCCCTTC GTGCCATCGA AGGCGGCGTG CCAATCAAGA	780
CTCTTAATGT TGGTTCTATG GCTCACTCAA CAGGTAAAAC ATTGGTCAAT ACCGTTTTGT	840
CTATGGACAA AGAAGACGTT GCTACATTTG AAAAAATGCG TGACTTGGGT GTTGAATTTG	900
ATGTCCGTAA AGTACCAAAT GATTCTAAAA AAGATTTGTT TGACTTGATT AACAAAGCCA	960
ATGTCAAATA AGCCATTATT TATGAAAGGA TTTTAAACAT GTCTATTATT TCTATGGTTT	1020
TAGTAGTCGT TGTAGCCTTC TTGTCAGGTC TTGAAGGCAT CCTCGACCAG TTCCAATTTT	1080
ACCAACCACT TGTAGCCTGT ACCCTTATTG GGCTTGTAAC AGGTCACCTG GAAGCAGGGA	1140
TTATCCTCGG TGGATCGCTT CAAATGATTG CCCTTGGTTG GTCAAATATC GGTGCTGCTA	1200
TCGCTCCTGA TGCTGCACCT GCTTCTGTGC CTGCTGCCAT TATCATGGTT CTTGGTGGTG	1260
ACTTTACCAA GACTGGTATC GGTGTTGCCC AAGCGGTTGC TATCCCTCTT GCTGTAGCTG	1320
GACTTTTCTT GACAATGATT GTTCGTACAA TTTCAGTTGG TTTGGTTCAT ACTGCAGATG	1380
CTGCCGCTAA AAAAGGTGAC TTCGGCGCTG TGGAGCGTGC GCATTTTCATC GCGCTACTTT	1440
TCCAAGGACT TCGTATCGCG CTTCCTGCAG CTCTTCTCCT TATGGTACCA ACTGAAACTG	1500
TACAAAGTAT CCTTAGTGCC ATGCCAGACT GGCTCAAAGA TGGTATGGCT ATCGGTGGTG	1560
GTATGGTCGT TGCCGTTGGT TACGCCATGG TTATCAACAT GATGGCAACT CGTGAAGTAT	1620
GGCCATTCTT CGCTCTTGGT TTCGTTCTCG CTGCTGTGTC AGATATTACT CTAATCGGAT	1680
TCGGTGCTAT CGGCGTTGCT ATCGCTCTTA TCTACCTTCA CCTTTCTAAA ACTGGTGGAA	1740
ATGGTGGCGG AGGAGCCGCA ACTTCTAACG ACCCAATCGG CGATATCCTA GAAGACTACT	1800
AAGATAAGAA AGGACTGAAA ACATCATGAC TGAAAACTT CAATTAACTA AATCAGATCG	1860
TAAAAAAGTT TGGTGGCGTT CAACCTTCTT ACAAGGGTCT TGGAACCTTG AACGGATGCA	1920

1208

AAACTTGGGC	TGGGCTTATA	CACTCATTCC	AGCTATCAAA	AAACTCTATA	CTAAAAAAGA	1980
AGATCAAAATC	GCTGCTCTTG	AGCGTCACCT	TGAGTTCTTC	AACACTCATC	CATACGTAGC	2040
TGCTCCAGTC	ATGGGGGTTA	CTCTGCGCT	TGAAGAAGAA	CGTGCTAACG	GTGTGGAAAT	2100
CGATGACGCT	GCTATCCAAG	GGGTAAAAAT	CGGTATGATG	GGACCTCTTG	CTGGTATCGG	2160
TGACCCAGTA	TTCTGGTTTA	CAGTACGCCC	AATCCTTGGA	TCTCTCGGTG	CTTCACTTGC	2220
CCTTACTGGC	AATATCTTGG	GGCCACTCCT	CTTCTTTGTT	GCATGGAAC	TGATTTCGTAT	2280
GTCATTCTTG	TGGTATGTTT	AAGAGATTGG	ATACAAGGCT	GGATCAGAAA	TACTAAAGA	2340
TATGTCTGGT	GGTATCCTTC	AAGATATCAC	TAAAGGAGCT	TCTATCCTTG	GGATGTTTAT	2400
TCTTGCTGTC	CTTGTTCAAC	GCTGGGTAAA	TATTAATTTT	GCTTTCGATG	TTTCTAAAGT	2460
TCAACTAGAT	GAAAAGGCTT	ATATCCATTG	GGATAAATTG	CCAGAAGGGT	CTAAAGGTAT	2520
CCAAGAAGCA	TTCGCACAA	TAGGACAAGG	ATTGTCTCAA	ACTCCTGAAA	AAGTTACTAC	2580
TTTCCAACAA	AACTTGGATA	TGTTGATTCC	TGGATTATCA	GGACTACTCC	TTACTTTACT	2640
TTGCATGTAC	TTACTTAAGA	AAAAAGTATC	TCCAATCACT	ATTATCCTTG	CCCTCTTCGC	2700
AGTGGGTATT	GTGGCACATG	TTCTTCACAT	CATGTAATCA	AGCAACTAAA	AAGGAACCAG	2760
GTTCTAAAAT	CTGATTCCTT	TTTTCTATGC	TTTTATTTCAG	CCAAGGCTCC	CATTGGATCC	2820
CATGGTGCAA	GTACGATTGG	TTCTGCTCCA	TAGGCAGCTT	GTTCTTCTGC	TGTCAGCAAT	2880
TCCTTACGAA	CAACGATTTG	GTATGTGTAT	TCGTCCATCC	AAGCGTCTGA	GGCAACAAAG	2940
TAACCATCTG	TACCGACCTT	GTCTCCCCAT	GAGTTTTCAA	CCTTCCACTT	GTTTGATTTA	3000
CCATTTTCGT	CCAAGTCAAC	ACCTGTCAAG	ACCATGGCGT	GGGTCATCAA	GCTTTCACTA	3060
TAGTCCAAAC	GTCCAGCCTT	GTCTTGAGTA	AGTTTAATGT	CCATGCTTGA	TTCAAAGTCA	3120
TAAACATCTG	TCGCAAGGAT	GCCAGCTTAC	GGTTGCTGAG	CTGGCCGACA	TCAGAACCAG	3180
ACCAAACAGT	CTCACCTGCT	TGCATTTGGG	CAATCGCCAA	TTCTTTCAAG	CGCTCCATTG	3240
GAACGTTGAT	GTAGCGAACT	GCACGGCTAC	CAACCACATT	CCCCAACATC	TCAACTGTGT	3300
AAGATTTTCC	GTAAGGTTTA	TCAGCAGTTG	GAGCATTGAT	AACAGAAACG	TAGTCTTCTA	3360
AAGGAAGATT	GACATATTTT	TTGTAAAACT	CTTGTGGTGT	GATTCCCTTT	TCACTTTTGT	3420
AGTTGTTATC	TTTATCGCGA	TAAGCAAAGT	CAAACCTGCG	TGGTGGAAGT	CCTAATGACA	3480
TAGCAAGAAA	GTTAAAGATT	TCTTGCAAGA	GTCCTTCTTT	CTTAGCTTGA	ACAGTCGCTT	3540
GATCTGCACC	AGAAACAAGC	AAGTCACGCA	AGATTTGAGC	ATCTTGACGA	AGCAATTTAT	3600
TAAGGATCGC	ATTTAGCTCA	CGACTGCTGC	TAGATGAAAC	AGACTCAGGA	TAAACTGACT	3660
TAGGCACGAC	ACCGTATTTT	TCAAAGAGGG	AAACGACCAT	ATCCCATTGA	CCGCCATCTT	3720

1209

GTTGAGGTGT TTGGAGTAAG AAGCTAACTT GCGGCTAGTC AATTCTTGGT CTGAAGTCGC	3780
AATGACTTGC TCCAAGAACC AGTTTGATTT CTCATACTTA TCCCAGAAGA AAGTGTGGGC	3840
TTGTGACAAC TCAAAGTTCT CCAATTTGTA TTGCGAGATG AGTTTGTGGC GGAAGGTGTT	3900
GAGAGCCGCA AACATCCAGC AACGACCAGA CGCTTTCTGG TTAGTGACCT TGTCCCTTGGT	3960
TAAATCCAAT GAGAAAACAG GTGTGTTGTC TACATGGCTT TGGCGACGTT CCAGAGCTGC	4020
AAAAATTCCG TTGTGGCTGG CAGCATTTTC AATCGCTTGG TATTTTACAT TTGCTTCATA	4080
GTTGGCAAAT AGTTTATCAG TAAATGATTC TTGAATCGCG TTCATAGATT CCTCCTTTTA	4140
GTCTACAGTG TATTGG	4156

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3902 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AAAAACAACA AAATAAAACA AAAACAAAAA TATCGAGGTT TATTTTCAAA ACTTTCGATA	60
TTTTTATTAA GTTATTATTT TGTGTTTCT AGTTTACTTT TTGATGGTTA AGAGTGGTGG	120
AGAATTATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAG CTAGCCGCAG GCTGTACTTG	180
AGTACGGCAA GGCGAAGCTG ACGTGGTTG AATTTGATTT TCGAAGAGTA TTAGTGCAAA	240
CCGTAGTTGT AGTCATCATC TTGCATGGCT TCAACTTCGC CAAGAAGGTA ACCATTTCCG	300
ACTTGAGAGA AGAAGTCATG GTTGAAGTT CCTGTTGAAA TACCGTTCAT AACGATTGGG	360
TTGACATCTT CAGCTGAATC TGGGAAAAGT GGATCTTGTC CCATGTTCAT GAGAGCTTTA	420
TTGGCATTGT AGCGAAGGAA GGTTTTAACC TCTTCAGTCC AACCAACACC GTCATAAAGA	480
CTCTCTGTGT AGCCTTCTTC ATTTTCATAA AGAGTATAGA GTAGGTCGTA CATCCATTCT	540
TTGAGTTTTT CTGCTCTTC TTCAGGTAAT TCATTGAAAC CAAGTTGGAA TTTGTAACCA	600
ATGTAGGTTC CGTGAACAGA CTCGTCACGA ATAATCAATT TAATGATTTC TGCAACGTTG	660
GCAAGTTTGT TGTACCAG AGTAGAGG GGAGTGAAGA AACCAGAGTA GAAGAGGAAG	720
GTTTCGAGGA AGACGCTGGC AACTTCTTT TCAAGTGGGC TGCCGTTTAG GTAGATTTCG	780
TTGACAATCT CAGCCTTCTT TTGTAGGTAA GGATTGGTAT TGGTCCATTC GAAAATTTCT	840
TCAATCTCAG CCTTAGTATT CAAGGTAGAA AAGATTGATG AGTAAGATTT AGCGTGGACA	900

1210

GATTCATATA	ATTGGATGTT	ATTGAAGACA	GCTTCCTCAT	GTGGTGTACG	GATGTCTGCG	960
CGAAGGGCTT	GAACCCAGT	TTCAGATTGC	ATAGTGTCAG	GAAGGGTTAA	ACCACCAAAA	1020
ACTTTTCCGA	CCAAGTCTTT	CTCTTTGTTA	GATAGCTTTC	TCCAGTCATC	CAAGTCGTTT	1080
GATAAGGGAA	TACGTGTATC	GAGCCAAAAT	TGCTCCGTCA	GTTTTTCCCA	AGTTGATTTG	1140
TCGATGACAT	CTTCGATGGC	ATTCCAGTTA	ATGGCTTTGT	AGTAAGTTTC	CATTTAAAAAT	1200
CTCTTTCTGT	GTTTAGTATT	GCGAACTCAC	AATTTATTTCT	ACTTTACCAT	AATTCCTATAG	1260
GAGTATCGCA	CAAAAAGTCG	GAAGCCCGAC	TTTTAAAAATG	TTACATAAAT	TATGTTATGA	1320
CATAGTAGAT	TTGATTTTAT	CAGTGCTGCT	TAGGGAAAAA	TAGTGTCTCT	ATGCTAGAAA	1380
CTAAATCACA	CAGCTTTCAC	ATTGGTTGGC	GCCGACTTCT	CCACCGTCAT	CTGTAAAGGT	1440
ACGGACGTAG	TAGATAGACT	TGATTCCTTT	GTTAAAGGCA	TAGTTACGAA	GGATGGACAA	1500
GTCACGTGTC	GTTTGTATTAT	TTTCCCTCTT	CCATTCGTAA	AGGCCTTTTG	GAATGTCACT	1560
GCGCATGAAG	AGGGTGAGTG	AAAGTCCTTG	ATCCACGTGT	TCAGTCGCAG	CAGCGTAAAC	1620
ATCGATGACT	TTACGCATAT	CCATATCGTA	GGCAGAAGTG	TAGTAAGGAA	TGGTTTCTGT	1680
AGACAAGCCA	GCAGCAGGGT	AATAGATTTT	ACCAATTTTC	TTCTCTTGGC	GTTCCTCGAT	1740
ACGTTGCGTA	ATCGGGTGGA	TAGAAGCAGA	AACGTCGTTG	ATATAGCTGA	TAGAACCATT	1800
TGGCGCTACA	GCAAGGCGAT	TTTGGTGGA	AAGACCATCT	TCTTGAACCT	TGTCGCGAAG	1860
TTTCAAGCAA	TCAGCAACAC	CAGGGATAAA	GACATTTTGT	AAGAGTTCTT	TAACACGGTC	1920
TGATGTGGGA	ACAAATTCAC	CAGTTACATA	CTTGTCAAAG	TAACTTCCGT	TAGCATAGTC	1980
TGATTTTTC	AAGTTGTGGA	AGGTAATACC	ACGTTACCGT	GCAATATTGT	TTGACTCTAC	2040
CAAGGTCCAG	TAGTTCATAA	GCATAAAGTA	GATGCTTGTA	AATTCACAG	ACTCAGGTGA	2100
ACCATATTCA	ATGAGTTGTT	GGGCAAGGTA	GCTGTGCAGT	CCCATGGCAC	CGAGACCAAA	2160
GGTGTGGGCT	TGGCTATTTT	CATGGTCAAT	CGTTGGTACA	GCTACGATAT	GTGAACATATC	2220
TGTAACGAAA	GTAAGGGCAC	GAACCATAGC	ACGGATAGAA	CGACCAAAAT	CAGGTGAAGT	2280
CATCATGTTA	ACCACGTTGG	TTGAACCCAG	GTTACATGAA	ACATCTGTTC	CCATTTGAAG	2340
GAATCTTGA	GCATCGTTGA	TCAAGCTTGG	TTCTTGAAC	TGAAGAATCT	CAGAACACAA	2400
GTTACTCATG	ATAATCTTTC	CATCAACAGG	ATTTGCACGG	TTAGCCGTAT	CGATGTTGAC	2460
TACATAAGGA	TAGCCAGACT	CTTGTGCAA	TTTAGAGATT	TCAGTTTCCA	AATCCCGCGC	2520
CTTGATTTTT	GTCTTGCGAA	TATTTGGATT	TGCGACCAAT	TCATCGTATT	TTTCAGTAAT	2580
GTCGATGTAA	TTGAATGGCA	CACCGTATTC	TTTTTCTACA	GAGTAAGGGC	TGAAGAGGTA	2640
CATTTCTTCA	TTTTTACGAG	CCAATTCGTA	GAATTTATCA	GGTACTACAA	CACCAAGTGA	2700

1211

TAGAGTCTTG ACACGTACTT TTTCATCAGC GTTTTCTTTC TTAGTTGAAA GGAAAGCGAT	2760
GATATCTGGG TGAAAGACGT TGAGGTAGAC AACACCAGCA CCTTGACGTT GCCCAATTG	2820
GTTGGAGTAA GAGAAGCTGT CTTCAAAAAG CTTCATAACA GGAACGACAC CTGAAGCAGC	2880
TCCTTCATAG CCTTTGATAG GTGCACCAGC TTCACGAAGG TTGCTGAGGG TAATTCCCAC	2940
ACCACCACCA ATACGTGAAA GTTGAAGAGC TGAGTTGATA GAACGCCCGA TAGAGTTCAT	3000
ATCATCCGTC ACTTGGATTA GGAAACAAGA TACCAACTCC CCACGACGAG CACGTCCAGC	3060
ATTCAAGAAG GAAGGAGTAG CAGGTTGGTA GCGTTGGTGG ATGATTTCAT TGGCAATATC	3120
GATTGCAACA GCTTCATTCC CATCAGCGAA ATAAAGGGCA TTGAAGAAGA CACGGTCTTC	3180
CATATTTTCA AGATAGTATT CACCGTCATT AGTCTTTAAG GCATATTGAT TGTAAAATTT	3240
ATAAGCTGCC ATGAATGACT TGAATTGGAA GTTTTGGTCT TTGATAAATT GAGCTAATTC	3300
TTCCAAGAAC TCTGGACGGT ATTTCTTGAT AAAGGCTGTT TCGATGTAGT TGTGTCAAT	3360
GAGGTAATTG ATTTTGTCTT TGATTGAATC AAAAACCATA GTGTTTGGA CTACATTTTC	3420
TTTAAAGAAA GCATCCAAGG CTTCTTGTC TTTATGAAGC ATGATTGTC CATTAAACAGG	3480
ACGGTTAATT TCGTTATTAA GACGGAAGTA AGTCACGTCT TCAAGATGTT TTAATCCCAT	3540
AAAATTTCCC TTATCTAATT ACAAAGAAA GGCTTCTAAG TTAGCCCTAA AAGCAGTTTC	3600
TTCTGGATGA TGTACTAAGA TTATGCTAAT TGTTCAGTT TTCCTGGTTG GAAACCTGAA	3660
AAGACTTCAG TTGGTGTG GATAACAGGA GCTGCGCTAA AACCAGAGCTC TTTAACTTGA	3720
TCGACGTACT CAGGTGCTC ATCAAGATTG ATTTACAGAT AAGAGACATT ATTACTGTCC	3780
AAGAAACGCT TGGTCATTTT ACATTGGACA CAATTGTTTT TAGAATAAAC GGTACCATT	3840
GTGTAATCC TCTTCAAAAT TTAATACTAT CTTAGTATAT CAGAAAATAA AATTTGTGCG	3900
GG	3902

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TATTGAAGCT ATTGTAGACT ACAAAGATAA GGATTTGCAG TTAGTAGGCG GTGAGACTCA	60
CTGATAACCT AAAAAGGATA GTCAATTATG CTTGTTTACT AACTATTAAC TATGCTAAAT	120

1212

CAATTGAGGT TGTTTACATA AAATCTCTATA TCAGAGAAGC CTGATATAGA GTTTTTTCTT	180
GCTAGTTTTTA GGATTTTTTT GTAAAATAGA AAAAGTGAAG AGAGGTATGA AATGAGCAAG	240
AAAGATAAAA AAATCGAAAT TCAAGTAGCG GATGCCAAAG TTAATGTTGG TAAAGACAGT	300
TTTGAAGGTT ATACATTGAC TATCGGTAAA AAAGTTATCG GAGAAATTGC CGAATTAGAC	360
GGACAATTG CCATTATAAA GAATGGGAAT GTCGATAGTT TTTATAAAAA ATTGGAAAAA	420
GCTGTGGAAT TTTTGATTGA AAATTATAAT TTAGCAAAAT AAGTCTTGTT TTTTGAAT	480
TTTCATGATA TAATAGTCCA TGTGATTGT AGGAGAGATA GCGAAGAGGC TAAACGCGGC	540
GGACTGTAAA TCCGCCCCCT CGGGTTCGGG GGTTCGAATC CCTCTCTCTC CATTTTCTTA	600
ATGGGGTATA GCCAAGCGGT AAGGCAAGGG ACTTTGACTC CCTCATGCGT TGGTTCGAAT	660
CCAGCTACCC CAGTTCTTAG GTAATAATCA AGATAGAAAG CAAAATATCT TAGGGTATTT	720
TATTTTTATA ATTGAAAGAC GTGAATGATA TGAACATGTC CTTGCGGGTG CTTAGGAAAA	780
AAATTATAAG TATGTCAAGT TTAAGAAAAA CTTGATTGTT GGAGGATTTT TTAGATGAAC	840
GAATTTGAAG ATTTGCTAAA TAGCGTTAGT CAAGTTGAGA CTGGTGATGT TGTAGTGTCT	900
GAAGTATGA CAGTTGATGC GACTCAAGCT AACGTTGCAA TCTCTGGAAC TGGTGTGAA	960
GGTGTCTTGA CTCTTCGCGA ATTGACAAAC GATCGTGATG CAGATATCAA TGACTTTGTT	1020
AAAGTAGGAG AAGTATTGGA TGTCTTGTA CTTCTGCAAG TAGTTGGTAA AGATACTGAT	1080
ACAGTTACAT ACCTTGATC TAAAAACGC CTTGAAGCTC GCAAAGCATG GGACAAACTT	1140
GTTGGTCGCG AAGAAGAAGT TGTACTGTT AAAGGAACGC GTGCCGTAA AGGTGGACTT	1200
TCAGTAGAAT TTGAAGGTGT TCGTGGATTT ATCCAGCTT CAATGTTGGA TACTCGTTTC	1260
GTACGTAACG CTGAGCGTTT TGAGGTCAA GAATTTGATA CTAAATCAA AGAAGTTAAC	1320
GCTAAAGAAA ACCGCTTCAT CCTTTCAGT CGTGAAGTTG TTGAAGCAGC TACTGCAGCA	1380
GCTCGCGCTG AAGTATTCGG TAAATTGGCT GTTGGTGATG TTGTAAGTGG TAAAGTTGCT	1440
CGTATCAGAA GCTTCGCGC TTTCTGCGC CTTGGTGGTG TTGACGGATT GGTTCACCTG	1500
ACTGAATTGT CACATGAACG TAATGTATCA CAAAATCAG TTGTAAGTGT TGGTGAAGAA	1560
ATTGAAGTGA AAATCCTTGA TCTTAACGAA GAAGAAGGAC GTGTATCACT TTCACTTAAA	1620
GCAACAGTAC CAGGACCATG GGATGGCGTT GAGCAAAAAT TGGCTAAAGG TGATGTAGTA	1680
GAAGGAACAG TTAAACGTTT GACTGACTTC GGTGCATTTG TTGAAGTATT GCCAGGTATC	1740
GATGGACTTG TTCACGTATC ACAAATTCA CACAAACGGA TTGAAAATCC AAAAGAAGCT	1800
CTTAAAGTTG GTCAAGAAGT TCAAGTTAAA GTTCTTGAAG TTAACGCAGA TGCAGAACGC	1860
GTGTCACTTT CTATTAAAGC TCTTGAAGAA CGTCCAGCCC AAGAAGAAGG AAAAAAGAA	1920

1213

GAAAAACGTG CTGCTCGTCC ACGTCGTCCA AGACGTCAAG AAAAGCGTGA TTTCGAACTT	1980
CCAGAAACAC AAACAGGATT TTCAATGGCT GATTTGTTTG GTGATATCGA ACTTTAATCA	2040
AATTGAAAAT TCACAAAATC CTTTGTTTAC TAAACAAGGG ATTTTCTGG CTCTTTGTCA	2100
ACTGTAGTGG GTTGAAGAAA AGCTAAGCTC GAGAAAGGAC AAATTTTGTC CTTTCTTTT	2160
TGATATTCAG AGCGATAAAA ATCCGTTTTT TGAAGTTTTC AAAGTTCCGA AAACCAAAGG	2220
CATTGCGCTT GATAAGTTTG ATGAGATTAT TGGTCGCTTC CAGTTTGGCG TTAGAATAGT	2280
GTAGTTGAAG GGTGTTGACA AGCTTTTCTT TATCTTTGAG GAAGGTTTTA AAGACAGTCT	2340
GAAAAATAGG ATGAACCTGC TTAAGATTGT CCTCAATAAG TCCGAAAAAT TTCTCCGGTT	2400
CCTTATTCTG AAAGTGAAAC AGCAAGAGTT GATAGAGCTG ATAGTGGTGT TTCAGG	2456

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10974 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AAATAGGATA TAGAGACATC CTTCTGATCT GCTTTTwACA AAGTCCAATT ATATGCGGAT	60
CTATACCTCC ACAATGTCCA TTATTATmCC TAACTATAAT ATGAGCCGAA AACACTATAT	120
CCTTAATGTC TCCATATCCA TCAGGGATAT TAATATTTAT TTTTCCACAA CTATATFGCA	180
TTGTAACCAT CTCCTTAAAC GACGCATTAT GATATTTGAT AGAGAAATTT TTATGAATAA	240
CTCAATAATT TTATAGTAAA TCATGCTTAT ATCTCAAAGA TACCTATTTT ATCTTGCTCTC	300
GACCTTCTCC AAAGAATTGC TATAATACTA TTACAAATCC ATCTGCACTA CACTTCAAAT	360
TTTAGCACTG TATAAAAACG TTTCAATACA CTAACCTCAA GAAAACCTCC ACTATTAATT	420
GAAAAAATG ATAGAGATAA ATTAAAAATC TATATTGAAA CTCATCCCGA TGCTTATTTG	480
ACTGAAATAG CTGCTGAATT CAACTGTCCT CCAACAATA TTCATTACGC TCTAAAGGCT	540
ATGGGATATA GTCTAAAAA GAGCCGTACC TACTGCGAAC AAGACCCAGA AAAAGTAAAT	600
CGGTTCCCTTA AAGAATTGAA TCACTTAAGC TACCTGACTC CTATTTATAT TTATGAGACA	660
GGGGTTGAGA CCTATTTTTA TCTCGAATAT GATCGAGCCT TGAGCAGGCA GTTAGTCTCT	720
CTGGAAGAAG ATATAATTAT TTGAATTAAG ATCGAGACAA CGCACACCAG AGATTGCGAT	780
ACTGTTATAG AAGTACTAAT GCCCTTTTTT GTTCAATAT ACTATGGCTC CGATGACCTA	840

1214

TAAAGATACG ATGACGAGTG ACTTTTTCGA AGCTTGCTTC CAAAAATCTCT TACTACCTAC	900
TTTAGATACA CCATCCCTTA TCATTATGGA CAATGCAAGG TTTCACAGAA TGAACATGTG	960
TAAGGAGCAG GGCATAGACT GTTACCACTT CCTACCTATT CACCCGAGTA TAATCCCATTT	1020
GAGAAAATAT GGGCTTACAT CAAAAACATC TCAGAATAAT ATTGTCAAAT TACGATGCTT	1080
TTCTTGAGGC ACTTTTGTCC TATTCTTGTT TCAGCCGACT ATACTCCGTT ATTGGGCAGC	1140
TACGGAACAG TCGATGGGAC GATGGGGGGA CATAAAAAA TCCTCCAGTT TGTGTTTTTA	1200
TAAACAGTATA CTGGAGAATT GACAATCTCG GTAGATACCT CGTTATAGCG CGGTTACTTA	1260
TTAGGCAGTT ACAAACAAC TGTGAACAGA AAACATTCCA GAGTCAGACA AGACTTTGGA	1320
ATGTTTTGGC TCTATAATTT CTGTAGTGGG TAATCCCACC CCAGGAATTA TAGGGTCGTT	1380
TCTTGTAGAA AAAAAGCCCC ATATGACCTA TAATGAAAAG CGTCTAACCA ACTCATTAGA	1440
AAGGGTTCAT ATGGAACAAC TTAAGAATAC CACAGATTG CTCGGATTGG AAGACAAAAA	1500
TATCAAAATC TTGTCTGTTT TGAATACCA AACCCATCTA GTCGTTTCAGG CAAAGTTGGA	1560
TTCCCCCGCT CCTCCTGTC CTCATTGTCA AGGGAAGATG ATCAAATACG ACTTCCAGAA	1620
AGCCTCTAAA ATTCCGCTTC TCGACTGTCA GGGTTTACCC ACGGTACTGC ATCTCAAAAA	1680
GCGCCGCTTT CAGTGCAAGA ATTGCCTTAA GGTGGTCGTT TCTCAAACAT CCATTGTCAA	1740
GAAAAATGTC CAGATTTCCT ACATGGTGAG ACAAAAAATC GCTCAGCTCC TCCTTGAAAA	1800
GCAGTCTATG ACTGAGATTG CCCACAGATT GGCGGTCTCA ACTTCCACCG TCATCCGAAA	1860
ACTGAGGGAA TTAAAGTTTG AAACCGATTG GACCAAGTTG CCAAAAGTTA TGAGTTGGGA	1920
TGAGTATAGC TTCAAAAAGA GCAAAATGAG CTTTATTGCC CAAGATTTTG AGTCCAAATC	1980
CATCCTCGCA ATTTTAGACG GGCGAACTCA TGCGGTGATT CGAAACCATT TCCAACGCTA	2040
TCAGAGAGAG GTTCGGGAGC TGGTCGAGGT CATCACCATG GACATGTACA GCCCTTATTA	2100
TCGGCTCGCT AAGCAACTCT TTCCAAAGGC GAAGATTGTT CTTGACCGCT TCCACATTGT	2160
CCAACATCTG AGCCGAGCTA TGAACCGAGT ACGAATCCAA ATCATGAACC AATTTGACCG	2220
AAAATCCTTG GAGTATCGGG CGCTCAAGCG CTTTGGGAAC CCTCGCTTTT TCGTTTCTAG	2280
GCTCGGGCTA AATCAGTCCA CTGGACTGAT TTAACACACC AGTATAGCTT CAAGCTCTGT	2340
CAGAAACGAT TCTATCAGCC CACGTTTCGA ATGCACTTAA CCCATCGGGA AGTACGAGAT	2400
AAGCTGCTTT CTTACTCTGA GGGATTACAG GTTCACTACG AACTCTATCA ACTCCTGCTC	2460
TTTCATTTTC AAGAGAAGAA TGCCGACCAT TTCTTTGGAT TGATTGAGCA AGAACTGCCA	2520
ACGGTTCATC CGCTTTTTC AACGGTCTTT TGGACTTTTT TAAGGGATAG AGATAAGATT	2580
ATCAACGCAC TTAAGCTGCC TTATTCCAAC GCTAAACTTG AAGCGACCAA TAATTTGATT	2640

1215

AAGATTATCA AGCGCAAAGC CTTTGGTTTC CGGAACCTTA ACAATTTTAA AAAACGGATT	2700
TTGATGACTT TGAACATCAA AAAAGAGAGT ACGAATTTTCG TACTCTCCAG ATTGCAGCTT	2760
TTCGCCTACC CACTACACTT GACAAAGAGC CACTCTTTAT TCCATGGTAT CAAAGGCAAG	2820
ACTTGGTTTG GCATTGAGGT CCCAGCCTGC GAAGTTTTCCT TTGTTCCACT CGCTGACGCT	2880
GGCATAGGCA ATCATACCTG CATTGTCTCC GCAGAGTCGC AGAGGGGGGA TGATAACCTT	2940
GACATCTGTG ATTTCCGGCTG CTAGGCGTTC TCTGAGACCT TTATTTGGCTG CCACACCACC	3000
TGCCACAACCT AGGATTTTAA CAGGATATTT CTCCAAAGCC TTCTTGGTTT TTGCCATGAG	3060
AATGTCCATA ACTGCTGCTT GGAAGGAAGC ACACAAATCT TCTGTAGACA GGCTTTCTCC	3120
CTTTTGCTCG GCATTGTGAT GAAGATTGAT AAAGGCAGAT TTCAAACCTG AGAAGGAGAA	3180
CTCCAGATTA TCTTCCTTAA TCATGGCACG GGGGAAATCA TAAATATCCT GCCCTGATG	3240
AGCCAGCTCG TCAATCTCAC GACCTGCAGG ATAGGTCAAG CCCATGACAC GGCCGACCTT	3300
ATCATAAGCC TCACCAACCG CATCATCACG GGTTCCTCCA ACAATCTTAT AATCTCCTGC	3360
CTCCGAAACA TAAACCAACT CTGTGTGTCC GCCGCTGACC AAGAGGGCTA GCAAGGGAAA	3420
CTCCAAAGGC TCCACACTCT GAGCTGCCAT GAGGTGCCA GCCATGTGAT TAACAGGAAT	3480
CAGTGAAGT CCGTGAGCCC AAGCAAAGGC CTTGGCAGCT GACAAACCAA CTAGCAAGGC	3540
TCCGACCAAG CCTGGTCCGT AGGTAACCGC AACAGCTGTC ACGTCCTCTT CGGTAATCCC	3600
TGCTTCTGCC AATGCCTCCT CGATACAGGC TGTAAATGACC TCGACATGGT GACGACTGGC	3660
TACTTCGGGC ACTACGCCAC CAAAACGTTT GTGACTCTCA ATTTGACTAG CAATGACATT	3720
GGACAAGAGC TCATCGTCGT TTTTCAAGAC GGCACACTG GTCTCATCAC AGGATGTCTC	3780
AAATGCTAAA ATATATCTAT CCTTCATCTA TTTCTCTCTT CATGATAATG GCGTCCTCGA	3840
CTGGGTCTAG GTAGTAGGCC TTTGCTCAG CGATAACTGT CATCTTTTCT TTCTTGTAAG	3900
ATGCTTGC GC TCGTTGATTT GACTGTCTGA CTTGAGGAA AATTTCTTTG TCTGTCGGCA	3960
ATTGAGCAA CAAGGCTGAC GCAATCCCCT GACCTGATA AGCTCCTTTG ACAGCGATT	4020
GCAGGACTTC TGCTTCAAAA AGATTCTCCT GCACAGCTAG AAATCCAATC ACTTCTGCCC	4080
CATCATAAGC CAATGCATAC CAAGTCTGGT CTTGGGACAG ATCTGCTTGG ATTTGCTCCA	4140
GAGTCCAAG ACTGACTAGG TAAACAGCTG CCATAACAGC GTAGATGGCT TGAGCTAGGT	4200
CAGGCTGTTG TTGAATTCGC TTGATTTCTA TCATAGGCGT TTAATGTAAG ACTCGCCAGA	4260
CTCGGTATGG TTCTTGAGCC AGTTTTCCTC AGCCTCGACT CGTTTGAGGT AATTCGGCAC	4320
AAAATCATGC AAGGAGTCTG CTTCTTGTG CCAGGCCAAA AGAGCTAGAT TAGCTGCATT	4380

1216

GGGCAATGTT TCTTTGTAAT CAGTCCTTGG CAAGTGT TTTT TGAATCTGCT CAACAAAGGG	4440
GCCAACTTCT CCGACAAAGG TTACCTGACT AGTACCCTTG ACTTTTCTA GCACCTCTTC	4500
AAAAGATAGG TCGCCTCTCG CCATGACAGG TTTGGCATT TCAATAAATC CTGCATAAAC	4560
ATTATTGCGA CGCGCATCCA TCAAGGGGAC AAACAAACCT TCTTGTGAT GGGGCACCAG	4620
AGCCAAGAGA CTCGACATAC CAACCAACTC GATGTTT CAGG GTGTGAGCTA AGGTCTTAGC	4680
AGTTGCTACC GCAATTCGCA AGCCTGTATA GCTACCCGGC CCTTCAGCTA CCACGATTCG	4740
GTCCAAATCC TTGGGTGTCC AATCCAAACT TGCCATCAAA AAATCGATGG CAGGCATAAG	4800
AGTAATACTG TGATTTTCT TAATATTAAT CGTCGTCTCG GCAAGAACCT GCTTATCCTC	4860
TAAAATAGCC AGAGAAAGAG CCTTGCTGGA CGTATCAAAA GCTAATACTT TCATAACACA	4920
TTCTATCTT TTTGTCTGCT TACTATTATA CTACAAAAGC TGGCACATGG GAATTTTCTT	4980
TGCCCCCAGA CAAGAGTGCC CTCACCTAAC TAAAAATAAT TAAAAAAAT GCTCACTTTT	5040
CCTTTTCTTT TCCGAATATA AAAGTGAACA AGAAAAAGG AGGAAAGTTC AATGACAAAT	5100
TTTGACATTC TTGACAATCA ATTTTATCC TTATCTGAAA ATGAATTATC AGATATTGAT	5160
GGCGGTCTCG CTCCCTTGGT TATCTTTGGA GTAGCAGTAT CTTGGAAGGC TATTGCAGGT	5220
GGAACAGCAC TTATAGGTTT TGGTTTGGCA GCTGGTTATT TTTTAGGAGG AGATTAATAT	5280
GATGAAAGAT TTGAACAATT ATCGTGAAAT TTCTAATAAG GAATGCAAG AAATCAAGGG	5340
TGGCTTTGGT GTCGGTGTG GTATCGCTTT ATTTATGGCA GGTATACCA TTGGAAAAGA	5400
CCTTCGTAAA AAGTTTGGTA AGTCATGCTA GATAAGAAAC ACATTTT TAG AAGGATAAAT	5460
TTTATTGTCT TCATCTCTTA CAGTTTGTCT AGCATCTCTA ATGATTTGAA CATTACTACC	5520
ATCCCTTTAC CATTGATTT ATCTGTTTGT ATGTTTAT TTTTATGCTT CAACTCTATT	5580
TTTGATCAGA ACAATGACTC CCATAAAAAT AATAAGCTTT GAAAATTCCA TTGTCATGTC	5640
ATGTTAGAAA AATGCAAAGA CCACCTCATC TTGATAGATG GGGTGGAATT TTCGTGTCGT	5700
AAATCTACTA TCTCTACATT CCCAAACAAA AAACCCAGC ATAAGCAGGG CATCTAAGCA	5760
TTTAATTCAA AGTAAATAC AAACCAAACG ACATAGGTCA CGAGGAGGAG AAAAAGCGAG	5820
TAGAGAGTCA CAAAGGTCAT TTTCCACAAG AACTTGGTTT GTCGTCGTTC CAGTTTGGCA	5880
AATAGAAGAT TCCCCGATA AACGCAAGCA ACAAAAACAA TAAAAGCTAC CAAGCGAGCT	5940
CCGATAGCAA AAGCAAATAA GTTATACATA GGGCAACCTC CTTGACTTAA AATCTATATG	6000
GAATTATGAC AAGCAATAAA TTTCACTTCC GTTATCAACA TAATACATTT TCTTTATTTT	6060
TGAAAACGCT TACCAAAGAA ATCGTCCCCT AACTTTCTCG TTTCCGTCTT TTAATAATTT	6120
TTCATTTTGT GGTATAATTG AAATAATTGT AACGAATCAA GGTCAATCTA GACACAAAAT	6180

1217

GGAATGAAAT CAAGCAAATA TCTGCTAAAA GTTTGGAATA AGCTGACCTG TAAATAGAAA	6240
GGAACATATAT GATTTACAAA GTTTTTTATC AAGAAACAAA AGAACGTAGC CCACGCCGTG	6300
AAACAACACG CACGCTTTAC CTAGACATCG ATGCCAGCTC AGAACTTGAG GGCCGTATCA	6360
CTGCTCGCCA ACTTGTCGAA GAAAATCGCC CAGAGTACAA TATCGAGTAT ATCGAACTCT	6420
TGTCTGACAA ATTGCTCGAT TACGAAAAAG AAACGGCGC CTTCGAAATT ACGGAGTTCT	6480
AATATGGCCT ACACTCTTAA ACCTGAAGAA GTCGGCGTTT TTGCCATCGG TGGTCTAGGA	6540
GAAATCGGGA AAAACACTTA CGGAATTGAA TACCAAGACG AGATTATCAT CGTCGATGCT	6600
GGGATTAAAT TCCCAGAAGA TGACTTGCTT GGTATCGACT ATGTCATTCG TGACTIONCT	6660
TACATCGTGG ACAATATCGA CCGCGTCAAG GCTGTTTTAA TCACACACGG ACACGAGGAC	6720
CACATTTGGT GGATTCCGTT CCTACTCAAG CAAGCAAATG TCCCTATTTA TGCTGGACCG	6780
CTTGCCCTTG CTTTGATCCG TGGGAAACTC GAAGAACACG GCCTCTTGCG CAACGCCAAA	6840
CTTTACGAAA TCAACCACAA CACCGAGTTG ACCTTTAAAA ATCTCAAGGC AACTTTCTTT	6900
AGAACGACTC ACTCTATTCC AGAGCCTTTG GGGATTGTCA TTCATACTCC TCAAGGGA	6960
ATCGTCTGTA CGGGTGACTT TAAGTTCGAC TTTACTCCAG TTGGAGAACC TGCGGACTTG	7020
CATCGTATGG CTGCGCTTGG TGAAGAAGGC GTGCTCTGTC TCCTGTCTGA CTCGACAAAT	7080
GCGGAAGTAC CAACCTTTAC CAACTCTGAA AAAGTCGTTG GTCAGTCCAT TATGAAGATT	7140
ATCCAAGGTA TTGAAGGACG TATCATCTTT GCATCCTTTG CCTCAAATAT CTTCCGTCTC	7200
CAGCAGGCAA CAGAAGCTGC TGTTAAGACT GGACGCAAGA TTGCGGTCTT TGGTCGTTCT	7260
ATGGAAAAGG CCATTGTCAA CGGAATCGAT CTTGGCTACA TCAAAGCTCC TAAGGGAACC	7320
TTTATCGAGC CAAATGAAAT CAAAGATTAT CCTGCAGGAG AAGTTCTTAT CCTCTGTACA	7380
GGTAGTCAGG GTGAGCCTAT GGCAGCCCTC TCTCGTATCG CCAACGGAAC CCACCGTCAA	7440
GTACAATTAC AACCAGGTGA TACCGTTATC TTCTCTTCTA GTCCCATCCC TGGAAACACT	7500
ACTAGTGTCA ACAAGCTGAT TAACATCATT TCTGAAGCTG GTGTGGAAGT TATCCACGGT	7560
AAAGTGAACA ATATCCATAC ATCTGGACAC GGTGGTCAGC AAGAGCAAAA ACTCATGCTC	7620
TGCTTGATTA AGCCAAAATA CTTTCATGCCT GTCCACGGTG AATACCGCAT GCAAAAAGTC	7680
CACGCTGGAC TAGCAGTGGA TACTGGTGTG GAGAAGGACA ATATCTTTAT CATGAGCAAT	7740
GGCGATGTGC TTGCCCTTAC TGCTGACTCA GCTCGTATCG CAGGTCATTT CAACGCCCAA	7800
GATATCTATG TCGATGGAAA TCGTATCGGT GAAATTGGCG CAGCTGTCTT CAAAGATCGT	7860
CGCGATCTAT CTGAAGACGG TGTCGTTCTG GCAGTTGCAA CTGTTGACTT CAAATCGCAG	7920

1218

ATGATTCTAT	CTGGTCCAGA	CATCCTCAGC	CGAGGCTTTG	TCTACATGAG	AGAGTCTGGC	7980
GACTTGATTC	GCCAAAGCCA	GCGTATCCTC	TTCAATGCCA	TTCGTATCGC	ACTGAAAAAT	8040
AAGGATGCTA	GCGTGCAATC	TGTCAATGGT	GCCATTGTCA	ACGCTATTCG	CCCCTCCTC	8100
TATGAAAATA	CCGAACGTGA	ACCGATCATC	ATCCCGATGA	TCCTCACACC	AGATGAAGAA	8160
TAAAGCAAGA	AAACAGCCCC	GTCTCGGAG	CTGTTTTTCT	CTATGCTTTC	TTTTGAGATT	8220
AAAACTCATA	CTCAATGAAA	ATCAAAGAGC	AAACTAGGAA	GCTAGCCGTA	GGTTGCTCAA	8280
AGCACTGCTT	TGAGGTGTGA	GATAGAAGTG	ACGAAGTCAG	TAGCCATACC	TACGGCAAGG	8340
CGACGTTGAC	GCGGTTTGAA	GAGATTTTCG	AAGAGTATCA	ATAAAAAATCG	AAATCAGACT	8400
AGAAGGCTAA	GCGAAAGCAT	AACTTGAGTT	AGCTCCCAT	GTTCGGGAAA	CTATGGGAGG	8460
CTGGAGATGA	ATCAAAGCCA	AGCTTTGAAC	TCATTTCGTAA	GAAGCCGACG	ACGTATCATT	8520
TTGATTTTGT	AAGAGTTTGA	GAAATACTAC	GATTTTACC	TTCCAGATAC	ACCATCAAAA	8580
TAGAAATATC	TGCTGGGTTT	ACTCCCGAAA	TACGGCTGGC	TTGGCCGATG	GTTTCTGGAT	8640
TGATGAGTTT	GAATTCTGA	CGGGCTTCGG	TTGCGATAGA	ATCAATGTCA	TCCCAGTCGA	8700
TATTTGGCCG	AATGCGTTT	TCTTCCATGC	GTTTCATCTT	GGCAACCTGG	TCCATGGCTT	8760
TGGAATATA	GCCTTCATAC	TTGATTTCTG	TTTCAATCAA	TTCGATAATC	TTGTCATCCA	8820
AGTCTTCTGC	AGCTGGTCCG	ATGAAGGCCA	CCACATCTTG	GTAAGAAACT	TCTGGACGGC	8880
GAAGGAATTC	CTTGGCTGTC	ACTGCATCGG	TCAAGGGTTT	GAAGCCCATC	TCCTCAACCT	8940
TGGCATTTGGT	TTCTTGACT	GGCTTGAGTT	TGATACTGTC	TAGGCGCTTC	ATCTCATTAT	9000
CAAAATTGATT	TTTCTTGATT	TCAAAACGAG	CCCAGCGTTC	ATCGTCCACA	AGGCCAATCT	9060
CGCGTCCCAT	CTCAGTCAAG	CGCATATCAG	CATTGTCATG	ACGAAGAATG	AGACGGTATT	9120
CAGCACGACT	GGTCAAGAGA	CGGTAGGGTT	CAATGGTTCC	CTTGGTCACC	AAGTCGTCGA	9180
TCATCACCCC	GATATAACCA	TCACTGCGCT	TCAAAATCAA	TTCAGGCTTG	CCTTGGATTT	9240
TCAGAGCCGC	ATTGATACCC	GCGATAATCC	CTTGGCCTGC	TGCCCTCTCG	TAACCTGATG	9300
TTCCATTTGT	CTGACCAGCA	GTGAAGAGAC	CTGAGATTTT	CTTGGTTTCC	AAAGTCGCAC	9360
GCAACTGATG	AGGCAAGACC	ATATCATACT	CAATAGCATA	ACCTGTCCGC	ATCATCTCTG	9420
CATTTTCCAA	ACCTTTGATG	GAATGCACCA	AGTCACGCTG	GACATCCTCA	GGCAGACTGG	9480
TTGAAAGTCC	TTGCACATAG	ACTTCCTCAG	TATTGCGCCC	TTCTGGCTCA	AGGAAGAGTT	9540
GGTGACGTTT	CTTGTCCGCA	AAGCGCACAA	TCTTGTCTTC	AATCGACGGA	CAGTAACGAG	9600
GCCCCACTCC	CTTGACCACA	CCTGTAAACA	TAGGCGCACG	GTGGAGGTTG	TTTTGGATAA	9660
TCTCATGACT	GGTACCATTG	GTATAGGTCA	ACCAGCATGG	TACTTGGTCC	TTGACATAAT	9720

1219

CCTCATCACG TGAAGTGTAT GAGAAATGAT TAGGCACTTC GTCTCCTGGC TGAATTTCTG	9780
TCACATCGTA ATTGATAGAA GAAGCCTTGA CACGTGGAGG GGTTCCTGTC TTGAAACGAC	9840
CGATTTTCGAG ACCCAGTTCC TTGAGATTGT CAGCTAGGTT AATAGAAGCC AAGCTGTGGT	9900
TAGGACCTGA TGAGTACTTG AGGTCTCCGA TGATAATTTT CCCACGGAGA GCAGTCCCTG	9960
TCGTCAACAAT AACAGCCTTA GCAGCATATT CTGATGGGT GGCTGTACGC ACACCGACAA	10020
CCTTGCCATC TTCCACCAAA ATCTCATCAA TCATGGTTTG ACGAAGGGTC AGATTTTCTT	10080
GGTTTTC AAC CGTCTTGCGC ATCTCCTTAG AGTAAAGTTC CTTGTACGCC TGCGCACGAA	10140
GGGCACGGAC AGCTGGCCCC TTCCCTGTGT TTAGCATCTT CATCTGGATG TAAGTCTTGT	10200
CAATGGTTT GGCCATCTCG CCACCGAGGG CATCGACTTC ACGCACGACA ATCCCCTTGG	10260
CAGAACCACC GATAGAGGGA TTACAAGGCA TGAAAGCCAG CATTTCAATA TTGATGGTCG	10320
CAAGCAGGAC CTTACAGCCC ATACGGCTAG CGGCCAAGGA AGCCTCAACC CCAGCGTCTC	10380
CCGCACCAAT TACAATAATA TCGTATTCTT CAGTAAAATG ATAAGTCATG TTTCTCTCCT	10440
ATTCTCAAG ATGAATGTGT CTTAGTTGGC CTTCCCAATC TGGTAGGGCT GTTTTAAAA	10500
AGACTGGAAC TAGCTGGATA TTCTGGAGCT TATCCAAGTC AATCCACTCA CAGGGCTGCC	10560
TTTTCTCATC TTCCTGCATG GTCAACGGGG CATCTTCAAG CAAATCCACC AGATAATGAA	10620
ACTCGATATT GTGATAGGAA ACGCCGTCCA CTTCAAAACG ATTTTCAACC ACAAAGCTA	10680
GCTGCCCAGC TTGAGCTTTG ACACCCAGTT CTTCCCTCAC TTCACGGACT ACCGCGTCTT	10740
CCGTGCTTTC ATTGACTTGA ATCGCACCTC CAATAGTGTA ATACTTGCCC TTGTCTTTGG	10800
TAAC TAGAAG CTTGTGATTT TGGACAATCA AGGCTGTAGC CCGAACACCA AAAACCGTAT	10860
TGTCTACTTT TGTCCGAAAG TCTTGTGAG TCATTCTTGT CCTTTCCCTT AAACGACACA	10920
AAAACAGTCA AAAC TACAAA GAAGTGCAGG ACAAAAAAGC CTGCAACATC CAGG	10974

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 987 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

CCCGTTATGA TTATGGATAG CGCTTTCAA TTTTAAACT CCTATCCCAT CCTTTATCT	60
ATATAATAAG TGAAATATA ATAAGTCA AGTAACTGAA GTGAATTTA TAAAAAATT	120

1220

ACAAGCCAAA TTTGTAAAGT TTACACTAAG CCGCTAGgCA ATCGTCTATC AGAATATCCG	180
TTTATTTGTC AATAATCCGA GAAAATCTTG CAACGCTTAG AAGTCTATAA AAATATCAA	240
CATTTATATG ACTTGCGAAT AGCAATCCTG CTAAACCTTT CCACACTCTA TCTATACAA	300
CAAGATAAAA ACATGTGTAA GCAAATCTGC TACACTTTAC TGGAGGACGC CAAGAATAAG	360
AAAAGCTACG ATAGGCTTGC TATCTGCTAT GTCCGTATTG GGATTTGTAC AGACGATTCT	420
AAACTTATCC AAAAAGGGTT CTCCCTTCTG GAGCTGACCG AGGAAACTTC TATGCTGTCT	480
CATCTCAAAA AAGAAGTAGA GACCCATTAT CAACCAAAGA AATTATAAAA AAAGTCGAGG	540
GAGCTCCTCG ACCTTTTCAT AGAATCGCCG AACGATTTAA CGAGAAAGTA TGACTTTTAC	600
GTTTATCCCA ACTCAATTAT GACATTTTTC TCAAAAAGTCA ATATATCTCA CTTTTCAC	660
GACAAGAAAG AGGCTGATAA TCTACCAACC TCTTATCTG AACCCATCAC TCCATCACTT	720
TTTAGCTTCA TTCGCTTCT TAGCGACTGC AATCTGGTAT TCGACTTGGT CATTCCTCTT	780
ACCGGTACAA CCATGAGCAA TTGTAGTCGC TCCTATCTGA TGCCTATTT CAACCAATTT	840
TTTAGAAATC AGAGGGCGGC TCAAGGCAGA TACCAAGAGA TACTTTTGTT CATAATAGGC	900
ATGTGACTGA TGAGCCACTA GCACATAATC TGTAGCAAAT TCGTCCTTAA CATCAATGAC	960
ATAAGATTCT ACTGCCCAA CCTTAAG	987

(2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CTGGGTCTTG TTCATAGTAG GTGTGGTtCT TTTTTCGAG TGTAGCCCAT AGCTTTGAGC	60
GCATAGTGGA TGGTAGTTGG ATGACAGCCA AAGTCAGAAG CTATTTTCACT CAAATAAGCA	120
TCTGGATTGT CAGTAAGATA GTTTTAAAGT CTATCTCTAT CAACTTTTCT TGGTTTGT	180
CCTTTTACTT GGTGGTTTAG CTCTCCTGTT TTCTCTTTTA GCTTTAACCA GCCATAAATG	240
GTATTACGTG AGATTGGAA AACGTGTGAT GCTTCTGTTA TACTACCTAT TCGCTCACA	300
TAAGAGAGAA CTTTTTTACG AAAATCTATT GAATATGCCA TAAGAAGATT ATACCACATT	360
GTGTACTATT TTTGGTTCAT TTTACTATAT TTTATAAGTT ATAGTGTAGC ATTCCAACCT	420
CAAAGCACTA TAAAGTAAAT TGAAACAAGA ACAATACAAA CAATTCTCGT AAACGGATTG	480
CAACCACAAA AAAGCAAGCA TTCACAAGAA TACTTACCTA TCATGGGAGG AACCAACCGTT	540

1221

CCTCTTTTTT ATTACTAAAA TTCAAAGAAT TCCAATGCTT TTTTCAAGAG CAAATCCGTA	600
TATTCTGGAT CTTCTTGGGC TACTTCTATT TCCCGCTGAA CTTTTTCCAA ATCATCTGTA	660
ATCACTCCAT CTA CTCTCTAA GTGAAGAGAT TTGCTGATAG CTTCTGAATC ATTGACAGTC	720
CAGACATAAA GTTCTGATC CGTTGTCCAT AGTTTGCTTA CAAAATATTC ATCCAAGGTT	780
GAGTACTCCA TAGTATATCC TGTCGCTCTT GTTTTAGGAA AGACAGAATT GTAGGGCATG	840
ATGAAATAAA CTGGTAGTTC GGCATCATAC TGTCTTACTT TTTGACAAC ATGGTAGTCT	900
AAAGACTGGA TTTGATGTCC ATAAATCTTG AGCTTTGCAG CATAACGGGC TAAAAAGCGG	960
TTTCATCATGT CTGGACTATC TTTTCTACTG GTTTTAATTT CAATTAGTAA TTTTGGACCA	1020
AGTTCGTTGG CTCGACTGAG ATAATCTTCA AAGCTTGAAA TTTTAGTCTG GTAGCCATTT	1080
TCAAAAATAT CAATCCCTTT AAGCTCCTCC AAGTTTAAGT CTTGAGGACT TTTATTGATA	1140
CCTGCTAGAT TTTTCAAGTT AGCATCATGC ATCATGACAA ACTGCCCCATC TTTTGTTC	1200
TGCACGTCGG TCTCCACCAA GTCTGGTTTG AGTTGTGCTG TAGTTTCCAA GGACTCTACT	1260
GTATTTTGAA TCCCATTTGC ATTGGAACCC CCTCGGTGAG AAATAAGTTG AGGTAGATGA	1320
ACCATGGGAG CCTCCAGATA AATATAACCT TCTAAGGCAA AGAAAAGACT GGCACAAGTC	1380
ATGACACCCC ATCGCACGAT GTGATCTTTT TCTCTCCTAG GAAGCATATC CAGCTCCTTT	1440
CCTGTCAAAA ATGAAACAAA TTTAACCAA AAATAAGTCA GAGCCATATA ATAGAGATTT	1500
TTAATCACGA CAAAATTCAA AATACCAAGA ATCAGAGACT CTCTCTGAGT GATATCATCT	1560
ACCAAAGTTT GAGCCAATAA TAAAGGAATC AAAGGAAGAT AATAATAA ATGTGCTTTG	1620
AGCAAGATGT AAAATAAAT CCAAGCATAA AAAGTAACTC TCTTCTTGGT TTTCTCCAAG	1680
CTAAACATCA CTGCTTCTCG AACAGTCAGC TGATCATATA CAATCTTCGG AAGGGCAAAC	1740
ATCAATCTGA CAGAGACATA GAGAAAGATA AGAGATAGAA GTAGGATGCT CAGCCACCAC	1800
ATCCAATATC TATCTTCTAA ATAAGCTTGG ATAACTCTG GAATGACGAT TTTATTAAGA	1860
TAATAAATCT TCAGCATTTT CCGTATAAAA GGAAACAGCA TAGCTATATA GAAAAGATA	1920
AACAAGGCTT TAGCGCAAGT TAGCTTTTC ATAAATCCAA AACTTTCATG GAAAACCTTG	1980
CGGATATACT CAATTAGCCT TCGCTTTTCA TTATAGAGGA GATGACGAGC ACCAATAAAG	2040
AGGAGTCTTA TTTGAAAATA AGCAACCAGA AGGTTAATTA CAATCAAGGC TAAAAAGCT	2100
AGACTAATCA ATGGAGAATG AGTAAGGATG GCTAAGACAT TGTTATAGGA AATAAAAAGA	2160
TAACCTGTCT GATCTAATAA GAAGCTAGCC AACCATGAAT TGAATGGTAC CCACAAATAC	2220
TCCACTATCA TAAAAATCAA GAAAAATAGA AAGAGGATTT TATCAAGATC GAGGTAAATC	2280

1222

TGTTTAAGAC CCAATTTTTT AGGTTTTTCA GGTTTCATAG GCACTCCTAG TCAAATAATT	2340
GAGACAAGTC CAAGCCACCA AAAGGATTGT TTGATAAGCT ACTTTCCTGTC TCTAACAATT	2400
CCCTAGCTTG ATCCGACTCT AAGAAGGATT CGTAAACACG CGCCGTCTATC CGAGCATCCT	2460
CTAAACTATT ATGAGACTGA CCTTGAAATC CAAGAAATGA GGCAACAGTT TGCAATTTGA	2520
GATTGGCAAT ACCATGTAAA TCTGAACTCC GACGTTCAAA AGCTTCATCA TACAAATCCA	2580
CCTTGTAATG TTGGCTATAG TCTAAACCAT GCTCTGCTAA AATAGGTAAA TCACTTTTAG	2640
CAGCATTGTA G	2651

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

C GTTATAATA AACTTGTGAA AAAATTAACA AAGGATATCG TTCCTTGAAA GCTATGGAGG	60
A AAATATGGC TGATAAAAAA ACTGTGACAC CAGAGGAAAA GAAACTCGTT GCTGAAAAAC	120
A ACGTAGATGA GTTGCTTCAA AAAGCTCTAG TTGCCCTTGA AGAAATGCGT AAATGGATC	180
A AGAACAAGT TGA CTACATC GTTGCCAAAG CATCAGTAGC AGCTTTGGAT GCCCACGGAG	240
A AATTGGCTTT ACATGCCTTT GAAGAAACAG GACGTGGTGT ATTTGAAGAC AAAGCAACTA	300
A AGAACTTGTT TGCCTGTGAA CACGTAGTAA ACAACATGCG CCACACTAAG ACAGTTGGCG	360
T TATCGAAGA AGACGATGTA ACAGGATTGA CTCTTATTGC TGAACCAGTT GGTGTTGTTT	420
G TGGTATTAC TCCAACAACA AACCCAACAT CAACAGCAAT CTTCAAATCA TTGATTTTCA	480
T GAAGACACG TAACCCAATC GTCTTTGCCT TCCATCCATC AGCACAAGAA TCATCTGCTC	540
A ATGCAGCTCG TATCGTCCGC GATGCAGCTA TCGCAGCTGG TGCTCCTGAA AACTGTGTGC	600
A ATGGATTAC TCAACCATCT ATGGAAGCAA CAAGTGCCTT TATGAACCAC GAAGGTGTTG	660
C GACAATCCT TGCAACAGGT GGTAATGCCA TGGTTAAGGC GGCTTATTCA TGTGGTAAAC	720
C AGCTCTTGG GGTAGGTGCC GGAAACGTTT CAGCTTATGT TGAAAAATCA GCAAACATTC	780
G TCAAGCAGC ACACGATATC GTCATGTCTA AATCATTTGA TAACGGTATG GTCTGTGCAT	840
C TGAACAAGC AGTTATCATT GATAAAGAAA TTTACGATGA ATTTGTAGCA GAGTTCAAAT	900
C TTACCACAC TTA CTTTGTA AACAAAAAG AAAAGCTCT TCTTGAAGAG TTCTGCTTCG	960
G CGTCAAAGC AAACAGCAAA AACTGTGCTG GTGCAAAATT GAACGCTGAC ATCGTTGGTA	1020

1223

AACCAGCAAC TTGGATTGCA GAACAAGCAG GATTTACAGT TCCAGAAGGA ACAAACATTC	1080
TTGCTGCAGA ATGTAAAGAA GTTGGCGAAA ATGAGCCATT GACTCGTGAA AAATTGTGAC	1140
CAGTTATTGC AGTTTGTAAA TCTGAAAGCC GTGAAGATGG TATTACTAAG GCTCGTCAAA	1200
TGGTTGAATT TAACGGTCTT GGACACTCAG CAGCTATCCA CACAGCTGAC GAAGAATTGA	1260
CTAAAGAATT TGTTAAAGCT GTTAAAGCTA TTCGTGTTAT CTGTAACTCA CCTTCTACTT	1320
TTGGTGGTAT CGGGGACGTT TACAATGCCT TCTTGCCATC ATTGACACTT GGATGTGGTT	1380
CTTACGGACG CAACTCAGTT GGGGATAACG TTAGTGCCAT TAACCTCTTG AATATCAAAA	1440
AAGTCGGAAG ACGGAGAAAT AACATGCAAT GGATGAACT TCCTTCAAAA ACATACTTTG	1500
AACGTGATTC AATTCAATAC CTTCAAAAAT GTCGTGACGT TGAACGTGTC ATGATCGTTA	1560
CTGACCATGC CATGGTAGAG CTTGGTTTCC TTGATCGTAT CATCGAACAA CTGGACCTTC	1620
GTCGCAATAA GGTGTGTTAC CAAATCTTTG CGGATGTAGA ACCGGATCCA GATATCACAA	1680
CTGTAAACCG TGGTACTGAG ATTATGCGTG CCTTCAAACC AGATACCATC ATCGCACTCG	1740
GTGGTGGTC TCCAATGGAT GCTGCCAAAG TAATGTGGCT CTTCTACGAG CAACCAGAAG	1800
TGGACTTCCG TGACCTTGTC CAAAATTCA TGGATATCCG TAAACGTGCC TTCAAGTTCC	1860
CATTGCTTGG TAAGAAGACT AAATTCATCG CGATTCCAAC TACATCTGGT ACAGGATCTG	1920
AAGTAACACC ATTTGCCGTT ATCTCTGATA AAGCAAACAA CCGTAAATAC CCAATCGCTG	1980
ACTACTCATT GACACCAACT GTGGCAATCG TAGATCCTGC TTTGGTATTG ACAGTTCCAG	2040
GATTTGTGTC TGCTGATACT GGTATGGACG TATTGACTCA CGCGACAGAA GCATACGTAT	2100
CACAAATGGC TAGTGACTAC ACTGATGGTT TAGCACTTCA AGCCATTAAA TTGGTCTTTG	2160
AAAATCTCGA AAGCTCAGTT AAGAATGCAG ACTTCCACTC ACGTGAGAAA ATGCATAACG	2220
CTTCAACAAT CGCTGGTATG GCCTTTGCCA ATGCCTTCCT AGGTATTTCT CACTCAATGG	2280
CCCATAAGAT TGGTGCSCAA TTCCACACAA TCCACGGTCG TACAAATGCT ATCTTGCTTC	2340
CATACGTTAT CCGTTACAAC GGTACACGTC CAGCTAAGAC AGCAACATGG CCTAAGTACA	2400
ACTACTACCG TGCAGATGAA AAATACCAAG ATATCGCACG CATGCTTGGA CTTCAGCTT	2460
CTACTCCAGA AGAAGGGGTT GAATCTTACG CAAAAGCTGT CTACGAACTC GGTGAACGTA	2520
TTGGGATCCA AATGAATTTT AGAGACCAAG GAATTGACGA AAAAGAATGG AAAGAACATT	2580
CTCGTAAATT AGCCTTCCTG GCTTATGAAG ACCAATGTTT ACCAGCTAAC CCACGTCTTC	2640
CAATGGTAGA CCATATGCAA GAAATCATCG AAGATGCATA CTATGGCTAC AAAGAAAGAC	2700
CAGGACGCCG TAAATAATTG TTTATCAGTC TAGAAGCAAG AAAAAACTC AATTTGAGGG	2760

1224						
AAAGATCCAG	TAATTTTCT	ATGATAAAAG	GCATCCTATC	AAGGTTTTTG	AACACCTGAT	2820
AGGATGCCTT	TTTATGATAT	TGAGGCCTTT	TTGCCCTTTT	TGAAAACTA	GAATAGAAAC	2880
AAAATATATA	ATAGATTGAA	ACTAGAATAG	TACATATCTG	CTTCTAAAAC	ATTGTTAGAA	2940
TTTCGATTGA	CTGTCCTGAT	CGATTGTGCC	TGTTCTTATT	TCATTTTGAT	ATATAAAAAA	3000
TATAGTATAG	TAGACTGAAT	CTAAAATAGT	ACGAAACAAT	TGCTAAAACA	TTTATAGAAA	3060
TTAATTTTAC	TTTTCTGATA	GAGTTGTTC	CATCTTATTT	CAATTCAC	TAGTTTAATT	3120
TAAGAGTAGT	ATTTACTAAG	GCCCAATTAA	AATCAAAGAG	CAAACTAGAA	AACGAGTGCC	3180
ATTCAGCTCA	AAACACTGAT	TTGAGATTGC	AGATAAGACT	AGCCCCCTCA	TTAACAGATT	3240
TACGATAAAA	CGATGACAAG	GTGTGTTGCT	TTTTGATTTC	TAAAGAGTAT	AATGATAGAT	3300
CTCTATAAAA	TAAGTGCGAA	GGAAATGAGC	TTTTATAGTC	CTTTCGTTTT	AAAATACTAT	3360
CTCAGATATT	CTTATATCGA	CAAGAAGTTT	TTGAGTCATT	CCCTCATCAT	ACATATTAAA	3420
TAAATAGTGG	CTCATTCAAT	TTTTCACTAG	AATAATAAGC	TAGTATAGTA	AACTGAAATA	3480
AGATATAAAC	AAATAAATTG	GAGCTTAACA	TCCATTTC	GCAATTTTTT	AGAACTACA	3540
GTGGACTATT	CTAGATTCAA	CATATTATAA	AACTAGAGT	AAAAGAAAAG	GATTGGATCT	3600
TGTGTAATGC	AGGATCCAAT	CCTTCAATC	ATTTTGTCCA	ACTTTTGAG	GTTCCTACAA	3660
TGTAGTCGTC	ATTAATAAAG	ACAGATGGGA	ATGACAGTGT	TCCTATTTAT	TTTGATAGAG	3720
ATCGATGAAT	TCTTTAGATA	GCAACTGAAT	AATCTCTGTT	GAAGCCATTT	GGTCTTCTGC	3780
ATGCATAAAT	AGCAAGGAGA	ATCCTATTTT	TTCTCCAGTA	GCTTCTTTTT	GTATGAGATT	3840
AGAGTGAATC	TTGTGCGCTT	CTACTAAGGA	GTCTTCCGCT	TCTTCAACTT	TAATTTTCGC	3900
TTCTTTTAAA	TTTCTGCCT	TAGCTAGTTG	GATGGCTTCA	ATAAAGGATG	ATTTGGCTGC	3960
TCCACTATTG	GCAATGAGCT	GAAAACAGAT	ATATTCCATT	TCTTCTGTCA	TCTTATTTCT	4020
CCTATCCATG	CAAGTGCTTG	TTCCAGAACT	TTTGCTCCAT	TCATCATTC	GTAATCCCGC	4080
ATATCAATGG	TATCTACAGG	GATATTTCTT	GCAATTTCTT	TCACAGCAAG	TAACTCATAA	4140
CGAATTTGTG	GCCCAATTAG	AATGACATCT	GCTTCATGGA	TATTCTTTTT	AGCTTCTGTC	4200
ATTGATTTTG	CTTGATAGA	GATTTCATC	CCACGTTGAG	TCGCACTTTG	TTGCATTTTT	4260
TTAACAAGCA	TACTTGTCGA	CATTCCCGCA	TTACATACTA	ATAAAATTG	TTTCATAATC	4320
TTAACCTTCC	ATTTCTTGTT	CAACAACCTT	GTCATTAACT	TTGATAAATG	GAATGTATAG	4380
AAGAACTCCA	AGTGCAAAGA	TGATGAATTG	AACTAGAACT	GCTCTCACGT	CCCCTGCTGT	4440
TGCTAACCAT	GCATTTAAGA	ATACTGGTGT	AGTCCAAGGA	ACTTGTATAA	ATGCAGGACT	4500
CATGAATTCT	GTAAGTGTG	CTAAGTAGCT	GATTAAAATA	CCAAGGACTG	GAACTGTGAT	4560

1225

AAATGGAATA GCTAATGAAA TGTATAAAC GATTGGGTAA CCGAATAATA CTGGTTCATT	4620
GATATTGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG TTTTGTAGAGA CAGCATTGCG	4680
ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT CCACTACCAC CCATTAAAGC	4740
GAATGTTTGT ATTTGTGATA GGTGATGAT GTGTGGAATG GCTTGTCCAT TATTTGCTGC	4800
AGTGATGTTT TCAGTAATGT TAATTAATAG TAATGGTCTT AGGATGGCAC TGTAAATAAC	4860
TGCTTGGTGA ATACCAAATA GCCATAACAT ATTTCTTAAA GAGTAAATAA TAATGACCCC	4920
GATTAAGCTT GTACCAATAT GACGAATTGG TTCTTGAATA AAGATTGTAA TGATTGAGAT	4980
TAAGTTCATT CCAGTTATAT TGAATAATAA TGCTGAAACA ACCCCAAATA AGGAGATGAC	5040
GGTCATGACT GGAAGTAATA CGCTAAATGA TCTACTAACA GCTGGTGGAA TATTTTCACC	5100
AAGGTTTCATT TGTAAGCTT TAACGTTTGA TAATTCAATG AATAATTCTG TTGCAATAAT	5160
CGTACGATAA CCCCGGCGAA CATTGCGCCT GTACCTGTGT TGTGTAATGA AAGAACACCT	5220
GAAATGTTTA CCGCATCTTT TGCTCCGTCA GGAAGTACAG AAAGTGTATT TGGCATCATC	5280
ACAATTAAAG AAAGTAATGA TAGCATGAT GCTGCTAACG GGTTTTCGAA ATCTCTGTTT	5340
TTAGCTAAGA AATAACCAAC CATTACAGCA ATAATCATACT CTGAAATACT TAAAGTACCG	5400
TTTGAATTG TTATCCCCA ATATTGGAAT CTGTGTAATG TATCCCCTTG GAAATCCAC	5460
TTAAATACCG TGTGTTCAA AAGAAGGATT AAACCTGCCA AAATATATAA TGGCATTACT	5520
GTTACGAATG CATCTCTTAG GGTTTTAAA TGAATTTGGT TCCCTAGTTT ACCAGCAAAG	5580
GATGGCAAAA AAATTTTTTT GGGGGGGGG GTTATTAAAC CCCCCTTTT AAAAAAA	5638

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CCGGAAGCTG TTGCCCTTGG AACTCCAAAT GAAGAAACAG CCTTTGTCTT GAACTATTTT	60
GGTGTGGAAG CACCACGTGT TATCACTTCT GCCAAAGCAG AGGGGGCAGA GCAAGTTATC	120
TTGACTGACC ACAATGAATT CCAACAATCT GTATCAGATA TCGCTGAAGT AGAAGTTTAC	180
GGTGTGTAG ACCACCACCG TGTGGCTAAC TTTGAAACTG CAAGCCCACT TTACATGCGT	240
TTGGAGCCAG TTGGATCAGC GTCTTCAATC GTTACCGTA TGTCAAAGA ACATGGTGTA	300

1226

GCTGTGCCTA AAGAGATTGC AGGTTTGATG CTTTCAGGTT TGATTTCAGA TACCCCTCTT	360
TTGAAATCAC CAACAACACA CCCAACAGAT AAAATCATTTG CTCCTGAATT GGCTGAATTG	420
GCTGGTGTGA ACTTGAAGA ATATGGTTTG GCAATGTTGA AAGCTGGTAC CAACTTGGCT	480
AGCAAATCTG CTGAAGAATT GATTGATATC GATGCTAAGA CTTTGTGAAC CAACGGAAAT	540
AATGTCCGTG TTGCCCAAGT GAACACAGTT GACATCGCTG AAGTTTGTGA ACGCCAAGCA	600
GAAATTGAAG CTGCAATGCA AGCTGCCAAC GAATCAAACG GCTACTCTGA CTTTGTCTTG	660
ATGATTACAG ATATCGTCAA CTCAACTCA GAAATCTTGG CTCTTGGTGC CAATATGGAC	720
AAGGTCGAAG CGGCTTTCAA CTTCAAACCTT GAAACAATC ATGCCTTCCT TGCTGGTGCC	780
GTTTCACGTA AGAAACAAGT GGTACCTCAA TTGACTGAAA GCTTTAATGC GTAAGATTTT	840
GGGTGTGAGC TCAAAATCGG AAAGTCTAGT TTGCCCTATA TCGCAAGGAG TTTCCGGCTCC	900
TTTTTTCTAG GAGTGAAGTA TGTTAGAAAA TGGCGATTG ATTTTGTGA GAGATGGGTC	960
AGACATGGGA CAGGCCATCC AGACTTCCAC AGGTAACAT AGCCATGTTG CCATTATTTT	1020
GGATGGGATG ATTTATCATG CTAGTGGACA GGCTGGTGTT GTCTGTCAAG AACCGGCAGA	1080
CTTCTTTGAG TCCAATCATT TATACGACCT CTATGTTTAC CCAGAAATGG ATATCCAGTC	1140
GGTGAAGGAA AGAGCTTGCA AACATCTTGG AGCACCTTAC AATGCTTCTT TCTATCCAGA	1200
TGCAGCTGGT TTTTACTGCT CCCAGTATAT AGCAGAAATC CTACCTATTT TTGAAACTAT	1260
TCCTATGAAA TTTGGAGwTG GGGAGCAGGA GATTAGTGAT TTTTGGAGGG AGTATTACAT	1320
AGAACTAGGT CTGCCTGTTT CTCTGAACCA AGCTGGTACC AATCCTAGTC AGTTGGCAGC	1380
ATCGCCTCTG TTACAATGTA AAGAAAGGAA TCTTCATGAT TCAGATTTTT AATCCATCTC	1440
GTTTGACGAG ACAGCCATTT TTGGAGAATT GATCCGCTAT CTGGATCAGT ATGAGGATGT	1500
GATTCTACGG GAAATTAAGG CTCAATTTCC AGATGTTGCA GTTGATAAAC TCATGGAAGA	1560
GTATATAAAG GCAGGCTTGA TTCTACGTGA AAATAAGCGC TATTACCTCA ATTTTCCTAC	1620
GCTTGAATCA CTTGATAGTC TTGAACTGGA TCAAGAGATT TTTGTCAGAG AAGCTAGTCC	1680
GGTCTATCAA GCCTTGTTGG AGCAGAGTTT TGAGACGGAA TTGCGCAATC AAATCAATGC	1740
AGCTATTTTA GTTGAAAAGA CGGACTTTGC GCGCATTAAT ATGACCCTGT CCAATTATTT	1800
TTACAAGGTC AAACAGCAGT ATCCTTTGAC AGAAAAACAG CAGGAGCTCT ATGACATTTT	1860
AGGAGATGTT AATCCTGAGT ATGCCCTCAA GTATATGACG GCTTTTTTGT TGAAATTTCT	1920
CAAAAAAGAC CAGCTTATGC AGAAATGCCG TGATATCTTT GTGGACAGTT AGGTTGTCTT	1980
AGGCTATATT GTGCAAAATG AAGATGGAAA GTATGAGTTG GCTATCGATT TTGATAAGGA	2040
GAGGTAACT TTCTACTTAG CGTGATTTCT TGTTTCTGAG TACATGTTT GACTTTCCTT	2100

1227

AGTATTCGGT ATAAACTATA TGTAACCGGT AACACATATC GGAATAAACT AAAGGAGACA	2160
ATCATATGTC ACTTGAAAAC AAATTGGAAC AAGCAACAGG CGCTGTCAAA GAAGGTTTGT	2220
GTAAAGTTAC TGGAGACAGC AAGACAGAAC TTGAAGGAGC TGTGAAAAA ACAGTTGCTA	2280
AGGCAAAAGA CGTTGTAGAA GACGCAAAAG GTGCTGTAGA AGGTGCCGTT GAAGGTTTGA	2340
AAAACGTTTT TACTAAAGAA TAGGAAAAA TCAAGGGTTT CATTTTCCCT TGATTTTTC	2400
TATTCCTATA AATAATTTTC TGCACGGCT GTATCTCCTG GGTAGGATTC TTTCTGCC	2460
TGGATGATTT GGTAACAATC GGCTCCCTTA CCCGCAATAA TAACTGCATC TAATTCGTGA	2520
TTTGTGATAG CCATGCGCGC CTGTGAGGCT TCTTGGCGAT CCGCAATCTT TTCAACAGGA	2580
TGATTGATGT AGCTACTAAT TTCATCTGCA ATGGCCATTG GGTCTTCATA GTTAGGGTCA	2640
TCAGCAGTCA GAAAGACTTG AATCTCAGGG TGTGATTGA GGAGGAGGCC AAAGTCCCTA	2700
CGACGACTTT CTCCCTTGT TCTGTTGAT CCCAGAACCA GAGCAATCTT TCCGGTTTGA	2760
TGAGTTTCAA CCACATTGAT GAGTTTTTTC AGACTATCCC CATTTGTGGGC ATAGTCGATG	2820
AAGACCTGG CTCCATTTT CTGAGTGAGG ACTTCCATAC GACCAGGAAC GCGGGTTGCA	2880
GCGATGCCTT TTTTGATGTC CTCAAGACTT GCTCCGAGAC GGAGACAAGC AAGTCCAGCA	2940
GCAACTGCAT TTTCTTGGTT GAAGTTGCCA ATGAGTTGAA TATCATAATC TCCAGCGAGT	3000
TTACCCGTAG CTGAAAAGCT AAAGCTTTG GAATCTCGA TTTGGTTATC AAATTGGCTA	3060
CCATAGAAAT CATGGTCTTG ATCTCAACC TGTCTTTCA AGACTGAGAA GTGGTCCATG	3120
TCACTGTAA TGATGACTGC TCGGCTCTT TCCATCAAGA GACGCTGTG GTAGAAATAG	3180
TCTTCAAAGC TAGGGTGTTT AATCGGGCCG ATATGGTCTG GGCTGATATT TAGGAAAAC	3240
CCCACATCAA AGGTTAGACC ATAGACACGT TTGACCAGAT AGGCTTGACT GGAGACTTCC	3300
ATGATGAGGT GGTACGGTC ATTTTGACA GCCTGATTCA TCATGTCAAA GAGTCAATA	3360
CTCTCAGGG TTGTCAACGC TGACTTAAAG AAAGTCTCGC CATCAAGAGT TGTGTTTATG	3420
GTCGACAACA TAGCAGGTCT ATGCCCTTGA GATAAGATGT TATAGGCGAA ATAGGCTGCT	3480
GTTGTCTTAC CCTTAGTACC AGTAAAGCA AGGAGTTTGA GTTTTCTCTG TGGATTACCA	3540
TAGAACTCCA TGGCAATCAA ACTCATGGCT TTCTTTATAT CGTTCACAAT GATGACAGGG	3600
ATACCGACTT CGTAGTCCTT TTCAGCTACA TACCAAGCTA ATCCTTGTGT TATAGCAGAA	3660
AGAAGGTATT CTTTTTAAA GGCAGCGCCT TTTGCGAAAA AAAGAGTGT TCTGTFACT	3720
TTTCGGCTGT CGTAGCTGAT GCTATCAAAA ATAACCTTGC TGTAGTTGTA GTGTAATGA	3780
CCTTGGTCAA TAATTCGCG AAAAAGGCCA TCTTCTTTA AAATATCTAA TACGGTTTCA	3840

1228

ATCTTAATCA TACTTTCTAT TGTAAACCGA AAGTCGTAAA TTTACAAGTA ACAAGGAAAA	3900
GTTTATAATG GAAGATAAGG AGTTTTTCCT AGTTATCAAA ATTGAATGAG GAATCTATGT	3960
CGCACGAAAA CAATCACCAG CAGGCCCGA TGTACGGGG GACTGCTTGG CTAACGGCTA	4020
GTAACTTTAT CAGTCGCCTA CTCGGGGCTG TTTACATTAT CCCTTGGTAC ATCTGGATGG	4080
GGGCTTATGC AGCTAAGGCA AATGGTCTCT TTACCATGGG TTACAATATC TATGCTTGGT	4140
TCTTGTGGT TTCAACAGCG GGGATTCCAG TTGCGGTGGC CAAGCAAGTT GCCAAGTATA	4200
ATACCATGCG AGAAGAAGAG CATAGCTTTG CCCTGATTCTG GAGCTTCTTA GGCTTTATGA	4260
CAGGACTAGG CCTGGTTTTT GCTTTAGTCT TGTATGTCTT TGCTCCTTGG CTAGCAGACT	4320
TGTCTGGCGT GGGCAAAGAC TTGATCCCAA TCATGCAAAG CTTGGCTTGG GGAGTCTTGA	4380
TTTTCCCGTC TATGAGTGT ATCCGAGGAT TTTTCCAAGG GATGAATAAC CTCAAACCCCT	4440
ATGCCATGAG CCAATTGCT GAGCAGGTCA TTCGTGTTAT CTGGATGCTC CTAGCAACCT	4500
TTATCATTAT GAAGCTCGGT TCAGGAGATT ATCTAGCAGC CGTTACCCAA TCAACCTTTG	4560
CTGCCTTTGT CGGTATGGTA GCCAGTTTGT CAGTCTTGAT TTATTTCCCT GCCCAAGAAG	4620
GTTCACTCAA AAGAATCTTT GAAACAGGAG ATAAGATTAA CAGTAAGCGT CTCTTGTTG	4680
ATACCATTAA GGAAGCCATT CCTTTTATCC TGACAGGGTC TGCCATCCAG CTCTTCCAGA	4740
TTTTG	4745

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CCTGATTGAC CTTATAATAA GGAACAAAAC ACAATGCACT ACCTTTTCAA CAAAAGAGTT	60
GCTGCTTGAT TAAAACCATC ACACCACTTA TACCATTTTG CTTCATACCC ATCTTGAGCT	120
AGGATACGAT CTTCTAAATC AAAACAGAG TAAATCTTTC TTTCTCGCA AGCTTGCGCA	180
TAGAGATGAT ATAGTTCATC ACCACCATCT CTATCCCACT CAGCAGAAAT CGTATCCCGA	240
CCTGCCAATA AAGCCTGATA AGCCCTGTGA TGCCCATCTG TAATCAGCAA ACAATCTCCA	300
AAGGCAAGAA TACTGATTGG ATCGACTTGG ATTGTTTCTG CCGACTGGTA AAGCATCTGA	360
ATATCTTGCA ACTTCTTTTC TGATAAATAT AGTTGAGTCA GATGAAGATC TGCTATATTG	420
ACTTTCATTT CTTTCTCCTC AAGGGAATTC GATACTCACT TCTGTTTGCC TTAAATCGC	480

1229

CATTGGAAGC GGAgCTTGTC ATAAAAGGGA AACTCGATAA ACAGGACTCC CAAGCCCACA	540
CAGAGACTGG CAAGGACGTC TGATGGGTAA TGAACCTCCA GATAGACTCT TGATACCAGC	600
ACACTGACTA GGTAGAGGCC AAGGACGATT TGTACGATTT TTCTCCAGAC CTGATCTTTA	660
ATCCGCTGAC TAAGAATAAC AATCAAAGTC CCTACCATCA GCGTTACAGC TAGAGAATGC	720
CCACTTGGGA AGGAAAATCC CTTCTCCTCC ACCAGATGTA AAATAGCTGG TCGTGGGCGC	780
TGGTAGATAT TTTTAAAGGT CACGATTAAA AGACCTGCCA AAGCCAGATT TCCCAGCATG	840
AAGAAACTTT CTATCTTCCA TCGCTTACGA TAAAAGACAA AAGCTGTAAT GACAACCCAA	900
GTGATAATCA CTGGGATATC AATCAGACGT GTGAGGGCTC GAAAAGAAT AGTCAAATAA	960
TCTGGTAAAGT CTCCTCGAAT GGCAGTCTGA ATCGATTGGT CAAAATTGAC CAACATTTCA	1020
GGGTAAAATT TGACCATGTA GCCAAGAATA ACGAAAAGTA AAAGGGCAAA ACTGCCCTTC	1080
ATTAAAAATG TTTGTTTATC TCTCATAATG TTTAAGGTT GGTTCGAAGA GAACATACAA	1140
CAACCAGAAT GAAACGGAAA AGATAACACC TTCAATCAAG TTAAGGTA ATACCATGGT	1200
CATTAGGTAG TTGGAAAGTC CAAAATTTT TCCAATATCA AAGTTAGCAA ACTTAGCGTA	1260
CAAAGGAACA GCATAACAT AGTTGAGAAC CAACATGGCC AAGGTTAAAC CAATAGTTCC	1320
AGCTAGAGAG CCTAGTAGGA AACGAAGGGT TGTCCGTTCC TTTTCCAAA TCAAAGCAAA	1380
TACGATGACA AAAACTCCCA AAGCTACGAT ATTCATCGGC AAACCAATGT AAGTATTCAC	1440
TCCTTGGCTG TTAAGAAGCA ATTTCAAGAG TGAGCGAAGC AAGAGCACTC CTAGAGmCsC	1500
AGGCAAAATCC ATGACCACCA GACCCACAAG GACTGGCAAG ATACTAAATT CGATCTTGAG	1560
GAAAGATGCC GCTGGTAAAA GCGGAAAGTC AAAGTACATC AGCACAAATG AGATGGCTGA	1620
TAGAATTGCA ATGGTCGAAA GTCGACGTGT GTTTGTCATA ACAGGTTCCCT CCAATTTTCT	1680
ATAAAATCAG AAGAAGTTGG AAAGGATTCC TCTATCTATT CTCACTTTTT ATATCCCAAA	1740
AGTTCCCTCT TACTCTATTA AAGAAAAACA AAGCAAGTGG TTACAATCCG GCTATAAATC	1800
TATCAAAACA GACAAGGCTA TTCTTTCGTC TTCTCCCATC CAGACTATAC TGTCGGTTGT	1860
GGAATCTCAC CACATCACGT TGCCTCAGC GACTCTTTTA	1900

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4692 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GGTTTTCCAG CAGGAGCTTC TCCTTTATCA GAATGACCAT CCCATCTGCT CACGATAGAT	60
GAATAATGAT ATTTTTTACC ATGATAGTAA TTTGAAAAAG CCTAACCACC TCCTGAACCT	120
TCTCCATATG TCCATACTCC TCCATCTGGA TATTATACAG CAGCTGATGC AGCTCCCAAT	180
AATGTAAAAC TTGAAATAAG AGCTAGAGCA AGTAATCTAT GTTTTTTCGT TTTCATTTTA	240
TTTTTCTTT CAAAAAAGC ACACCTTGAG CAACAATGCA ACAAATAAA TCCTCCTCTC	300
TCTTTTATG AAACCGCTTT CTTATGTGAT AAGAATAACT TTTTATATAT TGTGTGCA	360
GGAAAAATC GAATTTTTTA GATATTTTAC TATATTACCT CTGTGAATAA TATTATATAG	420
TAGTTTTATT TCAAAATAAT ATGCAACCAG TACTAACCAA ATATAAAATA GATGCCATTA	480
ACGAATTTTA TTCAAGTTTT TCCCATTCAT ACTATACAAG TAAAAGAGAT GGTGTTAACT	540
AAAAAGCAAT TCAAACTATT GTAAATTC TAGCAAAAAG AGAGCCGAAA CTCTCTTTTT	600
TATCTCTTT TACTTTTTTT GACTGGCATG AGTGTGATGT CTCTAACACT AAAGTAAGCT	660
AGGATCAACA TGGCTATGCG TAGGAATATT TCTGTTGGTA ATTGAAAAAT TTTCAGAAAA	720
GATAGAACCA ATAAATCAA GAGTGCCACT AAAATACATA CCATAGCGAC GATATTGACA	780
GTCCCTTTAA TGCTTTCTGG TGTGCGAAAT ACATAGAGTA GGAGCAGTAA AATTCCTAGG	840
ACTAAATAGA CCATCTTTCT CTCTTCTAG CTCTTATTCA GCTGATTTTT TCTTCTGTT	900
AGCTTTCTCA CGCTCTGCTT TGTTAAGGAT TTGTTTACGC AAACGGATAG ACTCAGGCGT	960
TACTTCCATG TACTCATCGT CGTTCAAGAA CTCAAGAGAC TCTTCAAGTG TCAAGATACG	1020
AGGCGTCTTG ATAACAGCTG TTTGGTCCTT AGTAGCTGAA CGAACGTTGG TCATTTGTTT	1080
TGCCTTCGTG ATGTTAACTG TCAAGTCATT TTCACGAGAG TTTTCACCGA TGATCATTCC	1140
TTCATAAACC TCAGTACCTG GGTGACAAA GATCGTACCA CGTCTCTCGA TAGACATGAT	1200
TGAGTAAGTT GTAGCCTTAC CAGCATCGAT AGAAACAAGG GCACCACGGT GACGTCCACC	1260
AATTTCCCTT GGAATCAATG GCAAGTATTG GTCGAAGGTA TGGTTCATGA TACCGTAACC	1320
ACGAGTCATT GATAAGAACT CAGTTGAGTA TCCAATCAA CCACGCGCTG GAACAAGGAA	1380
GACCAAACGA GTTTGACCAT TACCAGTTGA AATCATATCC AACATTTTAC CTTTACGTTT	1440
AGAAAGGCTT TGGATAACAG ACCCTTGGTA TTCTTCTGGA GTGTCGATTT GTACACGTTT	1500
AAATGGTTCA CATTTAATAC CGTCGATTTT TTTTACGATA ACTTCTGGAC GAGATACTTG	1560
AAGTTCATAG CCCTCAGGAC GCATTGTTTC GATAAGGATT GACAAGTGCA ATTCTCCACG	1620
TCCTGAAACA GTCCATTTAT CTGGTGAATC AGTTGGGTCA ACACGAAGGG AAACGTCTGT	1680
TTGCAATTCT GCCTGCAAGC GTTCTTCAC CTTACGAGAA GTTACCCATT TACCTTCTTT	1740

1231

ACCAGCAAAT GGTGAGTTGT TGACCAAGAA AGTCATTTGA AGAGTTGGCT CATCGATGTG	1800
TAGGATTGGA AGAGCTTCTA CTGCATCTGT CGGAGTGATG GTTTCACCGA CAAAGATGTC	1860
TTCCATACCT GAAACGGCAA TCAAGTCACC CGCTTTGGCT TCTTGGATTT CACGACGTTT	1920
CAAACCAAAG AAACCGAAGA GTTTTGTAAAC ACGGAAGTTT TTAGTTGTAC CGTCAAGTTT	1980
AGAAAGGGTA ACTTGGTCCC CAACCTTAAC TGTACCACGG AAGACACGAC CGATACCGAT	2040
ACGTCCAACG AAGTCATTGT AGTCCAAAAG TGACACTTGG AACTGCAAAG GCTCATCTGA	2100
GTTATCTACT GGAGCTGGGA TATGGTCGAT AATCGTGTC AAGATTGGTG CCATAGTCGC	2160
TTCTTGGTCA GCTGGATCAT CTGACAATGA AGAAGTCCG TTGATCGCTG AAGCATAAAC	2220
CACTGGGAAA TCAAGCTGGT CGTCATCTGC ACCAAGCTCG ATGAAAAGTT CCAAGACTTC	2280
ATCCACTACT TCTGCTGGAC GAGCTGATGG CTTATCGATT TTGTTAACAA CCACGATTGG	2340
GACAAGGTCT TGTTCCAAGG CTTTTTTCAA TACGAAACGA GTTTGTGGCA TGGTTCCTTC	2400
ATAGGCATCT ACGACCAAGA CAACACCGTC AACCATTTTC ATGATACGCT CAACTTCTCC	2460
ACCAAAGTCC GCGTGTCCGT GTGTGTCCAT AATGTTGATA CGACTCCGT TGTAAGCAAC	2520
GGCAGTATTT TTAGCAAGGA TGGTAATTCC ACGCTCTTTT TCGATATCGT TTGAGTCCAT	2580
AGCACGCTCT GCCAATTCAG TCCGTGCATC AAGCGTTTCT GATTGTTTCA ATAATTCGTC	2640
AACCAGGGTT GTTTTACCGT GGTCAACGTG GCGGATAATC GCAATGTTAC GGATATCTTC	2700
TCTTAATTTT GTCATGATTT CCTCTATAAT ATTCAAAATT TATTTTCTAA CTGAACGATT	2760
ATACCATAAT TTCAAATAAA TAACATAACT CAAGCAAGTG TAAATGTTTT CACTCTGCTT	2820
TTCTTTTCAC GTCAAGCCTT TTCAAAGCGA GCGACTTATG ATAAGATAGG CACAGTATGC	2880
GTTTAGATAA TTATTAGCT CAAGAAAAAA TCAGCCGAAA GGCCATGAAG CAAGCACTCC	2940
TCAGAGGGGA AATTCTAGTC GATGGTTGCC CAGCCCGCTC CCTAGCTCAA AATATCGATA	3000
CAGGACTACA AGAACTCCTT TTTCAGGATC GAATCATTCA AGGCTATGAA CACACCTATC	3060
TTATGCTTCA TAAACCTGCT GGTGCCGTTA CAGCCAACAA AGACAAGGAA CTTCGACCG	3120
TCATGGACCT GCTTCCATCT AACATCCAGT CTGACAAGCT CTATGCCGTT GGCCGACTGG	3180
ACCGAGATAC AACGGGACTC CTCCTCTTGA CCGATAACGG TCCCTTGGGC TTTCAGCTCC	3240
TCCATCCCCA ATATCATGTC GATAAGACTT ACCAAGTTGA GGTTAATGGA CTTCTAACAC	3300
CTGACCATAT CCAAACCTTT CAAAAAGGAA TTGTCTTTTT AGATGACACT GTCTGTAAAC	3360
CCGCAAAACT AGAGATTCTA TCTGCAAGTC SCTCCCTCAG TCAAGCCTCT ATCACCATT	3420
CAGAAGGAAA ATTCATCAA ATCAAGAAA TGTTCTCTC GGTGGTGT AAGGTGACTA	3480

1232

GCCTCAAAAG AATCCAATTT GGGGACTTCA CATTGAACCC AGATTTAGCA GAAGGTAAC	3540
ACCGCCCTTT GAACCAAAAA GAGTTACAAA TCATTAAAA CTATTTAGAG ATGAGTCGAT	3600
AAAACAAAA AAGCTTTAAA ACTAAAGCTT TTTTCTTTTA TTTACCGAAA AATTAAGGCG	3660
ATTGTACAA TCCAGTTAAC TACAGAAATC ACAATTCCTA AGATATTAAG AATCTTTTCT	3720
ATTTTATAGT CTAATTGTGA CTCTTTTGG TATGAAATAG CCAAGACCAA TCCTATGATA	3780
CCCCAAATCA GGCCTACAAT TGGAAATAAC AAACCAAGAA TAATCGACAA GATACCCACA	3840
AAAAGTGGAT TTTTCTTCTT TTCTTTTATG TTCTAAGAAC TCCTTAAATT TTATACAAAT	3900
TAATTATACT ATAAACAAT AGCTTCATCC TATCATTCGA CTAATTTGGA AATAAGGTTA	3960
GCTAGTCTTC ACTTTCCCTT TCCAAGAATC CAAGCCATAA GAAAGGATAT AAATCTCAGA	4020
AAAACCTTGT TTTTCAAGT AAAGAGCTGC ATTTGTAAC CGTTGCGCAC GTTGGTTTTC	4080
GTAGAGAAGG ACAGGTTTAT CTTTACGAAG GGCTGCAAGA CTAGTTTCA ACTGACTTGA	4140
AGGAATATTG CGTGCACCAA GGATATGTTT TCTGTGGAAT TCTGCTGGGT CGCGCAAATC	4200
AATCAATTGA CCCGTACGAA TCAAGGCTTC AAACCTCTCA TTGTCCACAA TTTAGCCGC	4260
ACGGCGAATA CGAAGATAGT TAAAGCCCAT CCACGCCAAC ATGCTAGTA TAAGTGCCCA	4320
CAAAATCCAA GTAACCATTA GTTCTTTTCT CCATTTTCT CAATATAATC CAATTCTACC	4380
TTGTGCTCTC TGCGAAGAAC TGCTTCTGCC TCTAGATAGT CTAATTTATC CATCAACCCT	4440
GCATCGTAAA TCCGAGATAG TTCCAATTC ATCAGTTCAA TATCATATAA GCGTTTCCC	4500
ATGTAAACAA TAATACCAA TCGTTTGAGG AATTGCTGCA CATCATAGAA TGTTTTCATA	4560
AGACTCATTC TAGCAAAAT TTTGTGTTTT TTCAAGAAGA GACTCACACA ATGCTCCTTA	4620
TTTTCCTATC TTCTTTAGCG ATTCTAAGGC AAGTATGGTA CAATAAAAAC ATGGGGATTC	4680
AACAATTACA TT	4692

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GCTAAAAAGC TGATAATCTT CGACTCCTGT ATATGATGTG TCTTTTCATG TAAGACACGC	60
GCCGCCAGAA TCATGGCAAG AGCTGCAAGA CTGGCAAGTA AGAAGCCGAT AAGATAGGCA	120
AAAAGATAAG TGAATTTGAC AAAGAAAGTC AAAAGAACTA GGAAACCAAA GCCTCCTCCA	180

1233

AAAACCTACCA AAGTCTTTTCG TAAATCCCAG ATTTTATCCA ACTGCTTGAC GAGGGAAGTC	240
GTCTGACGAA CGCCTACAAT AGTTGCTAAC ATACTTCCTA AAAAGAATGG ATAGACATGA	300
GTAAACTGG AGAAATAAAC AGAGGAATAA GAGGTCACTA GAAACTACC AATAACATG	360
GAGAAGAAAC TGATCAAGAA GGCAACAGCA GATAAGAGAA AGACCATCCC CTTCAACTGA	420
CCATTGATT TAGCTTGTTT GGATAAGAAC CAACTGCCA ATCCCCAAG AATATAGTAG	480
TGAACCTCAA CTGCCAACT CCAATTATGA ACAAACAAAT GAGGAATGAA CTGAGATTCA	540
TAACTCCAC CTGTTAGGAG TTCATAGAAG TTGGTCATAA AGCCTAAGAC GCCCGCAATC	600
TGGCCACCAA TTCCAGCAAC ATAGTCTTGG CGAACCAAGA AAGTAAAGG CATGGTCACC	660
AAGACCATCA AAACCACAGG TGGCACAATC TCGATAAAAG CGTCTT	706

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CAGCTGATGG GCAATATCAG TCATAGAAAT TTTTCAATT AACTTTTGAG CAATTTTGTG	60
GTGTGATGATA CGAGGATTT GGTGATTTT CTTTACCAGG GGAGTCTCAG CAACCATCAT	120
TTTTGAACAG TGATAGCACT TGAAACGGCG TTTTCTAAGG AGAATTCTAG AAGGCATACC	180
AGTTGTTTCG AGGTAAGGGA TCTTAGACGG TTTTGAAG TCATATTTCT TCATTAGACT	240
TCCACAATCA GGGCAAGATG GAGCCTCATA ATCCAGCTTA GCGATAATTT CTTTGTGGGT	300
ATCCATATG ATGATATCTA GAATCTTGAT GTTGGGTCT TTAATATCGA GCAGTTTGT	360
GATAAAATGT AATTGTTCCA TATGATTCTT TCTAATGAGT TGTTTGTGCG CTTTTCATTA	420
TAGGTCATAT GGGACTTTT TTCTACACAA AAATAAGCTC CATAATATCC ATAGGGGATT	480
TACCCACTAC AAATATTATA GAGCCGAAA ATATGGGAAA ACTGATCCTT GTTCTGCTT	540
TTGTCTATAG AAGAATAATA AAGATTATCT TCTTCAAATT CTCCGATATT CTCTAAAGTT	600
TTGTGCAAGT TGCACAGAAC TTGTTTATTT TTTTGGTCAT CTTGCCATAG AAATATAAG	660
CGTTTTTATA TATAATATAA TTATCAAAAG ACAAAGGAG TTCACCTCAT GGTAGAATTG	720
AATCTTAAAA ATATTTACAA AAAATATCCA AACAGCGAAC ACTATTCAGT TGAAGATTTC	780
AACTTGAACA TCAAAGATAA AGAATTTATC GTTTTCGTAG GACCTTCAGG ATGTGGTAAA	840

1234

TCAACTACAC TCCGTATGAT TGCTGGTCTT GAAGACATTA CAGAAGGTAC TGCATCTATC	900
GATGGCGTAG TTGTCAACGA CGTAGCTCCA AAAGACCGTG ATATCGCCAT GGTATTCCAA	960
AACTACGCTC TTTACCCACA CATGACTGTT TATGACAACA TGGCTTTCGG TTTGAAATTG	1020
CGTAAATACA GCAAAGAAGA CATTAACAAA CGTGTTCAAG AAGCAGCTGA AATACTTGGA	1080
TTGAAAGAAT TCTTGAACG TAAACCAGCT GACCTTTCAG GTGGTCAACG TCAACGTGTT	1140
GCCATGGGGC GTGCGATTGT CCGTGATGCG AAAGTATTCT TGATGGACGA ACCTTTGTCA	1200
AACTTGGAATG CCAAACCTCG TGTATCAATG CGTGCTGAAA TCGCTAAAAT TCACCGTCGT	1260
ATCGGAGCTA CAACTATCTA TGTAATCTAC GACCAAACAG AAGCGATGAC ACTTGCAGAC	1320
CGTATCGTTA TTATGTCAGC TACTAAGAAC CCTGCTGGTA CAGGTACTAT CGGACGTGTA	1380
GAACAAATCG GTACTCCTCA AGAAGTTTAC AAAAATCCAG TTAACAAATT CGTTGCAGGA	1440
TTTCATCGGAA GCCCAGCTAT GAACTTCATC ACCGTGAAAT TGGTTGGTAG CGAAATTGTT	1500
TCTGACGGTT TCCGTTTGAA AGTGCCAGAA GGAGCATTGA AAGTTCTTCG TGAAAAAGGC	1560
TACGAAGGAA AAGAATTGAT CTTTGGTATC CGTCCAGAAG ACGTGAATGC AGAACCTGCT	1620
TTCTTTGAAA CATTCCCAGA CTGTGTTGTA AAAGCGACTA TCTCTGTATC AGAACTGCTT	1680
GGTTCAGAAT CTCACCTTTA CTGTCAAGTT GGTAAAGACG AGTTTGTGTC AAAAGTTGAT	1740
GCTCGTGAAT ACTTGCAAAC AGGTGCAACA GTTGAGCTTG GATTTGACTT GAACAAAGCA	1800
CACTTCTTCG ATGTAGAAAC TGAAAAACA ATCTACTAAA ATAAATAAAA TTCAAAGCAC	1860
TACAAGAAAA GATATCTCTT TATCAATTGT AGTGGAGAGA TATCAGTTAA TCTAGGGAGA	1920
GAAACAAAT GCTTCTCTCC TTTTGTCTAG AGAAGTCATA TTATGCATCT ATATTGTGAT	1980
GCTCTTTAAT ACTCTTCGAA AATCTCTTCA AACCACGTCA ACGTCGCCTT GCCGTACGTA	2040
TGATTACTGA TTTCGTCAGT TTTATCTGCA ACCTCAAAGA TGTACTTTGA GCAGCTTACG	2100
GCTAGTTTCC TAGTTTGCTC TTTGATTTCC ATTGAGTATT ATTTGTGGGT ACCATCTACA	2160
AGTGAAGCTA TATGCGTAAA CTACGTGAGC AATTGAATTC GAACTAGAGA GGTAAATAATA	2220
AATTTATGCT ATAGTTATGG TGACTTGTAT GCTTTTGATT CTAGTTTATC AAATAATAGA	2280
TTAGAATTGT CAGATAATAT CATTTTGTGT TATAATGAAG AAAAAACAGA GGTGTTCAAA	2340
TGTCAGAAGC AGGTCATAAG TTTTGTAGCA AATTGGGGAA AAAACGCTTA CGTCCAGGTG	2400
GAAAGCGTGC CACAGATTGG TTAATTGCAG AAGGAGGATT TTCAAAAGAA AAGAGAATAC	2460
TAGAGGTTGC GTGTAATAGG GGAACACAG CAATTGAGTT GGCACAGCGT TTTGGTTGCA	2520
AGATAACTGC TGTGATATG GATGCTCAAG CTTTAGAAGT GGCTAAAAAA TCTGCTGGAA	2580
CGGCAGGTGT TGCTCATTTA ATCAGTTTGT AAAGAGCAAA TGCAATGAAA CTTCTTATC	2640

1235

AAGATGCTAG TTTTGATATT GTTATAAATG AAGCTATGCT GACTATGCAA GCCGATCAAG	2700
CTAAGAAAA ATGTGTAATG GAATATCTAA GGGTATTAAA ACCTGGAGGT CTTCTCTTGA	2760
CACATGATGT GCTTCTTAAG GAAGCTAAAG AGTCTATCAG ACAGGAATTA TCACAAGCAA	2820
TTCATGTAAA TGTAGGTCCT TTAACCTCAAG ATGGTTGGGA ACAGGTGATG ATAGAATCAG	2880
GTTATTGTGA TGTGAAAGCA TTGACTGGTG AAATGACATT AATGAAATTA TCGGGTATGA	2940
TTTATGACGA AGGTTTGCTA GGAACCTTGA AAATTTGTGT AAATGCTTGT AAAAAGGAGA	3000
ATAGAAAGCA GTTTTAACT ATGTATAAAA TGTTTGCTAA GAATAAACAG AAATTGGGCT	3060
TTATTGCGAT GGCTAGTTAT AAATCGTCAA AACGTTAGAT AATTATTGAA GTTAACTTTT	3120
CCTTTTTTCT TTCTTAAAA ATATGCTATA ATAGAGAGTA AAAAAGCTTTG AAAGAAAGAA	3180
AAAGATGAAT TTAAAAGATT ACATTGCAAC AATTGAAAAT TATCCAAAGG GTACCG	3236

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

CCTGACTTTT CAAATTGGTT AGTTTGCCAC ACTTGGTTTA TATGGTCGTG GAAAGCATGG	60
CTATTACTTC TCAAAGGGCG ATTTCTCACC CCATGAAAAG TGTCTATTTT TGTTTAGGTT	120
TGTAAGTTAA TTCATTGTCA CATATTACTC TTAACTGAT TGAGTGAGTA CCGCTTATAT	180
TTGATGCCAA ACGCCTTAAA AGTGTTACCC TCAAGTCCTT TTAGAATACG GCTATAATTC	240
CGCTCATTGT AAACATCTTT AAGCTCATCA CTATCTAGGT TGGTATTAAA AATGGTATTT	300
TCACGATTGT TTAGCACGTC AAAGAGTAAA TCCTGCTCCC AGTCACTCTT AGGCTTAATA	360
ACAGCATTTT TTGCTCCTAA ATCATCAATA ATTAAGTAAT CAACAGACTT CATGAGTTCA	420
GTAGCTTCAA ACTCTGTAAG TGTGACCTT TTACCATAAT TCCACCCCTC TTTAATTTGT	480
TTGATCATTT CGGTTAGGCT TACAAAAAGC AACTCTTAG GTTCTCCTTT TGTCTTATAC	540
CCCTCATTTA TACCTTTGGC AATAGCAACT GATAAAAGTG TTTTCCAAT CCCTGTACCT	600
CCTGTGATAA GCGTATTTCC CCTCATGCCA TCAAGATATT TTTGTACCTG ACCTTTTGCA	660
AATTCTAAAA ATCGCTTTTC TTCTGATGTT ACAGCATTA AATCATCAA AGTTTTAGTT	720
TTAACTCAT CTGCTACATA GCTCTTATTG CTCATCAACA CATTATAAGT TTGCATATAT	780

1236

AGTTTAGCAT TCAAATTATC AGCAATCGCA TCTTCTTCAT CTTGCTTTTT CTGTTCTTCT	840
TGGCATTGTT CACAATAGGG TGGGATACAG CGAACTTCTT TTATTGCCTC TCCGTTCTCA	900
TTCCACCCCA CTA CTACTACATG TCTTTCTCCT TTGATTGTG TTAGCTGTAT TTCATGCTTA	960
GGACACAATT CGTCTAGTTT AAATGTCTCA ATATTTCCTA AACTAGATTG TAATGATTTT	1020
ATTTTCTGAC CTCCTAAAAT GGTTTTTCTT GTGTTGGTAT CCAATCTCA TAGCTGGTAG	1080
GCTCTAGTTG ATTGGTTTGC TGTTTTTTAG CCTCACGCGC TGCCCTGCTA TTTCTAACAA	1140
GTTCCACCGT CAATAAATTG TCCTGTTTCC AACGGTTAAG GATTACCTTG ATGTATGCAA	1200
AGTTTGCTTT ACCCTGACTG ACAGCCTCTT TTAACGCCTC ATGGATAAGC TCTGGGCTAA	1260
AATCTTCTAG CATATACTGC AATCTTGAA TCTGTAACGG TGACAATGCT TTACCTGTCT	1320
CAGCTCGCTT CATATTCAAC AAGTCGTCTA TTTCCACACT GGTACTTTT TTATTTACAA	1380
AATCAGAAAT CAGTTGAAAA ATGTTTGAC TTTGTAGCTG GATTTAGCC ATTACCTCAT	1440
CAAATCTGC TTGTGTCATG TTGTCTAAAT CTAGTGTCAT TGCATTGCCT CCTCAAACCTT	1500
CTCTATAAGA CAACTTTAT TTGCTTTCTG AGTCCATTT TTAGAGTTAA AAAGAATATC	1560
TTTTAAGTT ACAGTAGCCT CTAAATACTC CTTTCAGCA TGCTCTATAT ACGCCTGTTG	1620
CTCTGCTTCG TTCTCAAAA AGTGCTTAGC TTGGCGTTTA AAGAATGCTT TTCGCATAGC	1680
GTCCATTCA AAAATAACCAG GGGCGAAAA CATTCCTGTA GTGCTTTTAG AGACCGCTTC	1740
GATTTTATGG CTTTCATTCA ATTCAGGAAG TTCAATCCAA AGTAAACGGG ACAACTCATC	1800
TTTGATGGAT TTTGTCTGAC TTTCCAATAA AGAAAGGATT CTTAGGCCAT TTTCTTCGCT	1860
AATTTCTCGC ATTTCTGCGC TAATCTGTC TATACGTCTA GTTAAATTCT CATATGTTGT	1920
TTCTGTCATG TTTTACCTC TGTTCCTTG TTGGTGTGAT TTTTAGCTT ATTTTCTTAC	1980
TTCTAAACAT CATGTCTTA ATTTCTGAT AACTCATTTT CAATCAATC ATAGCTATTG	2040
CCATATCCTC AAATGCCTGG TACTGCTCCA ACTCCTCACT AGTCAAGCTA TCGATACCGT	2100
TATAGCCCC ACGCTCTTCT CTTAACTGCT TAGCGTTCAT GTCTGTTACT GCCTTTAGTA	2160
GCAAGTTGTT CATGGTGCTA TGCGCGTGCT TTGGTGCAAT AGGCCATGTT TCTATACTGT	2220
CATGCAAGGT TTTTCTTTT GGTTTTCTA GCGCCCTCTG CAGACGAAT TCAGAAAGTT	2280
CCTCACGCAT TTCAAAGAAT GCTTTGACTA GGTTAGTTT GAATTGCCGT ACTGTTTCGG	2340
TATTCTTTAA ATAAGTGATC AGAAAAGTAG CCTGTTGCTC GTTCAGAATA TAGGATTTT	2400
TAGGTTGTCC TCTAGTATCT AATTATGGA TTTTAAATCC AAGTATCCC AACTCTTCAA	2460
AGTCAGCCTT ATTTCTCTT ATTAAGCGCG TGATAGTGTG GTGTTGTA CTAGCACATT	2520
CAGCGATGAT CTCGCTGTG GTGTACGGCT CTTCTTACC GTCCATGTAA ACTAGTTCCA	2580

1237

TTACGGTTCT ACCTCCTGTA TAAATCTGGT TAGCTTACTT TTAAATTGCC TCCTCTAGCC	2640
TCTTTTTTAG CCTCTAAAAC GGCTTTGGCT AGTGGTTAAT ATTATTTACC ACTTGTCTCT	2700
ATAAACGTGT TAGAGGCCTT TATAACGACT TGTATCGCTG TATCGATATC CTCCTGGAA	2760
TAGTAGATTT ATTTTCTAAT ATCATTCAAG ACTTGTTTAA CCCATTTCTT GAAAGAAATA	2820
AAATTACATC TTCTTTATCC TTGGCATCTG CTTTGTCTGA GACAAATTAG AATGTCAATA	2880
CTTGG	2885

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

TATCAATCCT TTCCCATTAT AGGAGCAACA GAGTGGGAGT AGTCATCTAA GGACTAATTT	60
ATGTATTTTT ACGAGTCAGT ATCTTGGGAT ACTGGTTTTT ACTTTTCTAG ACTTTTGTAC	120
TACTTGTTAA AACTGGGATA ATTTTCGACT GTTTAACAGT TATTATGCAA AGTCTAAAAG	180
ATTAGAATTG TCAAAACAAT CCGTCTAGGC TTGATTTTAT CCTTTATTTA CTATAAAATG	240
AGAAGGAAAA ATGTCAAAC TTTATATTGC AAATAGGAGA AATCATGACA AAAACATTAA	300
AACGTCCTGA GGTTTTATCA CCTGCAGGGA CTTTAGAGAA GCTAAAGGTA GCTGTTCACT	360
ATGGAGCAGA TGCTGCTTTT ATCGGTGGTC AGGCCTATGG TCTTCGTAGC CGTGCGGGAA	420
ACTTTACTTT CGAACAGATG GAAGAAGGCG TGCAGTTTGC GGCCAAGTAT GGTGCCAAGG	480
TCTATGTAGC GGCTAATATG GTTATGCACG AAGGAAATGA AGCTGGTGCT GGTGAGTGGT	540
TCCGTAAACT GCGTGATATC GGGATTGCAG CAGTTATCGT ATCTGACCCA GCCTTGATTA	600
TGATTGCAGT GACTGAAGCA CCAGGCCTTG AAATCCACCT TTCTACCCAA GCCAGTGCCA	660
CTAACTATGA AACCCCTTGAG TTCTGGAAAG AGCTAGGCTT GACTCGTGTC GTTTTAGCGC	720
GTGAGGTTTC AATGGAAGAA TTAGCTGAGA TCCGCAAACG TACAGATGTT GAAATTGAAG	780
CCTTTGTCCA TGGAGCTATG TGTATTTTAT ACTCTGGACG TTGTACTCTT TCAAACCACA	840
TGAGTATGCG TGATGCCAAC CGTGGTGGAT GTTCTCAGTC ATGCCGTTGG AAATACGACC	900
TTTACGATAT GCCATTTGGG AAAGAACGTA AGACTTTGCA GGGTGAGATT CCAGAAGAAT	960
TTTCAATGTC AGCCGTTGAT ATGTCTATGA TTGACCACAT TCcAGATATG ATTGAAAATG	1020

1238

GTGTGGACAG TCTAAAAATC GAAGGACGTA TGrAGTCTAT TCACTAyGTA TCAACAGTAA	1080
CCAACTGCTA CAAGGCGGCT GTGGATGCCT ATCTTGAAAG TCCTGAAAAG TTTGAAGCTA	1140
TCAAACAAGA CTTGGTGGAC GAGATGTGGA AGGTTGCCCA ACGTGAAGT GCTACAGGAT	1200
TTTACTATGG TACACCATCT GAAAAATGAGC AGTTGTTTGG TGCTCGTCGT AAAATCCCTG	1260
AGTACAAGTT TGTCGCTGAA GTGGTTTCTT ATGATGATGC GGCACAAACA GCAACTATTC	1320
GTCAACGAAA CGTCATTAAC GAAGGGGACC AAGTTGAGTT TTATGGTCCA GGTTCCTGTC	1380
ATTTTGAAAC CTATATTGAA GATTTGCATG ATGCTAAAG CAATAAAATC GACCGCGCTC	1440
CAATCCAAT GGAATATTG ACTATTAAAG TCCCACAACC TGTTCAATCA GGAGACATGG	1500
TTGAGCTCT TAAAGAGGGG CTTATCAATC TTTATAAGGA AGATGGAACC AGCGTCACAG	1560
TTGCTGCTTA ATGTAGTTGT TTAGTTTTAA AAAACTATGC AAAGCTCCAT ATACAACACT	1620
TAAACGAGAT TAAAGAATGG CGAAATCCCT TGATGCGCAA GAGATTAGCT GTCTTTTTTA	1680
TTTTTTAAGT GATAAAGTCG GAGTTTAGGC ATCAAAGCCT ATCAAATTAA ACAAAGAAGC	1740
GATGTCTTAG ATATTTTGAA AAAAATTAAT AAGCAGAAAA CTCTCTATTA TTTGTTGTA	1800
GAGAGTTTTT TGTTAATAAA ATTTACAAA ATGACATTTA TATATTGCAT TAAGTTAGAT	1860
ATATGATATA ATATTGTAA AAAGAGGCGC AACTTTTTAA AATTAATGAG AATCAAAGAG	1920
AAAACCAATA ATATTAATGG AGGAATAAAA AATGTAAGTA AGCATTATGG TCATTCAATC	1980
ATTCTCAAAG ATATAAATTT TGCACTTAAC AAGGGTGAAA TTGTTGGTCT AGCAGGGAGA	2040
AATGGAGTTG GTAAGAGTAC GTTGATGAAA ATCTTGTTTC AGAATAATCA ACCGACTTCA	2100
GGTAATATTA TAAGCAGTGA TAATGTTGGG TATTTAATCG AAGAACCAAA ATTATTTTTA	2160
TCTAAACAG GTTTAGAGAA TTTAAAATAT TTGTCAAATT TATATGGTGT TGA CTACAAT	2220
CAAGAAAGAT TTAGATGTTT GATCCAAGAG TTAGATTGA CTCAGTCTAT TAATAAAAAA	2280
GTAAGACCT ATTCTTTGGG TACAAAACAA AAATTAGCTT TGCTTCTAAC TCTCGTTACG	2340
GAACCTGATA TATTGATTTT AGATGAACCG ACTAATGGTT TAGATATTGA ATCATCACAA	2400
ATAGTTT TAG CCGTTCTAAA AAAATTAGCT TTACATGAAA ATGTGGGAAT TTTAATATCG	2460
AGTCATAAAT TAGAAGACAT TGAAGAAAT TGTGAGAGAG TTCTTTTCTT GGAGAACGGG	2520
CTTTTGACAT TTCAAAAAGT AGGAAAAGAT AGTCATAATT TCTTGTTTGA GATAGCTTTT	2580
TCATCAGCTA CAGATAGAGA CATTTTCATT ACCAAACAAG AATTTTGGGA TATTGTTTAG	2640
GAAGAGGGAT TGAGAATTAC TATGTCTGGG AATATTCAA ATAGTGAGCT TTTTAAATTT	2700
TTTAACGAAA ACTCTATTAA AGTAGTTGAT TTTGAAACTA AAAAAGAGAC GCTTAAAGAT	2760
ATTTACCTAA ATCGTTCAA ATAAAGGAAG GTTATAATCA TGAAATTAA TAAACAGAAG	2820

1239

AATCGGATGA TTTACGTCCT GTCTAATTTT CTATATGCTA TCTCAGTTTC CATTATTTAT	2880
GCTTTGAATG GCATTGTGTT ACTAGTCATA GTAAGTAAAT TGGGTATTCC AGGTGATTTA	2940
GGATTAAATT TTATAGTAGC TATTGTAGTC AATACAATTT TGTTAGTCCT GTTTTATTTT	3000
CTATTATCTT ACATTTTCTA TTTATACAAA TTGAAAAGTG GCTTGGTATw TGGTATTTTA	3060
GTAGCTTTAC TACTCTTTAT CTCTAATATA TTAAATACGA TGATGATGAA TACTAGTAAT	3120
GATTTGTTTA TCAAAGCAAT TGAA	3144

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TACGGTATTA TTTTAAAGGA GAAAGAATCA TGAAAATCAA AAAATGGCTT GGTCTAGCAG	60
CCCTTGCTAC AGTCGCAGGT TTGGCTCTTG CAGCTTGCGG AAACCTCAGAA AAGAAAGCAG	120
ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG CGGTTCTGAA GAAAAACGTT	180
GGGACAAAAT CCAAGAATTG GTTAAAAAG ACGGAATTAC CTTGGAATTT ACAGAGTTCA	240
CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA AGTAGATTTG AACGCTTTCC	300
AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG AAAAGACCTT GTAGCGATTG	360
CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT GAATGGAAAGT GCCAACAAGT	420
ACACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC TGTACCGAAT GACGCTACAA	480
ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT GATTAAATTG GATGTTTCTG	540
GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC AAAGAACTTG AAAATCACTG	600
AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT TGACGCTGCC GTTGTAACA	660
ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC ACTTTTCAAA GAACAAGCTG	720
ATGAAAACTC AAAACAATGG TACAACATCA TTGTTGCAAA AAAAGATTGG GAAACATCAC	780
CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA CACAGATGAC GTGAAAAAAG	840
TTATCGAAGA ATCATCAGAT GGTTTGGATC AACCAGTTTG GTAATAAGAA ACAGGGAGGT	900
GGGAGAGAAA ATTCCACCTC TTGCTTTTGT ATAGAGTATA GATTGTAAAG AAGACTATTC	960
GTCATAGAA AGGTAGAGAG AATATGGTTT TTCCTAGCGA ACAAGAACAG ATTGAAAAAT	1020

1240

TTGAAAAGGA TCATGTAGCC CAGCATTATT TTGAGGTTTT GCGTACCTTG ATTTCTAAGA	1080
AATCAGTCTT TGCCCAGCAG GTTGGACTCA AGGAAGTCGC AAATTATCTG GGTGAGATT	1140
TCAAGCGTGT TGGAGCTGAA GTGGAGATTG ATGAGAGCTA TACAGCGCCC TTTGTCATGG	1200
CACATTTCAA GAGTTCGCGT CCAGATGCCA AGACCTTGAT TTTCTATAAC CACTATGACA	1260
CTGTGCCAGC GGATGGGGAT CAGGTCTGGA CAGAGGATCC KTTTACGCTT TCGGTCCGCA	1320
ATGGCTTCAT GTATGGGCGT GGGGTTGATG ACGACAAGGG TCATATCACA GCTCGCTTGA	1380
GTGCTTTGAG AAAATATATG CAGCACCATG ATGATTTACC TGTCAATATC AGCTTTATCA	1440
TGGAGGGAGC GGAGGAATCG GCTTCAACAG ACCTAGATAA GTATTTTGAA AAGCATGCAG	1500
ACAAACTCCG TGGGGCGGAT TTGTTGGTCT GGGAAACAAG GACCAAAAAT GCCTTGGAAC	1560
AGCTGGAAT TTCTGGTGGC AATAAGGGGA TTGTGACCTT TGATGCCAAG GTAAAAAGCG	1620
CTGATGTGGA TATCCACTCG AGTTATGGTG GTGTTGTGGA ATCAGCTCCT TGGTATCTCC	1680
TCCAAGCCTT ACAGTCTCTT CGTGCTGCGG ATGGCCGTAT CTTGGTTGAA GGCTTGTACG	1740
AAGAAGTACA AGAGCCCAAT GAACGAGAAA TGGCCTTGCT AGAAACTTAT GGTCAACGAA	1800
ACCCAGAGGA AGTTAGTCGG ATTTATGGAT TGGAGTTGCC TCTCTTACAG GAGGAGCGGA	1860
TGGCCTTTCT AAAACGTTT TTTTTCGATC CAGCGCTTAA TATCGAAGGA ATCCAGTCTG	1920
GTTATCAAGG TCAGGGTGT AAGACTATTT TACCTGCAGA AGCCAGTGCC AAGCTAGAGG	1980
TTCTGCTGGT TCCGGGCCA GAACCGCATG ATGTTCTGGA AAAAATTCGG AACAGCTAG	2040
ACAAAAATGG CTTTGATAAG GTAGAATTAT ACTATACCTT GGGAGAGATG AGCTATCGAA	2100
GCGATATGAG CGCACCAGCC ATTCTCAATG TGATCGAGTT GGCCAAGAAA TTCTATCCAC	2160
AGGGCGTTTC AGTCTTGCCG ACGACAGCGG GGACAGGACC TATGCATACG GTCTTTGATG	2220
CCCTAGAGGT ACCAATGGTT GCATTGCGTC TAGGAAATGC CAATAGCCGA GACCACGGTG	2280
GAGATGAAAA TGTGCGAATC GCTGATTATT ACACCCATAT CGAATTAGTA GAGGAGCTGA	2340
TTAGAAGCTA TGAGTAGAGA TATTATCAAG TTAGATCAGA TCGATGTGAC TTTTCACCA	2400
AAGAAGAGAA CCATCACAGC GGTAAAGGAT GTGACCATTC ACATCCAAGA AGGGGATATC	2460
TACGGAATCG TTGGATATTC TGGAGCAGGA AAATCAACCC TTGTACGGGT GATTAATCTC	2520
TTGCAAAAAC CATCTGCAGG GAAAATTACC ATTGACGACG ATGTGATTTT TGACGGCAAG	2580
GTGACCTTGA CGGCAGAGCA GTTGCCTCGT AAACGTCAAG ATATCGGAAT GATTTTCCAG	2640
CATTTTAACC TGATGAGCCA AAAGACAGCA GAGGAGAATG TAGCCTTTGC CCTTAAACAC	2700
TCTGAACTCA GCAAGGAAGA AAAGAAGGCT AAAGTAGCTA AGTTGTTGGA CTTGGTTGGT	2760
TTGGCAGATC GTGCTGAAAA CTACCCTTCA CAACTATCTG GAGGGCAAAA ACAGCGTGTG	2820

1241

GCAATTGCGC GTGCCTTGGC CAATGATCCA AAAATCTTGA TTTCAGACGA GTCAACTTCT	2880
CCCCTTGATC CGAAGACAAC CAAGCAGATT TTGGCCTTGT TGCAAGATTT GAACCAAAAA	2940
TTAGGCTTGA CTGTTGTCTT GATTACGCAT GAAATGCAGA TTGTCAAAGA CATTGCCAAC	3000
CGTGTTCAG TTATGCAGGA TGGGCATTG ATTGAAGAGG GTAGTGTGCT TGAAATCTTC	3060
TCAAACCTTA AACACCTTT GACTCAAGAC TTTATCTCAA CAGCTACAGG TATTGACGAA	3120
GCCATGGTCA AAATCGAGAA GCAAGAAATC GTGGAACACT TGTCTGAAAA CAGTCTCTTG	3180
GTGCAACTCA AGTACGCTGG AGCTTCAACA GACGAGCCAC TTTTGAATGA ATTGTACAAG	3240
CATTACCAAG TAATGGCTAA TATTCTCTAT GGGAAATATCG AAATCTCGA TGGTACTCCT	3300
GTTGGAGAAT TGGTGGTGGT TTTGTGAGGT GAAAAAGCAG CGTTGGCAGG TGCCCAAGAA	3360
GCCATTCGTC AAGCAGGTGT ACAACTAAAA GTATTGAAGG GAGTACAGTA AGATGGAATC	3420
ATTGATTCAA ACCTATTTAC CAAATGTCTA TAAGATGGGT TGGGCTGGTC AGGCAGGCTG	3480
GGGAACGGCT ATCTACTTAA CTCTTTATAT GACAGTTCTT TCCTTCATTA TCGGAGGCTT	3540
CTTGGGGCTA GTGGCAGGTC TCTTTCTCGT CTTGACAGCG CCAGGTGGTG TCTTGGAGAA	3600
TAAAGTCGTA TTCTGGATTT TAGACAAAAT TACCTCAATT TTTCGTGCGG TTCCCTTTAT	3660
CATCCTCTTG GCAATCTTGT CACCACTTTC TCACTTGATT GTTAAACAA GTATCGGGCC	3720
AAATGCAGCC CTGTGCCAC TTTCTTTTGC AGTCTTTGCC TTCTGG	3766

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TGTTGCTGAG TTAATCGGTA CGTTCATGTT TGTATTCGTC GGGACAGGAG CTGTTGTTTT	60
TGGAAATGGT CTTGATGGCC TTGGTCACCT TGGAATCGCC TTTCCTTTG GTTGGCAAT	120
CGTGGTGGCA GCCTACTCAA TCGGAAGTGT TTCAGGTGCT CACTTGAACC CGGCTGTTTC	180
GATGCTATG TTTGTAAACA AACGTTTGTG ATCTTCAGAA CTTGTAAACT ACATCCTTGG	240
TCAGGTTGTT GGAGCTTTCA TCGCTTCTGG CGCTGTCTTC TTCCTCTTGG CTAACCTCAGG	300
TATGTCAACT GCTAGTCTTG GTGAAAATGC CTTGGCAAAC GGTGTCACTG TCTTTGGTGG	360
TTTCTTGTTC GAAGTCATCG CAACTTTCTT GTTGTATTG GTTATCATGA CTGTGACTTC	420

1242

AGAAAGCAAG GGCAATGGCG CGATTGCTGG TTTGGTAATC GGTTTGTCTAT TGATGGCGAT	480
GATTCTTGTC GGATTGAAGA TTTACTGGACT TTCAGTAAAC CCAGCTCGTA GCTTGGCACC	540
AGCTGTCTTG GTAGGCGGCG CAsCCTTCAA CAAGTTTGA TTTTCATCCT TGCACCAATC	600
GCTGGTGGAG TTCTTGCAAG CCTTGTGCA AAAAATTTCC TTGGAACAGA AGAATAATTG	660
AAACTCAAAA AGCCTTGCTC CTCATCTTGA GGAACAGGGC TTTTTCGTAT GATACTCTTC	720
GAAAATCTCT TCAAACCACG TCAGCTTCAT CTTGCCGTAG TATGGTTACT GACTTCGTCA	780
GTTCTATCCA CAACCTCAAA ACAGTGTTTT GATCTGACTT CGTCAGTTCT ATCTGCAACC	840
TCAAAACAGT GTTTTAAGCT GACTTCGTCA GTTCTATCTG CAACCTCAAA ACAGTGTTTT	900
AAGCTGACTT CGTCAGTTCT ATCTGCAACC TCAAAACAGT GTTTTAAGCT GACTTCGTCA	960
GTTCTATCTG CAACCTCAAA ACAGTGTTTT AAGCTGACTT CGTCAGTTCT ATCCACAACC	1020
TCAAAACAGT GTTTTGATCT GACTTCGTCA GTTCTATCCA CAACCTCAAA ACAGTGTTTT	1080
GATCTGACTT CGTCAGTTCT ATCCACAACC TCAAAACAGT GCTTTGAGCA ACCTGCGGCT	1140
AACTTCCTAG TTTGCTCTTT GATTTTCATT GAGTATGACT TTAGCGGTG TCAATTTTCT	1200
CTGGATAAAG GTCGTGTTGG AAGAGGCGTT GTTCTGCCAA GCCCTCATAC TTAGTTCCTT	1260
GCTTACCGTA GTTGTAGTAG GGGTCGATTG AAATGCCACC GCGCGAGTG AATTTTCCCC	1320
AGACTTCTAA ATAGCGAGGG TCTAGCAAGT TGACCAAGTC TTTCCCGATG GTGTTGATAC	1380
AGTTTTCGTG GAAATCTCCG TGGTTTCGGT AGCTAAATAG ATATAGTTTG AGGGATTTTG	1440
ACTCGACACA GAGCTTGTC GGAATGTAGG AAATATGAAT CGTCGCAAAG TCTGGCTGAG	1500
CAGTGATTTG TCCCAGCAGA GACATATCGA GGATATGGTG ACGAATGCCC TGTTCCTTAG	1560
CGATTTCTCT AGTAATTGA ATTTGAGGT GATGACGTTG GCCGTAGGCA AAGGTGACAG	1620
CTTCGACTGT TTCATAGTGT TGCAATGACC AGAAAAGGCA GGTTGTTGAA TCTTGACCAC	1680
CACTAAAGAC GACCAAGGCT AATTGACGTT TCATAGTACT CCTTCCAAAA TGGGAAATGT	1740
TCAGAGCAG CAAAAGCTC CCATTAGGGA GCTAAAAAAT ACCAAATCGA GGTTTTTTTA	1800
GCGATGGCAT ATCCCAAACA TCGTAATATT CTACTTATAT AGTAAATGA AATAAGAACA	1860
GGACAAATCG ATCAGGACAG TCAAATCGAT TTCTAACAAT GTTTTAGAAG TAGAGGTGTA	1920
CTATTCTAGT TTCAATCTAC TATAGTCTAG CATATTTTTT GAAAAATGGC AAAGGGCAAG	1980
AAAAAAGAGA CCAAAGAAAG TACTTGGTCT CTCGTTTGAT TAGCTCAATT CAGCAATGAT	2040
GGCCTTGATT TGTTCGCTG TGTGAACACC TGCAACTTGT TTGACAACTT GGCCGTCTTT	2100
TTTGAAGAGA AGAGTTGGAA TAGACATGAT TCCAAAAGCA CGAGCTGTGT TTGGATTTTC	2160
ATCAACGTCC ATTTTAACGA TTTTCAAGAC ATCTTCTGAA AGTTCCTCAG ACAATTTGTC	2220

1243

CAAGATTGGA CCTGTCATAC GACATGGACC ACACCAAGTT GCCCAGAAGT CTACTAAGAC	2280
CAAACCGTCT TTTGTTTCTT GTTCGAATGT TGCATCTGTA ATTGCTTTTG CCATTGTATT	2340
TCTCCTTTTT TTAGTTATAT TGGCTTAAAT CTTGTTTCAT GAGATAGAAG AAGATATCTC	2400
CATAAGTCCC ATGGTAGTCC AAATTATGAC CCTTGTAAGT TAATTTTGG ACAGGGTAGT	2460
AkkCTGCGAC GCCGATAAGG CAAGCTTGTT GCGAACGTTT AAAGTCTTCA TAAGACTCGG	2520

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ACTCAGTTAG ATTTTGTTTT CAAAAACAAC GAAGAAAAAG ACCATGTTGC TCTACTTGGA	60
AGAATTGGCT CCGAACGTGT TTATCGATAT ATTAATAAAA AATATTTAGA TTTACCGGAA	120
ACATTGCAA ATTATAATGT TTTGTACCA GAAGCTAATG GAAGTGGTGC CTTAGGTGAA	180
GTCTTATCAA CACCCTAAT CGGGGAACCC CTAATCGGGC ATACAGATAC TTTTATCT	240
ATTGGTAATT TAAAAACAA ATTTGAAGCC GATGCTTGTA TTAAATTTAT TAAACTAAA	300
TTCGCTAGAG TATTATTAGG TGTTTTGAAA GTTACTCAGC ATAATTCACG CAAACTTGG	360
TATTACGTCC CCCTCAAGA CTTTACGGTC AATTCCGACA TTGATTGGAC ACAATCAGTG	420
ACTGATATTG ACCGCCAGCT TGATCAAAAA TATGACTTTT CCCCTGAAGA AATTGCCTTT	480
ATTGAGAATC ATGTAAGGA GATGGATTAG AAAAGTATTT TTATTTGACA AATAGTGCTC	540
AATGATCTAA AATGACTATA TAGGATTAGG TCAGGAAGCA TACGATGCCC TGACCCTTTT	600
TGTACTTATG AGATGAGAAA GTCATTTGTT AGATAAATG ACTCGTTAGC AAACGTTCAA	660
AAAAGGAAAA CTTATGCCAG TAGAAATTAA AACCCTAAA GAAATTCATC CTAAATCTA	720
TGCCTACACC ACACCGACAG TAACCGTAA TGAAGGCTGG ATTAAGATTG GGTATACAGA	780
ACGTGATGTC ACACAACGTA TCAAGGAGCA AACGCATACA GTCATATAG CTACAGATGT	840
CTTATGGACT GGTGATGCAG CTTATACAGA AGAGCCTGAT AAGGGGAAAA CTTTCAAGGA	900
CCATGATTTT CACCATTTCC TTTCTTTCCA TGATGTAGAA CGTCGTCCCA AGACGGAATG	960
GTTCTATTTT AATGGAATC CTGAAAAATC AAAAAATCTT TTTGATAAGT TTGTTACGCA	1020
TGATTTGTCT GGTATCAGC CTGGAAGG ACAGGACTAT ACTCTGCGAC AAGAGCAAGA	1080

1244

AGAAGCAGTT GCTAAGACAT TAGCTTATTT CCAAGAACAT GCTGGAGGCA AGTTTCTCTG	1140
GAATGCCAAG CCACGCTTTG GTAAAACCTT GTCTACCTAT GACCTAGCTC GACGGATGGA	1200
AGCTGTCAAT GTCCTAATTG TAACAAACCG CCCTGCCATT GCTAACTCAT GGTATGATGA	1260
TTTTGAAACA TTCATAGCAG GTCAAACGAC TTACAAGTTT GTTTCTGAAT CAGATAGCCT	1320
TAAGAGTCGT CCAATCTTGT CACGACAAGA ATTTCTTGGT ATTTTAGCTG ACGATGTAAG	1380
ACAACCTGCT TTTATCAGTC TCCAAGACTT GAAAGGATCT GTTTATTTAG GTGGAGAGCA	1440
CGATAAACTC AAATGGGTAA CTGATCTGCA TTGGGACTTG TTGGTTATTG ACGAGGCTCA	1500
TGAAGGAGTT GATACCTTCA AGACTGACCA AGCCTTTAAT AAGATTGAC GAAATTTTAC	1560
TCTGCATTG TCAGGTACAT CATTTAAAGC ATTGGCTAAA GGAGATTTTA CAGAGGAACA	1620
AATCTACAAC TGGTCTTATG CTGATGAGCA GGCTGCTAAG TATTCGTGGT CTCTTGAGCA	1680
AGAAGAGGAA AATCCTTATG AAAGCTTGCC TCAGTTGAAT CTCTTTACCT ATCAAATGTC	1740
TCAGATGATT GCGGAAAAGT TAGAAAAAGG CGCTCAGATC GATGGTGAAA ATATTGACTA	1800
TGTTTTTGAC TTAAGTGAAT TTTTCGCTAC AGATGATAAA GGGAAATTTA TTCATGAGCA	1860
TGATGTCAGA AATTGGTTAG ATACTCTATC AAGCAATGAA AAATATCCAT TTTCAACCAA	1920
AGAACTCCGT AATGAACCTA AGCATACTTT TTGGCTTTTA GAACGTGTCG CTTCGGCCAA	1980
AGCATTAATA GCCCTACTAG AAGAACACCC AATCTATGAA AACTATGAGA TCGTTCTAGC	2040
TGCTGGTGAC GGACGTATGT CCGAAGAAGA CGATAAAGTC AAACCTCAAAT CCTTGGACTT	2100
GGTTAGAAAA GCGATAGCAG AGAATGACAA AACCATTACC CTATCCGTTG GTCAGCTGAC	2160
GACAGGTGTC ACTATCCCTG AATGGACAGG TGTATTGATG TTATCAAATT TGAATCACC	2220
AGCTCTTTAT ATGCAGGCCG CCTTCCGTGC TCAAAATCCT TACTCATGGA GCGATAACAA	2280
AGGAAATCAC TTTCGCAAAG AAAGAGCCTA TGTATTTGAC TTGCGCCGG AAAGAACCTT	2340
GATTCTCTTT GATGAGTTTG CCAACAACCT ATTGCTTGTA ACTGCAGCTG GTAGAGGAAC	2400
TTCAGCTACA CGCGAAGAAA ATATTAGAGA ATTATTAAC TTCTTTCCAA TTATTGCCGA	2460
AGACCGTGCT GGTAAGATGG TTGAAATTGA TGCAAAGGCA GTTCTAACCA CTCTCGCCA	2520
GATAAAAGCT AGAGAAGTTC TTAAACGAGG TTTTATGTCC AATCTCTTAT TTGATAATAT	2580
TAGTGGTATT TTCCAAGCAA GTCAAACAGT TTTAGATATT TTAAATGAGC TGCCAGTTGA	2640
AAAGGAAGGG AAGGTACAAG ATAGTTCTGA TTTATTAGAT TTTTCAGATG TTACAGTCGA	2700
TGATGAGGGA AATGCAGTAG TAGACCATGA AATTGTAGTT AATCAGCAA TGCGACTTTT	2760
TGGTGAAAAA GTTTATGGAC TTGGTGAATC TGTTGCTGAG TTAGTCACAA AAGATGAGGA	2820
ACGAACTCAA AAACAGCTGG TCAATGACTT GAGTAAGACC GTTCTTTCAG TGATTGTAGA	2880

1245

GGAATTGAAA GCAGATTATT CTCTAAAAAC AAGGGAACT GAGCAAATTA AGAAACAAAT	2940
TACAGCAACA CTTGAGAATG AAATTCGAAA AAATGATATC GAAAGAAAAA TTTCTGAAGC	3000
TCATATCAAG CAAGAGTTGC AACAGCAGCT CAAAGAAGCA AATGATAAAG CGCAAAAAGA	3060
TAAGATTCAA GAAGATTGG AAAACGTTT AGAAGAAAAT AAACTCATTC ATAAAGAAAA	3120
ACTAGAACAA AACTCAAAA AAGAAGTGGA AAAAATGCCT GAGAAATTTA TCGAACAGGT	3180
TGAGATAAAA CGTGTGGAAC AGTTGAAACA ATCAGCTCAA GATGAAATTC GTGACCATTT	3240
ACGAGGGTTT GCAAGAACAA TTCCAAGTTT TATTATGGCT TACGGTGATC AAACCTAAC	3300
ACTTGATAAT TTTGATGCCT TTGTTCTTGA ACATGTTTTT TATGAAGTAA CAGGGATTAC	3360
GATTGATCAG TTTAGATATT TGCAGATGG TGGGCAGGAT TTTGCAGGGC ATCTCTTTGA	3420
TAAAGCAACA TTTGACGAAG CTATTCAAGA ATTTCTTCGC AAGAAAAAGG AGTTGGCGGA	3480
TTATTTTAAA GATCAAAAAG AAGACATTTT TGAATATATT CCACCGCAGA AGACCAACCA	3540
AATTTTCACT CCTAACGAG TGGTGAAGG GATGGTAGAT GATTTGGAAA AGGAAAATCC	3600
AGGGATTTTT GATGATCCAT CTAAGACTTT TATTGATTTA TATATGAAGT CAGGCCTCTA	3660
TATTGCAGAA CTTGTGAAGC GGTATATAA TAGCAATGGC TTGAAAGAGG CCTTTCCAAA	3720
TCCTGAAGAA CGCTTAAAC ATATTTTGGA AAAGCAAGTT TATGGATTG CTCGCTCTGA	3780
GATTATCTAT AACATTTCCA CTAATTTTAT ATTTGGCAAT CTTTCTAAAG ATATCAGTAG	3840
GAAGAATTTT GTTTTAGCAG ATACCATTC AGCGGCTAAA GAAGGGAGCA TTCAAAAGTT	3900
GGTTGATTC TATTTTGAAA ATAATTAAAA AGAAGGCCGA GTCAAAATTC TTTGAAATCA	3960
GAAAAACGC ATAATATTGA GTGCTTTTGT ACTGCCCCC AAAAGTTAGA CAGAAAAAT	4020
CTAACTTTTG GGGGCGAGT CAGACAATCC TTGGTATTAT GCGTTTTATT GTGGGAAGAT	4080
GTATAATGGA TTGAAATAAG ATATGAACAA ATCAATTAGG AATTAAAGC ATTTTATAAC	4140
AACGTTTTAG AGTAATGGG GGCTATTTCA ACTCAACCT ACTATAATAC AGAAAAAAC	4200
AACTCCCTGA TAATCAAGG AGTTGTCTAT AGTTAAATTA GTTTTAGAA GCTTCTTGGA	4260
ATTCTGGGTT TTTCCATGCT TCGTCAATGA TAGCTTGTA TTCTTTAGCA GATGCTTGCA	4320
TTTTTTGAGT TTCTGCGTCG TTCAATGGGA TATTTACTGG ACGAACGATA CCATGTGCAC	4380
CAACAACAGC TGGTTGACCG ATAAAGACAT TCTCAACTCC GTATTGACCT TCTTGAATA	4440
CTGAAAGTGG AAGTACTGCG TTTTCATCGT CAAGGATTGC TTTAGTGATA CGAGCAAGGG	4500
CTACTGCGAT ACCGTAGTAT GTTGACCTT TTTGTTGAT GATTGTGTAG GCTGCATCAC	4560
GAACACCTTC GAACAATTCA ATCAATTCAG CTCTTGAAC ATTTTGAGTG TCTTTAAGGA	4620

1246

ATTCTTCAAG GTTTACACCA GCGATGTTAG CGTGTGACCA AACAGCGAAC TCAGAGTCAC	4680
CGTGTTCACC CATGATGTAG GCGTGCACTG AACGAGCATC CACATCCAAT TTTTCAGCAA	4740
GTGCTTGACG GAAACGAGCT GAGTCAAGTG AAGTACCTGA ACCGATAACG CGTCTCTTAG	4800
GGAAACCAGA GAATTTCCAA GTTGAGTAAG TCAAAACGTC AACTGGGTTA GCAGCAACAA	4860
GGAAGATACC TTTGAAACCA GATTCAACAA CTTGAGTTAC GATTGATTTG TTGATAGCAA	4920
GGTTTTTACC TACAAGGTCA AGACGAGTTT CACCTGGTTT TTGAGGTGCA CCTGCAGTGA	4980
TCACAACAAG GTCAGCGTCT GCACAGTCAG AGTATTGAGC TGCATAGATT TTTTtaggtg	5040
AAGTGAAGGC AAGGGCGTGA CTAAGGTCAA GCGCATCACC AACAGCTTTT TCATGCAATT	5100
GTGGAATTTC GATAATTCCA AGCTCTGTG CAATTCCTTG GTTAACAAGT GCAAAAGCGT	5160
AAGATGAACC TACAGACCA TCACCGACAA GGATAACTTT TTTGTGTTGT TTAGTTGAAG	5220
TCATTGTTTT AAACATCTCC TTAATTTTAT TAGGGGATTT TCCCTAGACA ACTTCATT	5278

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

ATAAGGAATC TCTAAAAAT TTTAAGGAGA ATCTAGCAAA TGGATTTAC ATGGGCACTG	60
AAGTAGCCA CTGAATTTTT GGGAACTGCC ATTTTGATCA TTCTTGGGAA TGGTGCACTT	120
GCCAACGTTG AACTTAAAGG TACGAAAGGT CACCAAAGTG GCTGGATCGT CATCGCTGTT	180
GGTTATGGTA TGGGGGTTAT GATCCCAGCC TTGATGTTTG GTAACGTATC TGGGAATCAC	240
ATCAACCCTG CTTTCACTCT AGGGCTTGCA GTTAGCGGTC TTTTCCCTTG GGCACAAGTG	300
GTACCTTACA TTATCGCGCA AGTCTTGGGG GCTATCTTTG GCCAAGCCTT AGTTGTGGCA	360
ACATACCGTC CATTCTACTT GAAAACTGAA AACCCAAATA ACATCTTGGG AACTTTCTCA	420
ACTATTTCAA GTATTGACCA TGGTACAAAA GAAAGTCGCT ATGCAGCAAC TGTCAATGGT	480
TTGATTAATG AGTTTGTGG TTCATTTGTT TTGTTCTTTG CAGCTCTTGG TTTGACTAAA	540
AACTTCTTTG GTGCTGAAGT GCTTCAATTC ATGAAACAAA AGGCAACAGA AGCAGGACAA	600
ACAGTTGATT TTTCTGACTT GGCTATTAAA GCACAGGTGG CTCCACACAC TGCTTCAGGA	660
CTTTCTGTGG CTCACTTGGC ACTTGGATTC CTCGTTATGG CTTTGGTAAC ATCACTTGGA	720
GGACCTACAG GACCTGCCTT GAACCCAGCC CGTGACTTGG GACCACGTCT CCTTCATGCT	780

1247

TTCCTTCCCA AATCAGTTCT TGGTGAGCAT AAAGGCGATT CAAAATGGTG GTATTCTTGG	840
GTACCAGTAG TAGCACCTAT CGCAGCAGCA ATTGCGGCAG TAGCTGTATT CAAATTCCTT	900
TATCTCTAAG AAATAGCTCC TTTAACATTT GAGTGAGCAC CATCTATAAG TAAGAGAGGA	960
TCAGACTGGk TCTCTCTTTT kGATTTTtaG GGAAATGAAA GAAcTCTAAA CAAACTCCTC	1020
TCCAGCAGTG GTTTAGAAGT CTCAGTGGGC TATTCCAGCT TCAATGGACT ATAGTAGGTT	1080
GCAGTTGAAA TAATAGACCC TTGTTTCTAA AACATTGTGA GAAATTG GTT TGAATTCTCC	1140
AATCAAATTG TGCAGTTTTC ATTCTACTAT ATATTATCGG AATATTATCG GAGATGGGTT	1200
CCCTATCTTG TAAGTCTGCT TTATAGTGGG TTGAAGTTGG AATAGTCCTC CCTTCTTCT	1260
CAAACATTGT GAGGAATTGA TTTACCTTCC TCAACAAAAT GTTCAGTTTC TATTTCATTT	1320
TACTATAAAA TAAGCGATTA GGGGGGCTAT TCTTCGACCT ACATTGACTC TGCTGAGTCC	1380
TATGATTGTT ATCGTTTAT CTGCAATTTT ATACTCAATG AAAATCAAAG GGCAAACATA	1440
GAAGCTAGCC GCAGGTGTT CAAAACACAG TTTTGAGGTT GTATAGTAGA TTGAAACTAG	1500
AATAGTACAC ATCTACTTCT AAAACATTGT TAGAAATCGA TTTGACTGTC CTGAACGATT	1560
TGCCCTATTC TTGTTTCATT TTACTATATA AACCAGAGAC TGTTTACATT TTCAGCAAGT	1620
GAGTGGATGG ATAATGCTGA AAACCTCTTG AAGGATAAGT CTATTTAGTA CTTTCTATTA	1680
ATTAGTTAAA TTTTACCAA GAATAATTCA CAAAACGTT GTAAAACACT TGCAATTTAG	1740
CTGAAATTG ATAAATAGT AAGGAAAGT AGACTGTATT GCCTACTGTC TATCTATAAA	1800
ATATATTTTA TTGGAGGCTT TTACTCAAAT GGCAAAAGAA AAATACGATC GTAGTAAACC	1860
ACACGTTAAC ATTGGTACTA TCGGACACGT TGACCACGGT AAAACTACCC TAACTGCAGC	1920
TATCACAACT GTTTGGCAC G	1941

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATTTGAAGAA ATTGAAGAAA TCGTAGCCCC TACAGATGGT GAATTTTGG GGAAGTTTT	60
ACTTGGAAGT GGGGTAGTTC TCTTAATTGG AGTAGCCTGT TGTTAAAAAG ATAGGGAGTG	120
ATAATCATGC AAGATAACTT TTTATTTGAG GAAATTGAAG AAATTTCACT ACCAGTTAAT	180

1248

GATTTTTCAG CTGGACTTGC AACAGGTATC GGATTTGGTT TAGCAATCCT TGCTCTTGCT	240
GGTTGTGAA GTTTGTTCAT TTAATAACAT CAAGCTTTTT CAATTTTCATT TTAGACAGTC	300
ATTTAAATTT TCCGTATTAG TCTTGCAGCA AGAGATTAAT AGAATTAGTC ATTATTTTAT	360
TGATTGCGGA CTGAGGGACT AGAGTATGTT TACTTAACC CCTCTTTTAT TTATTAAAGG	420
TTAGGTTTGT TATGAGAATT GTTGATAAGA TTAAGATATT ACCTACTCCT TATGAGGGAC	480
ACTATCATTT ATATATACCA TCCAGTAAGA AACATGTATT AGTTGGGAAA CAGGAAAAAA	540
ATGGTTAGAG CAACTAATAG GTCAAGAATT TACCATATCG GACTTATTAG TGTTAGTAGG	600
GAAGAAATAT TTTTAAATA TCTTGGGACT TTAATATAAC ATTATCTGAA AAATTAAACT	660
ATAAAGATT TAATAAGAAT TTTGAAAAA TCCTATCTTG TTGTCATTAT ATTTGCAACG	720
ATACATGAAA TTAGTCATGC AATAATTGCT AATAA	755

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CCAGAAAAAC CGTAGTGGAG CTCGTGGAAC AGTGAATTG ATTTTCCAAA AAGAATACAA	60
TAAATTTTCA AGTATCTCAA AGAGGGAGGC ATAAGATGTC AGATGCATTT ACAGATGTAG	120
CCAAGATGAA AAAAATCAAA GAAGAAATCA AGGCACATGA GGGACAAGTC GTAGAAATGA	180
CTTTGGAGAA TGGTCGTAAG CGCCAAAAAA ATAGATTGGG TAAGCTAATT GAAGTTTATC	240
CATCTCTATT TATTGTGGAG TTTGGGGATC TGAAGGAGA TAAACAAGTT AATGTTTACG	300
TTGAATCCTT TACTTACTCA GATATTCTTA CAGAAAAGAA TTTGATTCAT TATCTTGAAT	360
AAAGTGAGAA ATTTTCTCAC TTTTCTTTT TTCTCCGAAT AATTTAGGTG AAGGCAATCA	420
TCGCTTTATA TTATTTTCA AGGAGGAAGA ATGAAAATTT TACCGTTTAT AGCAAGAGGA	480
ACAAGTTATT ACTTGAAGAT GTCAGTTAAA AAGCTTGTTT CTTTTTTAGT AGTAGGATTG	540
ATGCTAGCAG CTGGTGATAG TGTCTATGCC TATTCAGAG GAAATGGATC GATTGCGCGT	600
GGGGATGATT ATCCTGCTTA TTATAAAAAT GGGAGCCAGG AGATTGATCA GTGGCGCATG	660
TATTCTCGTC AGTGACTTC TTTGTAGCC TTTCGTTTGA GTAATGTCAA TGGTTTGTAA	720
ATTCGGCAG CTTATGAAA TGCGAATGAA TGGGGACATC GTGCTCGTCG GGAAGGTTAT	780
CGTGTAGATA ATACCCGAC GATTGGTTCC ATTACTTGGT CTACTGCAGG AACTTATGGT	840

1249

CATGTTGCCT GGGTGTCAAA TGTAATGGGA GATCAGATTG AGATTGAGGA ATATAACTAT	900
GGTTATACAG AATCCTATAA TAAACGAGTT ATAAAAGCAA ACACGATGAC AGGATTATT	960
CATTTTAAAG ATTTGGATGG TGGCAGTGTT GGAATAGTC AATCCTCAAC TTCAACAGGC	1020
GGAACCTCATT ATTTTAAGAC CAAGTCTGCT ATTAAACTG AACCTCTAGC TAGCGGAACT	1080
GTGATTGATT ACTATTATCC TGGGGAGAAG GTTCATTATG ATCAGATACT TGAAAAAGAC	1140
GGCTATAAGT GGTGAGTTA TACTGCCTAT AATGGAAGCT ATCGTTATGT TCAATTGGAG	1200
GCTGTGAATA AAAATCCTCT AGGTAATCT GTTCTTTCTT CAACAGGTGG AACTCATTAT	1260
TTTAAGACCA AGTCTGCTAT CAAACTGAA CCCCTAGTTA GTGCAACTGT GATTGATTAC	1320
TATTATCCTG GAGAGAAGGT TCATTATGAT CAAATTCTCG AAAAAGACGG CTACAAGTGG	1380
TTGAGTTATA CGGCTTATAA CGGAAGTCGT CGCTATATAC AGCTAGAGGG AGTGACTTCT	1440
TCACAAAATT ATCAGAATCA ATCAGGAAAC ATCTCTAGCT ATG	1483

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1027 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CCCGGAAAAC AAGTTAAAGT TGAAGTTGGT CAAGCAGTTT ACGTTGAAAA ATTGAACGTT	60
GAAGCTGGTC AAGAAGTTAC TTTTAACGAA TTGTTCTTGT TGGTGGTGAA AACACTGTTG	120
TCGGAACTCC ACTTGTGCT GGAGCTACTG TAGTTGGAAC TGTTGAAAAA CAAGGAAAAC	180
AAAAGAAAGT GGTACTTAC AAGTACAAAC CTAAAAAAGG TAGCCACCGT AAACAAGGTC	240
ACCGTCAACC ATATACAAAA GTTGTCATCA ACGCAATCAA CGCTTAATTT TAAGGAGAAC	300
ACATGATACA GGCAGTCTTT GAGAGAGCCG AAGATGGCGA GCTGAGGAGT GCGGAAATTA	360
CTGGACACGC CGAGAGTGCC GAATACGGCT TAGATGTCGT GTGTGCATCG GTTCTACGC	420
TTGCCATTAA CTTTATCAAT TCTATTGAGA AATTTGCAGG CTATGAACCA ATCCTAGAAT	480
TAAACGAAGA TGAAGGTGGC TATCTGATGG TTGAAATACC AAAAGATCTT CCTTCACACC	540
AGAGAGAAAT GACCCAGTTA TTCTTTGAAT CATTTTCTT AGGTATGGCA AACTTATCGG	600
AGAACTATTC TGAGTTCGTC CAAACCAGAG TTATCACAGA AACTAACAC GGAGGAAAAC	660
ATTATGTTAA AAATGACTCT TAACAACTTG CAACTTTTCG CCCACAAAAA AGGTGGAGGT	720

1250

TCTACATCAA ACGGACGTGA TTCACAAGCA AAACGTCTTG GAGCTAAAGC AGCTGACGGA	780
CAAACGTGTA CAGGTGGATC AATCCTTTAC CGTCAACGTG GTACACACAT CTATCCAGGT	840
GTAACGTG GTCGTGGTGG AGATGATACT TTGTTGCTA AAGTTGAAGG CGTAGTACGC	900
TTGAACGTA AAGGACGCGA TAAAAACAA GTGTCTGTTT ACCCAATCGC TAAATAAAAA	960
GGTCCATTGA ACCTTTTATC CCGAACCTTG AAATGTAGAG GTGAGGAAGC TAGAAACAGC	1020
TTAAAAAT	1027

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1990 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CGGTTCAAAT GGTGCAGGTA AATCTACGTT AATTAATTCT ATTGTAGGTT TTCAAGAGAT	60
TTATTTAGGA GAAATAGAGT ATTGTGATAA AGATTGATA GTTAGTTCTC AACCTTTTGC	120
TCATTTAGGC TTTACTCCTC AAACCACAGT AATTGATTTT TATACTACTG TGAAGGACAA	180
TGTAATATTG GGGCTGAACC TTGCTGAAA GTTTGGGAAA AATGCTGAGA AGTTGTGTCA	240
AATAGCCTTA GAAATTGTTG GGTAGCTGA TAAAAAAAT AATTGGTAG AAACATTGTC	300
AGGTGGACAA CTGCAACGCG TCCAGATTGC TAGAGCAATA GCTCATAATC CAGATTTTTA	360
TATTTTAGAT GAACCTACCG TTGGTTTGA TACTGAATCT GCCGAAAAAT TTTAATGTA	420
TTTAAAGAT AAGAGTTTGG AAGGAAAAC TATTATCATA TCTTCACATG ACATAAATCT	480
ACTCGAAAAG TTTTGTA AAAATACTTTT TTACAAAAT GGCTCCATAT CATTTTGTG	540
TGATATGCGT GACTTTGTAG ATAATTCAAC TATCAAATTA AATTTTTCAT TGCAGAATAG	600
AATTTCTAGA TATCAAATTG AATTTTGA AAATTTTGA TTAAAGTTC ACATCGAAGA	660
TAATGATAGT TTTACAATAG AAGTCCCTAT AGAAGAAAAG ATCTTAGATG TTATCAATGA	720
GGTAGGAAAA GCATGTGAAA TTA AAAACTT TTCAACAAGT AAATTAACCT TACAAGAAAG	780
TTATTTGCAA AGAATAGGAG GAGAAAAATG AAGGCTGATC AATTAAGGCA CAAATCGGAC	840
TTAGGTTTAA GAGGTCTAGC GATTATTGCT AAAAATGAGA TTATTGCTTT TTTTGAAGT	900
AAAGGTTTAA TTATTCTCA GTTCTACAA CCAATCTTAT ATGTTGTTTT TATAATAATA	960
GGATTAAATT CTTGATAAAA GAACATTCAG TTTAATGATA TAAAAACCTC TTATGCAGAA	1020
TATACAATCA TTGGTGTAT AGCTTTATTG ATAATCGGGC AGATGACTCA AGTTATTTAT	1080

1251

AGGGTGACAA TAGATAAAAA ATATGGGCTA CTTGCTCTTA AGTTATGCAG TGGAGTTCGT	1140
CCTTTATATT ATATTTTAGG GATGAGTATC TATTCTATAT TAGGGTTGAT AGTTCAAGAA	1200
ATTATTATAT ATATAATTAC GTTAGCGTTT GAGATAAATA TCGCAATGGA TAGATTTTTT	1260
TATACAGTTT TGTATCTAT TGTGTTTTA TTATTTTGGG ACTCCCTTGC AATTTTACTT	1320
ACAATGTTTA TCAATGATTA CAGAAGACGT GATATTGTAA TACGTTTTGT ACTAACACCG	1380
CTTGGTTTTA CAGCTCCTGT TTTCTACTTA ATAGATTCTG CTCCTAGTAT TGTGAGATGG	1440
ATTGGTCAGT TAAATCCCTT AACTTATCAA TTAACATTTT TGAGAAACTT TTATTTTAAA	1500
AATCAACAA CTTTGGGAAT AGTTTCTTA TTGTTAACAT CATTACTTGT CCTTATATCT	1560
GTATCTTTTA TTATACCAAA GATAAAATTG ATACTGATAG AAAGATAAAA GTTGGGTCAT	1620
CCAACTTTTT TGTGTCTCC CGAAAACCAC TAGCTATGCT AGTGGTTCCA TAGAGCTTTT	1680
AGCGTGGTAA CAAAAGAAC CTCCTAAAT GATAAGATAG AAGTGGTTT TCCGCCACTA	1740
CAACATATCA TACAGGAGGT ACCTCATGAG AGAGGATAAT CAAAGTTTAT CACATACCAC	1800
ATGGAATTGT AAATATCATA TTGTTTTTGC ACCCAAATAT CGTCGTCAA TCATTTATGG	1860
CAGATACAAA GCTAGTATCG GAAGAATCAT ACGTGACTTA TGTGAGCGTA AGGGTGTAAAT	1920
AATCCATGAA GCGAATGCTT GTTCAGACCA TATTCACATG CTTATCAGTA TTCCTCCGAA	1980
ACTTAGTGTT	1990

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GAACATATTT GCATATATTT CTAGCAATGA TCATGGCGAA TCTTGGTCTG CACCAACTTT	60
ATTACCTCCT ATAATGGGAC TTAATCGGAA TGCGCCATAT TTAGGTCCTG GACGTGGAAT	120
CATTGAAAGC TCAACTGGAC GTATTCTTAT TCCGTCTTAC ACTGGTAAAG AGTCTGCGTT	180
CATTTATAGT GACGATAATG GAGCATCTTG GAAAGTTAAA GTAGTGCCAC TTCCTTCTAG	240
TTGGTCAGCA GAAGCACAAT TTGTAGAATT GAGTCCAGGA GTAATTCAAG CATATATGCG	300
TACAAATAAT GGTAAAATTG CATATTTAAC AAGTAAAGAC GCAGGTACTA CTTGGAGTGC	360
ACCGGAATAT TTGAAATTTG TTCAAATCC AAGTTATGGA ACACAATTAT CAATCATCAA	420

1252		
TTATAGCCAA TTGATTGATG GTAAAAAGGC TGTCATTTTA AGTACTCCAA ACTCCACAAA	480	
TGGTCGTAAA CACGGACAAA TTTGGATTGG TCTAATTAAT GATGATAATA CAATTGATTG	540	
GCGTTATCAT CACGACGTTG ATTATAGTAA CTATGGATAC TCATATTCAA CATTGACAGA	600	
GTTACCAAAT CATGAAATTG GATTGATGTT TGAAAAATTT GATTCATGGT CTCGTAATGA	660	
ACTTCATATG AAAAATGTTG TACCATATAT AACATTTAAG ATTGAAGATC TGAAAAAGAA	720	
TTAAAGCTGA AATTGAAAA TATATAAAAA GAGGATAAAA ATTATGGTAA ATTACGGTAT	780	
TGTTGGAGCT GGATATTTTG GAGCTGATTT AGCTCGCTCA ATGAACAAAA TTGAAGATGC	840	
AAAAGTGGTT GCGGTATTTG ACCCAAATCA TGGAGAAGAA GTTGCTCAAG AGTTGGGATC	900	
AGATGTTTGT GCAAGTTTAG ATGAACCTGT AGCACGTGAA GATATTGATT GTGTGATCGT	960	
AGCTTCACCT AGCTACCTTC ACCGTGAACC AGTTGTGAAA GCTGCTCAAC ATGGCAAACA	1020	
CGTATTTTGT GAAAAGCCAA TTGCATTGTC TTATGAAGAT TGTAAGCCA TGGTTGACGC	1080	
ATGTAAAGAA AATAATGTCA TCTTTATGGC TGGTCACATC ATGAACCTCT TTAACGGTGT	1140	
ACACCATGCT AAAGAATTGA TTAICTAAGG TAAATCGGT AAAGTTCTTT ATTGCCATGC	1200	
TGCTCGTACA GGTGGGAAG AACAACAACC AACTGTATCA TGGAAGAAAC TTCGTTCTCA	1260	
ATCTGGAGGA CATTTGTACC ACCATATTCA TGAATTAGAT TGCATTCACT TTATCATGGG	1320	
AGGACTTCCT GAAAAAGCGA CAATGGTAGG AGGCAATGTA TATCATAAAG GTGAAAACCT	1380	
TGGTGATGAA GATGATATGC TCATTGTAAA CTTAGAATAC TCTGATGATC GTTATGCTGT	1440	
TTTGGAATAT GGTAATGCTT TCCGTTGGGG TGAACACTAC GTCTTGATTC AAGGAACTGA	1500	
AGGAGCTATC AAACCTGACT TGTTCAATAC TGGCGGTACT CTTCGTGTTA AAGGTGAAGG	1560	
AGAATCACAC TTCTTAGTTC ATGAACTCA AGAGGAAGAT GATGATCGTA CAGCTATCTA	1620	
TACCGGTCGT GGTATGGATG GAGCAATTGC GTACGGTAAA CCAGGAGTAC GTTGCCCAT	1680	
ATGGTTGCAA ACATGTATTG ATAAAGAAAT GGAATATCTA CATGACATCA TTAAAGGTGG	1740	
AGAAATTACA GAAGAATTTG AAAAATCTCT CAATGGTGTA GCTGCTTTAG AATCAATCGC	1800	
TACCGCTGAT GCATGTACTT TATCAGTTAA AGAAGATCGA AAAGTAAGTC TTTCAGAAAT	1860	
CACAAATGCT TAACTTTTGT AAAACAGAAT AGTAAATTCT TGTCATTATA TAATTTCTAA	1920	
AGTTCTGTGA TACAACATCAT TGAATAAAGA AATAGAGATG GGAAGGGAT AATGCCCAGT	1980	
CCCATTTTAT ATCAAAAAGT AATGAGATCA AAAATGTGGG AGTGTTGAAA TGAAGATTAT	2040	
AGGTATCGAT ATTGGCGGAA CAACAATTAA GGCAGATTAA TACGATGAGT TTGGAACGAG	2100	
TTTGAATCAT TTCAAAGAGA TAGAAACAAT TATTGACTAT GATTTGGGAA CGAATCAGAT	2160	
ATTAAATCAG GTCTGTGATT TAATTGGTGA GTATACTTTA AATCATTCOA TTGATGGTGT	2220	

1253

TGGGATTTC	ACTGCTGGAG	TTGTTAATGC	TAATACTGGA	GAAATCATCT	ATGCAGGCTA	2280
TACAATACCA	GGGTATATCG	GAGTAACTT	TACTGCCGAA	ATAGAAAAAC	GTTTGGGTT	2340
GTATACTTTT	GTTGAAAATG	ATGTTAATTG	TGCTGCATTA	GGTGAATTGT	GGAAGGGACA	2400
AGCCAAAGAT	AAGAAAAATG	TAGTAATGGT	TACTATTGGA	ACAGGTATAG	GAGGCAGTAT	2460
TATTGTCAAC	GGACAAATTG	TTAACGGATT	TAATACTACT	GCTGGTGAAG	TAGGTTATAT	2520
TCCTGTAGGT	AATTCGGATT	GGCAAAGTAA	AGCCTCAACA	ACCGCATTGA	TTCATTTATA	2580
TCAAAAAAG	AGCTTGAAAA	CTAATCAAAC	TGGACGTACT	TTCTTCACTG	ATTTAAGATC	2640
TGGAGATAAA	GTTGCTGAAG	AACTTTTGA	AATTTTGTGA	GAAAACTAA	CAAAAGGTTT	2700
ATTAACGATT	TCTTATCTAC	TTAATCCAGA	AATTCCTATA	TTAGGAGGTG	GGATTCTGGA	2760
TAGTAAGGAT	ATTTTGTTAC	CTGAAATTCA	AAGTTCTTTA	GCTAAAAATG	CAATGGATAA	2820
TAGGTTTTTA	CCTAAAAATC	TTGTGGCAGC	TACATTAGGA	AATGAAGCTG	GTCGTATAGG	2880
AGCTGTAAAA	AATTTCTTAG	ATAGAATTTT	TAATAAATAG	TATGTAAGAT	AAGGAGGTGT	2940
CACAATGACT	AACTCTGTAT	TTTCGACAAT	GCAAGATATT	GAGAATGTTG	CAACCGATAT	3000
TATAAAATCA	TATGATAATG	AGATTTATAC	TTATAAAGCT	GTTTCCCAAG	AAGAATTGGA	3060
AAAAC TAGAA	AAAAGTTATG	ATGAAAAAAG	TCACGAAGAA	TTAGTTTCAA	TAGAAAGCAA	3120
TTTAGAAATG	AAACAACAGA	ACCTTATTGA	TGAGGTAAAT	AAAACAATCA	AGGAAAAATGA	3180
TGCAAATATT	CAGTATATTT	CATCAAGTAG	GAGAGGAGAA	TTGTAGAAA	AAATTATTGG	3240
TAGGGTGGTA	GAAAAATATG	GCCATTAGTC	AGATGAAAAG	AATCTCTCTA	CTATTTTCTA	3300
AAAGTAGTCT	TGATGATGTT	TTAAAACTA	TTCAAGAACT	AGAGTCAGTG	CAGTTCCGTG	3360
ATTTAAAGGT	TCAGGATAAC	TGGTCAGAAG	CTCTAGAAAA	AGATGAAGTT	GTATTTCCAA	3420
CTATTCAAAT	TTTTCATACT	TCTAATTCCA	ATCATGGGGT	TATTGAGGGA	AATGATGCCT	3480
TGACTTATTT	GATGAATCAA	CAACAACATT	TAGAAGCAAC	TGTAGAGAAA	TTACAAGAAT	3540
ACCTACCGAA	AGAAAACACG	TTTAAATTAT	TGCAGCAACC	TCCGATAACT	ACCTCTTATG	3600
AAGAATTAGA	GAAATTTGGT	AAAGCTAATG	TTGCTGAGGG	TGTTCTTAAA	AAAGTGAATC	3660
ATCAAATTAA	CAGAGTTCAT	GAATTAGAAA	GACACATTCA	AAGTAATAAT	GAGGAAATAG	3720
AGCGATTAAT	AAAGTGGGAA	AAATTAGAAA	TTGTTCTCTG	GAATTAGAAA	CAATTTTCTT	3780
TCTGTAAAGG	AAAAGTCGGA	ACAATTCCAA	GGACTGAAGA	TAATCGCTTA	TACAATAGTC	3840
TTTTAGAAAA	CAATATTGAA	GTTCAAGAAA	TATTTTCTAA	TGATAGAGAG	TACGGTGTGTG	3900
TTGTTTCTA	TCAGTCTAGT	TACTCTATAG	ATTTTGATGA	ATACTTATTT	GAACCATTTG	3960

1254

ATTATTCTAG AAAGGAATTA CCGAAGCAGC GAGTAGTAGA TTTAGATCAA GAAAACATGC	4020
AGTTAATAAC TGAAAAAGAG AATATTATCG CATCGTTGCA AGATTCAAAG AAATATTTGA	4080
TAGATTTACA ATGGCAAATA GACTATATTT TATCTATCTA TGCTCGTCAA ATCTCTAAGA	4140
ATAACTTTTT GTGCACTCCG CATCTAGTTG CATTAGAAGG ATGGATAGAA GAAACTCGTA	4200
TTTTATATTT TATAAAAGTT ATGGATGAGC ATTTTGGACA TTCTATTTAT ATTTATGAAT	4260
CGGAAACATT GACGGATAAT CAAGATGAAA TACCTATCAA ATTAACGAAT CATTCTTTAA	4320
TTGAACCATT TGAATTATTG ACAGAAATGT ATGCTCTGCC CAAATATTAT GAGAAAGATC	4380
CTACACCTGT ATTAGCACCA TTTTACTTTA CATTTTTTGG AATGATGGTT GCTGATTTAG	4440
GCTATGGTTT ACTATTGTTT TTAGGAACAA TGTTAGCATT AAAAATTTTT CATCTACCTT	4500
CAGCAACTAA GAGATTTTTA AAATCTTTA ATATATTAGG GGTAGCCGTT GCAATTTGGG	4560
GTGGAATCTA TGGCTCATTT TTTGGATATG AGTTGCCATT TCATCTGATA TCTACAACCT	4620
CTGATGTCAT GACTATATTA GTAGTGTCAG TTGTGTTTGG GTTTATTACA GTATTTGCAG	4680
GTTTGTTAGC TTCAGGACTA CAAAAGTAA GAATGAATAA ATATGCAGAA GCATATAATT	4740
CAGGATTGTC GTGGTGTGTT ATTCTG	4766

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CCTTTTAGAA AAAATTAAAG AATACGACAC CATTATCATT CATCGTCATA TGAAACCAGA	60
CCCTGATGCC TTGGGAAGTC AGGTGGGATT GAAAGCCTTG CTGGAACATC ATTTCCCAGA	120
AAAAACCATC AAAGCCGTCG GTTTTGATGA ACCAACTCTT ACTTGGATGG CTGAGATGGA	180
TCTTGTGAA GATAGAGCCT ACCAAGGCGC ACTTGTCATC GTCTGTGATA CAGCTAATAC	240
TGCTCGTATC GATGATAAGC GCTATAGTCA AGGTGATTTT CTCATTAGA TTGACCACCA	300
TCCAAATGAT GATGTATACG GTGACCTGTC TTGGGTCGAT ACTAGTTCAA GTAGCGCTAG	360
aGaTGATTAC CCTATTGACC CAAACAACCC AACTAGCCTT GGCAGATCGC GATGCTGAGT	420
TGCTCTTTGC AGGAATTGTC GGTGATACAG GTCGCTTCCT CTACCTTCT ACCACTGCAC	480
GGACTCTTCG CCTGGCTGCT TATTTGAGAG AACATAACTT TGACTTTGCG GCTCTCACTC	540
GCAAAATGGA CACTATGAGC TACAAAATTG CTAAACTGCA AGGCTACATC TACGACCATC	600

1255

TGGAAGTGGA TGAAAATGGT GCTGCTCGCG TTATCCTGAG TCAGAAAATC TTGAAACAAT	660
ACAATATAAC CGATGCTGAA ACTGCGGCCA TTGTAGGTGC ACCTGGACGC ATTGACAGAG	720
TGAGTCTCTG GGAATTTTT GTGGAACAGG CTGATGGCCA CTACCGAGTT CGCTTACGCA	780
GTAAAGTCCA TCCTATCAAT GAAATTGCCA AGGAGCATGA TGGTGGAGGC CACCCTCTAG	840
CAAGTGGTGC TAATTCCTAT AGCCTAGAAG AAAACGAAAT CATCTACCAA AAGTTAGAAG	900
ACTTGCTTAA AACTGATAA AATACTTGCC AAACCTTTCA GAATCTGATA GACTAGTATA	960
GTAACAATCT ATGGCTCGCA AAGAGACCAT GGCAGAAAGG AAATATTGCA AAATGAAAAT	1020
AGATATCCAT CCAGAATATC GCCCAGTTGT CTTCATGGAC ACAACTACTG GTTACCAATT	1080
CCTTAGCGGT TCAACAAAAC GCTCTAACGA AACAGTTGAG TTCGAAGGCG AAACCTTACCC	1140
ATTGATCCGT GTGGAATTT CATCAGACTC ACACCCATTC TACACTGGAC GTCAAAAGTT	1200
CACTCAAGCA GATGGACGCG TGGATCGTTT CAACAAAAAA TACGGTCTCA AATAATGATA	1260
AGAGAACAGT TTTGGCTGTT CTTTTTGT TCTTGAAATC AACTGCTGTT TTCATGTTCC	1320
AGACTCATCT GTAGGTTGCA TTTCCATGCT ACTAGGCAGG AAGGAAATAG CTGTTTCAAC	1380
ACGTCCATAA TGAGCTATAC TATTGTCACG AACCACACTT TCATTGATGG TCCAAGTGGA	1440
ATTCAATTTT TTAAGGCTT CTCGGACTTT TTCCAAATCT TTGGAGGCAA TGGCCTGCTC	1500
TAAGGTTTCA AAACGAGGAC TTATACTCAT CTGCTTTCAA AAAGCATTC AGTCCATCTC	1560
CGATTACCGA TGGACTTTAT CACCTCCTTC TCCAGTCCTT GTATGACATC TTGAAGTTGA	1620
TTCATGACAT CTTCCAAAGT TC9AAAGGCT TTATTCTTAA ATCCACGTTT ACGAATCTCT	1680
TTCCACACTT GTTCAATGGG TTCATCTCTG GTGTGTATGG AGGAATAAAG GTAAAATCAA	1740
TATTAGTCGG AATATTTAAG GTACTTGATT TATGCCATAT AGCATGTGCC ATAACGAGTA	1800
AAAGGATAAG CTTGTGAAAG CTCTTCTAAA AAGGCGTTCA TCCACACTCC TTTTATATAA	1860
CCTGAAATAA GGCATCAATT GTAACAAATT CTCCTGCCTC TGTAGCCTTC AAATGACGGG	1920
CAAGAAAGGC TTTCTCTTCC TCAACTGTCA TATATGCATG GTTACGACCA CCACGTGTTT	1980
CTTGAAGGAG AGAGTCGAGT CCGAACTCCT CATATTTTTT TACGTTTCGC CAAATCGTTG	2040
TTTGATTACA GTCTAAAAGC TCTATAATCT CTTTATAAGA TTTGCCCATC AGACGAAATA	2100
TAGTAGATTG AAAC TAGAAT AGTACACCTC TACTTCTAAA ACATGTGTAG AAATCGATTT	2160
GTCTGTCTCT TGTTCATTT TACTATAGAA CGATTTGAAG GCGTTTATAA TATTTAGCTG	2220
TACGAGAGTC TTTTAAAAGT GTTTTGATGG TTTGGATTTT TTCTTTAGTT GATTTTCATAT	2280
TACTATTATA TAATGCTTTT TGATTTTAGT CTGGTATAAA TATTGCTTTC CTCCAAAATG	2340

1256

GTCATAGTTT TACTGGCAAA TCTAACATAT CACGGATAAA TTAACAAGTG ATTTCTGAAT	2400
TGCTAAACAT TTTCTTTTCT TATAGCATAC TTAAAGATT TGTCTTTGAG AAAGATATTT	2460
CCAAGAAAA CGTTCGTTTT TTGG	2484

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CTAGATATAG CTATAATTTT ATTTATAACA AGAGGATAGA AATGACCGAA TTAGAAAGAA	60
AAAAATCGAAA AATTAGCTAA GAAATATTCT GATAACTTAA ACATCAAAGT TCAAGAGAGA	120
GTTCGTGAAA TGGCAAATGA TAATAAGAGC CATTATTTGA TATACAGAGT TTTAGGTATT	180
TCATTTGAAG AAGGAGAAAA TATCGATTG TATCAAAATA AAGGTCGTTT TTTATACAAA	240
TATGCTGGTT CATTTTGTAGA AGAAGCTGCA GTACTATGCT TTAACGAAAA ATTTGGTACA	300
GAAAATACTT AAAAAGTTAA CATTCCTAAT TCTGAAAGTA CAAAACCTAA GACTTTTGAA	360
ATTGATTGTT TAGTCGGAGA AAAACACGCA TACGAAATAA AATGGTGGGA TGCAACTACA	420
GATGGAGACC ATATAACTAA AGAACACACT AGAATAAAAG TTATTCATAA CAAAGGATAT	480
ATACCAATTC GGTTAATGTT CTACTATCCA AATAGAACTC AAGCTATAAA AATTCAGCAA	540
ACTTTAGAAA CATGTGTATA CGGTATTGGA GGGAAATATT ATTATGGAGA TTCTGCCTGG	600
GAACATTTAA GAGCAGTGAC CGGTATTGAT TTAAGTAGTA TTCTAACAGA TATTGCAAA	660
AAAAAAACAG GGGTAAAATC AAAATGACAG TATTAAAAGG AGATAACTTA GAAATATTAA	720
AAACTATTGA ATCCTCAAGT ATTGATTTAA TCTATATGGA CCCTCCTTTC TTTACACAGA	780
AAACCCAAAA ATTATCTAAT AACAAAAATA TTATGTATTC ATTCGAAGAT ACGTGGACTT	840
CGATTGAGGA TTACAAAGAA TTTTGTCTG TAAGATTAGA AGAATGCAAA AGAGTGCTAA	900
AAAATAGTGG CAGTATTTTC GTTCATTGTG ATAAAATTGC AAATCATCAT ATTAGATTAA	960
TTTTAGATAA TATCTTTGGA GTAGATATGT TTCAAAGCGA AATTATATGG AACTATAAAC	1020
GGTGGTCTAA TTCAAAAAAG GGATTATTGA ACAATCATCA AAACATTTAC TTTTATTCAA	1080
AGTCAAAAGA TTTTAAATTT AATACAATTT TTACAGAGTA TTCTTCTACT ACAAATATCG	1140
ACCAAATACT AGTGGAAACGA AAACGAGATG GAAACTCTAA AACTATATAT AAGGTTGATA	1200
ATAATGGTAA CTATATTCTA GCAAAAGAGA AAAATGGAGT TCCCCTTCA GATGTTTGGA	1260

1257

ATATACCATT TCTTAATCCA AAAGCTAAAG AAAGAGTAGG TTATCCTACA CAAAAACCTA	1320
TTCTGTTATT AGAACAAATT ATAAAGATTG CTAAGTATA AAATGATATA GTTTTAGACC	1380
CGTCTGTGG AAGTGGAAC ACTTTAGTAG CCTCCAAGAT TTTGAATAGA AATTATATGG	1440
GGATTGATTT ATCTGAGGAA GCTATCAATA TAACTCAGCA ACGTCTGGAA AATGTTATAA	1500
AAACAAGTTC AAATTTATTG AATAAAGGAA TCGAAGCATA TAGAACCAAA ACTGAGGAAG	1560
AGGAAAACAT TCTTAAATTA TTACAGGCAA AAATTGTTCA AAGAAATAAA GGAATTGATG	1620
GTTTTTTACC TAAACATTTT CAAAAAAAC CGATACCTAT AAAAATTCAA AAAAATAATG	1680
AATGTCTGAA TGAGAGTATC TCTTTATTAC AGAATGCTAT AAACCTCAA AACTTGATT	1740
TTGGAGTAGT TATAAAAACT CATTTCG	1766

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 748 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CCGAAAATCA AATTCAAACC ACGTCAACGT CGCCTTGCCG TACTCAAGTA CAGCCTGCGG	60
CTAGTTTCCT AGTTTGCTCT TTGATTTTCA TTGAGTATTA AACTAAATTA AATAATATTA	120
GCGCGGAGAA TTTCTAATTC TTCCTTGCTC AAGCGACGCC ATTCCCCTCG TTCTAGGTTC	180
TCATCTAATA CTAAAGTTC CATAGTCAAT CGTTGCAAGT CCACCACTTC CTTGCCACAG	240
TAGCCACCA TACGCTTGAT CTGATGAAAC TTCCCTTCTG CAATGGTCAC ACGGATTG	300
CTTTGATTCT TTTCTGTATC TATGGATACA AGCTCCAGTA TAGCGGGTTG ACAGGTAAG	360
TCTTTGAGAG GAATACCCTC AGCAAAATGTC TCCACATCTT CTGGGGTCAT GATTCCCTTG	420
ACTTGTGCCA GATAAGTCTT GTCCACATGA CGCTTGGGCG AAAGAAGAAC ATGAGCCAGC	480
TGACCATCAT TGGTCAAGAG CAAAGACCA TGCCTGTCAA TATCCAAGCG TCCTACTGGG	540
AAACTTCCT TACTCCGCGC CAAGTCATCC AACAAGTCCA GAACGGTTCT GTGCTTGGGA	600
TCCTCAGTCG CTGAGATAAC TCCTTTGGGC TTGTTTCATCA TGTAGTAGAC AACTCTTCA	660
TACTCCAACA CTTGCCCATC AAAGCGAATC TCATCTATTT TTTCATCAAT CTGCAATTTA	720
GCTGATTTTT CTTTTTGACC ATTTACAG	748

(2) INFORMATION FOR SEQ ID NO: 237:

1258

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

AAAAGATTAC ATTGCAACAA TTGAAAATTA TCCAAAGGAA GGCATTACCT TCCGTGATAT	60
TAGTCCTTTG ATGGCTGATG GAAATGCTTA TAGCTACGCT GTTCGTGAAA TC GTTCAGTA	120
TGCTACTGAC AAGAAAGTCG ACATGATCGT GGGACCTGAA GCTCGTGGAT TTATCGTGGG	180
TTGTCCAGTT GCCTTTGAGT TGGGAATTGG TTTTGC GCCT GTTCGTAAGC CAGGTAAATT	240
GCCACGCGAA GTTATTTCTG CTGACTATGA AAAAGAGTAC GGTGTCGATA CCTTGACTAT	300
GCACGCGGAT GCCATTAAGC CAGGTCAACG TGTCTTATT GTAGATGACC TTTTGGCGAC	360
AGGTGGAAC GTTAAGGCAA CTATCGAGAT GATTGAAAAA CTG GTGTG GTG TTATGGCAGG	420
TTGTGCCTTC CTTGTTGAAT TGGATGAATT GAACGGCCGT GAAAAAATTG GTGACTACGA	480
CTACAAAGTT CTTATGCATT ATTAATGAAA ACAGTCCCTA GGGCTGTTTT CTCTACACTA	540
GGATATAAAA ATAGACTATA ACTAGTTAGA GAAAACTAT AATTGAAAAC TATATCTTCT	600
TGCAGTATAA TAAAGGACT AAGTGTGGA GATTTGTCTT CAAACATATG CAATTATTCC	660
TGAAAGAGTA CAGTTAGGAG AGGGTTATGC CGATTCGAAT TGATAAAAAA TTGCCAGCTG	720
TTGAGATTTT ACGGACAGAG AATATCTTTG TCATGGATGA TCAACGTGCT GCCCACCAG	780
ATATCCGTCC TTTGAAGATT TTAATTTTAA ATCTCATGCC ACAGAAAATG GTCACAGAGA	840
CCCAGTTGTT GCGCCACTTG GCTAATACAC CCCTACAACCT GGATATTGAT TTTCTCTATA	900
TGGAGAGCCA CCGTTCTAAA ACAACTCGTT CAGAGCACAT GGAGACCTTC TATAAACTT	960
TTCTGAAGT CAAGGATGAG TATTTTGATG GGATGATCAT CACGGGTGCT CCAGTTGAGC	1020
ATTTACCATT TGAGGAAGTG GACTATTGGG AGGAATTTAG ACAGATGCTT GAGTGGTCTA	1080
AGACTCATGT CTATTCGACC CTTCATATCT GTTGGGGGGC TCAGGCTGGG CTTTATCTGC	1140
GCTATGGTGT AGAAAAATAC CAGATGGACA GTAAGCTATC AGGTATTTAT CCTCAGGACA	1200
CCCTAAAAGA GGGTCACCTT CTATTTAGAG GCTTTGATGA TAGCTATGTA TCCCCTCATT	1260
CACGGCACAC GGAGATTTCT AAGGAAGAGG TCTTAAACAA GACCAATCTC GAGATTTTAT	1320
CAGAAGGACC TCAGGTTGGG GTTCTATTW TGGCCAGTCG TGATTTACGA GAAATTTATA	1380
GTTTGTGTC TTTGGAGTAT GACCGTGATA CTTTGGCAAA AGAGTATTTT CGAGATCGTG	1440
ATGCAGGTT	1449

1259

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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TACCCGCTTC TTTCAAGAGT TGGAGCAGGG CTTGTTTGCG ATCTTTTGTC ATAGTTCTTC      60
CTTTTAACGG CGTTTTCGAA GCACCTTATA GACAGCTAGT GCTAATGTAT AGTCTACCAT      120
ACTATGGATA ATTGTACCAA ATCCAACTAG TACAAATAGA ACATAAAACA TATTTTCTAC      180
ATTGGTACCA GAAGTTGCGT AAAAAACGAC ACAGGCCAAT ACTTCAGCAA GGGCATGAAC      240
AACAGCCAAA ACAAAGTTGA AAATCCAGGA AGATTTTGGT TTATCTAGGG TATCGGGGAA      300
TTTTTGTAGG TAAAGAGCTC CTAAAGCACC AAAAGATATA TGGGAAAAAG CCCGAAAAAC      360
GATAACCATG GGATAGCCAG CCATCAAAAA TCCAAACTA GAGGCTAGGA TGACAAAAAC      420
TGCCATCAAG GGCGACAAGA ACATGGCTAT AAAAAAGCG ATGTGGCTCC CCAAAGTATA      480
GGAAGCAGGT GGAATGACAA TCTTGAAAGG CATAACAATT GGAATCAAAA TCGCAATAGC      540
CGTTAAAAGG GCTGTCATTG TCATAAATTG TGTCTTTTTC CGTGTATTCA CAAGAATCTC      600
CTTTTAACT GCATATACAC TAGTATGGTA CAATAACCA GACAATAAAG CAAGAATTTA      660
CTTGGGTTTA TAGATCATTT TTTAGTAAA AGTTATAGTA GATTGAAACT AGAATAGTCC      720
ACCTCTACTT CTAAACATT GTTAGAAATC GATTTGGCTG TCCTGATCGA TTTGTCCTGT      780
TCTTATTTTCG TTTTACTATA GTAAAGATT CATTAAGGAG AAAGTGTATA GAGCAAAATC      840
TCCACCTTCA GGTTTGAAA GCGGAGATTG TTTTATTATT TTTCCAGGGT TTGTAGTCGT      900
GGGA                                                                    904
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(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

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CACTCAAACA TGACTTATAT CAAGACGGAT GGACTTCAAG ACGATGCCAA TCGCTTGAAT      60
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1260

CGTAACATTC AGTTTGGTGT TCGTGAATTT GCAATGGGAA CAATCTTGAA CGGGATGGCC	120
CTTCATGGTG GACCTCGTGT ATACGGTGGA ACTTCTCTCG TCTTCTCTGA CTATGTGAAG	180
GCAGCTGTCC GCTTGTGAGC CTTACAAGGA CTTCTCTGTA CTTATGTCTT TACCCATGAT	240
TCAATCGCAG TTGGGGAAGA TGGTCCGACT CATGAACCAG TTGAGCATTT AGCAGGTCTT	300
CGTGCTATGC CAAATCTAAA TGTTTTCCGT CCAGCAGATG CGCGTGAAAC GCAAGCAGCT	360
TGGTACCTTG CAGTGACAAG TGAGAAAACA CCAACTGCCC TTGTCTTGAC ACGTCAAAAT	420
TTGACTGTTG AAGATGGAAC AGACTTCGAC AAGGTTGCTA AAGGTGCTTA TGTGTATAT	480
GAAAATGCAG CCGACTTTGA TACCATCTTG ATTGCGACAG GTTCAGAGGT TAATCTTGCT	540
GTCTCAGCTG CTAAAGAATT GGCTAGTCAA GGCGAAAAA TCCGCGTAGT CAGCATGCCA	600
TCTACAGATG TCTTTGATAA ACAAGATGCA GCTTACAAGG AAGAAATTCT TCCAAATGCA	660
GTCCGCCGTC GTGTTGAGT CGAAATGGGT GCAAGTCAA ACTGGTACAA ATATGTTGGT	720
CTCGATGGTG CCGTTCTAGG TATTGATACT TCGGAGCCTC TGCCCCAGCA CCAAAAGTAT	780
TGGCAGAATA TGGCTTTACT GTAGAAAATC TTGTAAAAGT TGTTCGAAAC TTGAAATAAT	840
CCTAAAAATC AGGGCGTAAG CTCTGGTTTT TCTTACCAGA AAAGTAAGGT ACAATCTTGT	900
AAAAGTAGCT GAAATTTGAT ATAGTAGTCC TATGTAAAAG ACAAAG	946

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2764 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CGGGGCTCCC TAGTTCTTAG GGAGCTATTT TTGTTTTTC AAGAAGTTAT CTTCTGTAT	60
TTTATACTCA ATGAAAATCA AAGAGCAAGC TAGGAACTA GCCGTAsTG CTCAAAACAC	120
TGTTTTGAGG TTGTAGATAA GACTGACAAA GTCAGGAACA CATATCTACG GCAAGGCGAC	180
GTGACGCGG TTTGAAGAGA TTTTCGAAGA GTATTAGTTG TGAATCTGGT GCAGTCGTCC	240
CAGATTATTC TTATTAGTAG GGTCTTGTTT TCTATATCCC CTCGTAGTTA ACAAGACCTT	300
GAGCATTTTA GAAAGAGGAA TCTATGTCTA CGAAATATAT TTTTGTA ACT GGTGGTGTGG	360
TATCGTCCAT TGGGAAAGGG ATTGTGGCAG CGAGCTAGG CCGTCTCTTG AAAAATCGTG	420
GTCTCAAAGT AACCATTCAA AAGTTTGACC CTTATATCAA TATTGATCCG GGAACCATGA	480
GTCCTTACCA GCACGGGGAA GTTTTTGTGA CAGATGACGG AGCTGAGACA GATTTGGACT	540

1261

TGGGTCAC TA TGAACGTTTC ATCGATATCA ATCTCAACAA ATATTCCAAC GTGACAACTG	600
GGAAAATTTA CAGTGAAGTT CTTCGTAAAG AACGCCGTGG AGAATACCTT GGGGCAACTG	660
TTCAAGTCAT TCCTCATATC ACAGATGCTT TGAAAGAAAA AATCAAGCGT GCCGCTCTAA	720
CGACCGACTC TGATGTCATT ATCACAGAGG TTGGTGGAAC AGTAGGAGAT ATCGAGTCCT	780
TGCCATTCCCT AGAGGCTCTT CGTCAGATGA AGGCAGATGT GGGTGCCGAT AATGTCATGT	840
ATATCCATAC AACCTTGCTT CCTTACCTCA AGGCTGCTGG TGAAATGAAA ACCAAACCAA	900
CCCAACACTC TGTCAAAGAA TTGCGTGGCT TGGGAATCCA ACCAAATATG TTGGTTATTTC	960
GTACAGAAGA GCCAGCTGGT CAAGGAATTA AAAATAAACT GGCCCACTTC TGTGATGTGG	1020
CACCAGAAGC CGTTATCGAA TCGTTGGATG TTGAACACCT TTACCAAATT CCACTGAACT	1080
TGCAGGCACA AGGGATGGAC CAAATTGTTT GTGATCATTT GAAATTAGAC GCACCAGCAG	1140
CGGATATGAC AGAATGGTCA GCCATGGTGG ACAAGGTCAT GAACCTCAAG AAACAAGTTA	1200
AGATTTCCTT TGTGGTAAG TATGTGGAGT TGCAAGATGC CTATATCTCA GTGGTCGAAG	1260
CCTTGAAACA CTCTGGCTAT GTCAATGATG CAGAAGTTAA AATCAATTGG GTCAATGCCA	1320
ATGATGTGAC AGCAGAGAAT GTAGCAGAAC TCTGTCTGA TGCGGACGGG ATCATCGTAC	1380
CAGGTGGTTT TGGTCAACGT GGTACAGAAG GGAAAAATCCA AGCCATCCGC TATGCGCGTG	1440
AAAATGATGT TCCAATGTTG GGAGTCTGCT TGGGAATGCA GTTGACATGT ATCGAGTTTG	1500
CTCGTCACGT TTTAGGTCTT GAAGGTGCCA ATTCTGCAGA GCTTGACCA GAAACAAAAT	1560
ACCCTATCAT TGATATCATG CGTGATCAGA TTGATATTGA GGATATGGGT GGAACCTTC	1620
GTTTGGGACT TTATCCGTCT AAGTTGAAAC GTGGCTCTAA GGCTGCTGCT GCTTATCACA	1680
ATCAAGAAGT GGTGCAACGC CGTCACCGTC ACCGTTATGA GTTTAATAAT GCCTTCCGTG	1740
AGCAGTTTGA GGCAGCAGGT TTGTCTTTT CAGGAGTTTC TCCAGACAAT CGTTTGGTAG	1800
AAATCGTGGA AATTCCTGAA AATAAATCTT TTGTAGCTTG TCAGTATCAC CCTGAACTGT	1860
CAAGCCGTCC AAACCGACCA GAAGAACTCT AACTGCCTT TGTTACTGCA GCAGTTGAGA	1920
ACAGCAATTA GCAAAATCAG AACCTTTGAG AAAAATCTCA GAGGTTTTTT GCATACGATG	1980
ATATTGCAGT ATATCTGAGG TAGGGTCCT CTGTATGTAC CTGCTACCGT TGAAATCAAT	2040
AGCGACTCCC TCTTGCCCTG TGCTAGTGAA TGGATTATC AGTATATTGA AATGAAATAA	2100
AATTTGAACA AATTAATTCG GAAAGCCAAA TCAATTTCTA GCAAAGTTTT AGGAACTGGA	2160
TTGTATAGTG AATTGAAATA AGATGTGAAC ATCTCTATCA GGAAAGTCAA ATTAATTTAT	2220
AGAAATATTT TAGCAGTCAA GATGTACTGT TATAGATTCA ATACATTATA CTTTTTTAAT	2280

1262

TTAATCCACT ATAGTAAAAT GAAATAATAA CAGGACAAAT CGATCAGGAC AGTCAAATCG	2340
ATTTCTAACA ATGTTT TAGA AATAGAGGTG TACTATTCTA GTTTC AATAT ACTATCCCAA	2400
ATCATTCATA CCTCTCTCAA CTAGATGTAA CTTACAAAAC CCCTGACCTC ATGAGCCACT	2460
TTCTTCCTCC TCATGAGGTC AGTTTTACTT TCTGCTGTTC CAGTATCGTT TTTCCCTCGCT	2520
AGATTTCTCTC AAAAGGGCAG ACTCCTCCCT TGGTGCCTCA CACGATTTTT TCATCTCGAC	2580
TGTTCTTTAA TGCATCATTA ACGACGCTTT TCTTCTAGGT GGTTCATAAG GAACAGGAAG	2640
ATTCAGGTTG ACTTTTCTAA TCCTAGAATA AAGTGCTGAA AACAAATTCGG AATAGGCATA	2700
GAGACTAGAC AATTGAGGA GCTGCTTGGC TCCTGTTCGA ACACATTTTC CCACCACGTG	2760
AAGA	2764

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCGTTTTTTT CATTTGTTT CAG TACTACAAC TACGTTGTAG CGCCCTGCAC ATTGGTTCGT	60
CTTGTTT CAGT TTTCAAAGGT CTTTGTTCACT TGCTTCTCTC AAGCGACAAC TATATTAGTA	120
TATCACAAC T GCTTTCGCTT GTCAACACTT TTTTGAAGAT TTTTAAGTTT TTTTAAACTT	180
TTTTTCATCA AGTGGTCTG ACGCAACATA CCATAGTCCG TACGGGATTC GAACCCGTGT	240
TACCGCCGTG AAAAGGCGGT GTCTTAACCC CTTGACCAAC GGACCTGAGT TGTATTATTC	300
AACTCTTACT ATTATACAGT CTTTTC A A C TTTGTCAACT ACTTTTTTAA ACTTTTTTTA	360
TTAATTTTAC AACAGCTTCA GTTCGAGCTG TATGTGGGAA CATATCGACC GACTGGATAT	420
AATGAAGATC ATAGACTTCT ACTAAGCGTA CCAAAATCACG AGCCAAGGTC GAAACATTAC	480
AAGAAATATA AACCATTTTT TCTGGTACAT AAGTAAGAAT AGTATCTAAT AACTTATCAT	540
CCAGACCTGT ACGTGGTGGG TCAACAATCA AAGCATCTGC TCGGTAGCCT TCCTTG TACC	600
AACGAGGAAT AATCTCTTCT GCCGTTCAG CTTTATAATG AGTATTGTCA AATCCCATT C	660
TTTTAGCATT TCGCTTGGCA TCTTCAATAG CTTCTGGAAT AATATCCATA CCTCTGAGTG	720
TTTTTACTTT CTTTGCAAAG GCAAATCCAA TCGTTCCAAC TCCACAATAA GCGTCAATCA	780
AATGGTCTTC TTTATCAACA TCCAGCGCTT TTAGTGCTTC GCTATAGAGG ACTTCTGTTT	840
GCTCAGGATT TAGTTGATAA AAAGCTCGAG GGGATAGTGA AAATTCATAA TTGAGTACAC	900

1263

CTTCTTGAAT ACTCTCTTGC CCCAGATAA TCTCTGTCTT TTCACCATAT ATCTCACTGG	960
TTTTAGCTGT ATTTGTATTA ACAGCTACTG TCACAACCTC TGGGAAATCT TTAACCAACT	1020
CTTTTACCAA TTGAGTTAAA TTAAGCTGGC GGTTCGTAAC AATAATAATC TGAACCTGTC	1080
CGGTCTTTCT CGCGCGTCGG ACCATAATAG TACGGACACC TAGAACTTTT CTCTCATCCG	1140
TGATTGGAAT CTGGTGATAA GTAAGTAATT CTGCTAAGCG ATTAGCAATC ACTTGGGTTT	1200
CCTTATCTTG TACCAGGCAG TCTTTCAACT CTACTAAATA GTGAGAGTTT TGTGCATATA	1260
AGCCCGCCTT GACCTGATTT TTAAATTTTC GAGTCTGAAA TTGTAACCTA GCTCTGTAAT	1320
ATTTTGGTTC CTGCATTCCA ATAGTTGGAC GAATTCATA ATTTTCATAT CCTGCAGGAG	1380
CAAATTTTTT CAGCGCTTGA TGAAGTAAGT CCGTCTTGAA CTCCAGCTGC TTATCATAAT	1440
GCAGGTGCAT GATTTGGCAG CCTCCGCATT CATTATAAAT AGTACAAGAT GGCACAATTC	1500
GAAATTTAGA CTTCTTGTG ACCTTCAGTA ATTTTGCTTC AACAAAGTTG CGTCTAATAG	1560
AAGTAATCTG ACAATAGATA TCTTCGCCTT TGAGAGCTCC TGGTACAAAG ACTAATGTTT	1620
TTTGGTAAAA GCCGATTCCTC TCACCGTTAA TTCCCATGCG CTTGATTTTT AATGGTATTT	1680
TT	1682

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TTAACTTTGG TCAATTCCTT AAAGTCATCC TCTGTAAGCA TGTCTAACCA TTGATGTTTC	60
CCTTTATGTC TAAAATCACC AATTCGACT ACAGCTATAT CTAAATCTTT CCAACTATTT	120
TTCAAATTTT CAAAATATCT TGATTGCAAA ATACCATCTG CTAACAATTT ATTTCTTGC	180
ACAATCGTTG CATTCATAAA TGTACACTCT CCATGAAATT TTCTAGACAT TTCATAAATC	240
AGTGTATTCA CATGGTATTT AGCGTGTATG TGA CTAGGAC CACCTGCTAG AGGATAGAAG	300
TGAACATTTT GGACACTTTT ACTGTGAATT AAATCTACTA AATTACTTAA ACTTTTCCCC	360
CAAGAAAAGC CAATTTTCAT ATTATCATCA ATTAGATTCC TAAGGACGCC TGCTGCAACT	420
TGAGAAATTC TTTCAGATAA AATTGTTGGA GTATCATCAA ATTCATTTGG AATAATTTCT	480
AAACTTTCCA AACTGTATTT TTCTTTTACA TAATTTTCCA ACTTAAACAT ATGGGTATCA	540

1264

AAATTCTCTA TTTCAATTTT AACAAATCCT ACATTCCTTG CTTCTGTTAA CATTCTACTA	600
ATAGAGGTTC TATAAATTCC TAATTTTGCT GCTATTTGTG ACTGATTTAA GTTTTCAATA	660
TAATACAGAT AAGCAATTTT AGAAAGCAGT TTATTCCTAT CTTGATTCAT ACACTTAACC	720
TCTTACGAAA CTACCTTAAC CATTATCCCA GCATTTTCTA ATGTAGCTAT ATTTTGTTTA	780
GAAAGTTTTT CGTCTGTTAT TACTTCATAG ACTTGACTTA AAGCAAATCT TCTTACTGTA	840
CCTCTTTTAT CAAATTTACT TGAGTCAGTT AGGACAATGA CTTTATCCGA CACTGCTGAA	900
ATATATTGAA CTACCTCACT GCGCATTAAA TCTTTTCCGG TAAAGCCCAT CTCTTTATCG	960
TAACCATCTG TCCCAACAAA AGCTTGACAC ACATGAAAAG TCTGTATCAT TTCTTTTAAT	1020
AAAGGTCCTA CAGTCACCTG TGAATCTTTC TGAAACTCAC CACCAAGAAC AATAACACGA	1080
CATGAATCAT AAGCTCTCAC AAAATTTGCT ATAAAAACG AATTTGTTAC AATCGTAACA	1140
TTTCTTTTTT GCTTGCAAAT TTCCTCAGCA AGTAAAGCAC AGGTCGATCC AGATTCTATC	1200
ATTATTGTTT CATTATCTGA CACCAATTTT ACTGCTTCCT GAACAATTTT TCTCTTAGTT	1260
TCATAATTAA TTGACAAACG TACATTTAAG TCATCTCCAC TATTTAATAC AGCATATCCA	1320
TGCTCTCTGT GTAATAAACC TTTTGACTCT AATTTATCTA AATCTTTTCT AATCGTTACT	1380
TTGATACAT TTAATTTTTC CGATAATGTA TTAACGTCGA TCTTTTCATA TTCTGATACT	1440
AATTTAATAA TTTGTTCCAA TCTTTTCATT TTACACCTCC GTTTTATTCT ACCAAAAATA	1500
AAAGCAAAAA ACAACAAATT AACCTTTCGT TCGTAATGT TTTTCTTTTCG TTTTGTGAT	1560
AGGATAGACT TATGAAGAGG AGGAACTCTT ATGAAATAT CTAAAGGAAT TATTTTAAT	1620
ATTCAACACT TTTCAATTCA TGACGGTCCG GGTATTCGTA CAACTGTTTT TTTAAAAGGA	1680
TGTCCTCTGC GCTGTCCATG GTGTTCTAAT CCTGAATCTC AAAGAATGAA ACCTGAAAAA	1740
ATGAAAGATG CTCAACGAGA GAAATTCACC TTAGTCGGTG AAGAAAAGAC TGTAAGAAGAA	1800
ATTATTACAG AGGTATTAAA AGACAAAGAA TTTTACGAAG AATCCGGTGG AGGTTTAACT	1860
TTATCAGGAG GTGAAATATT TGCTCAGTTT GAATTTGCTA AAGCCATCTT AAAATCAGCT	1920
AAAGAACATC ACATACACAC TGCCATTGAA ACTACTGCCT TTGTTGATCA TGAAAAATTT	1980
ATTGATTTAA TTCAATATGT GGATTTTATC TACACAGACC TAAAACATTA TAATTCTATA	2040
AAACATAAAA AAGTGACTGG GGTTTTTAAT CAAATGATTA TTAATAACAT TCATTATGCT	2100
TTTTCACAAA ATAAAACTAT CGTTTTAAGA ATCCCAGTTA TTCCTAATTT TAACAATAGT	2160
TTAGAGGATG CAGAAAAATT CGCTACTCTA TTAACTCAT TAAATATCGA CCAAGTTCAA	2220
CTACTCCCTT TTCATCAATT TGGTGAAAAC AAATATCGTT TATTAAATCG GAAATATGAA	2280
ATGGATGGAA TCAACGCACT TCATCCWGAA GATCTTATTG ATTATCAAAA GGTATTCTG	2340

1265

AACCACCATA TTAATTGTTA TTTCTAGTTT ATTTCCTTGA AATGCTCTAG CTATTTGCAG	2400
ATAACAAGCA TCTATAATAC ATACTTAAC TTTCAAAAGG TTTAGCTAAA AAATTTTAGC	2460
CAAACCTTTT CTATTTTACC TTGCTCTAGA ATTTTAAAC TGCTATACTT ATCACAAAAA	2520
AACG	2524

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

CGTGCTTGGG GGCTTGTTGGT CAAAAGGAAA GTCAGACAGG AAAGGGGATG AAAATTGTGA	60
CCAGTTTTTA TCCTATCTAC GCTATGGTTA AGGAAGTATC TGGTGACTTG AATGATGTTC	120
GGATGATTCA GTCAAGTAGT GGTATTCAC TCTTTGAACC TTCGGCAAAT GATATCGCAG	180
CCATCTATGA TGCAGATGTC TTTGTTTACC ATTCTCATAC ACTCGAATCT TGGGCAGGAA	240
GTCTGGATCC AAATCTAAAA AAATCCAAAG TGAAGGTCTT AGAGGCTTCT GAGGGAATGA	300
CCTTGGAAACG TGTCCCTGGA CTAGAGGATG TGGAAGCAGG GGATGGAGTT GATGAAAAAA	360
CGCTCTATGA CCCTCACACA TGGCTAGATC CTGAAAAAGC TGGAGAAGAA GCCCAAATTA	420
TCGCTGATAA ACTTTCAGAG GTGGATAGTG AGCATAAAGA GACTTATCAA AAAAATGCGC	480
AAGCCTTTAT CAAAAAGCT CAGGAATTGA CTAAGAAATT CCAACCAAAA TTTGAAAAAG	540
CGACTCAGAA AACATTTGTA ACACAACATA CAGCCTTTTC TTATCTAGCG AAGAGATTTG	600
GGCTTAATCA ACTTGGTATT GCAGGTATCT CTCCTGAACA AGAACCAAGT CCACGACAAC	660
TAACAGAAAT TCAGGAATTT GTTAAGACCT ATAAGGTAA AACGATTTT ACAGAAAGTA	720
ACGCTTCTTC AAAAGTAGCT GAAACTCTTG TCAAATCAAC AGGTGTGGGT CTAAAACTC	780
TGAATCCTTT AGAGTCAGAC CCACAAAATG ACAAGACCTA TTTAGAAAAT CTTGAAGAAA	840
ATATGAGTAT TCTAGCAGAA GAATTAAAGT GAGGAAAGAA TGAAAATTAA TAAAAAATAT	900
CTAGCAGGTT CAGTGGCAGT CCTTGCCCTA AGTGTGTTGT CCTATGAGCT TGGACGTTAC	960
CAAGCTGGTC AGGATAAGAA AGAGTCTAAT CGAGTTGCTT ATATAGATGG TGATCAGGCT	1020
GGTCAAAAGG CAGAAAACCT GACACCAGAT GAAGTCAGTA AGAGGGAGGG GATCAACGCC	1080
GAACAAATTG TTATCAAGAT TACGGATCAA GGTATGTGA CCTCTCATGG AGACCATTAT	1140

1266

CATTACTATA ATGGCAAGGT TCCTTATGAT GCCATCATCA GTGAAGAGCT CCTCATGAAA	1200
GATCCGAATT ATCAGTTGAA GGATTGAGAC ATTGTCAATG AAATCAAGGG TGGTTATGTC	1260
ATTAAGGTAA ACGGTAAATA CTATGTTTAC CTTAAGGATG CAGCTCATGC GGATAATATT	1320
CGGACAAAAG AAGAGATTAA ACGTCAGAAG CAGGAACGCA GTCATAATCA TAACTCAAGA	1380
GCAGATAATG CTGTTGCTGC AGCCAGAGCC CAAGGACGTT ATACAACGGA TGATGGGTAT	1440
ATCTTCAATG CATCTGATAT CATTGAGGAC ACGGGTGATG CTTATATCGT TCCTCACGGC	1500
GACCATTACC ATTACATTCC TAAGAATGAG TTATCAGCTA GCGAGTTAGC TGCTGCAGAA	1560
GCCTATTGGA ATGGGAAGCA GGGATCTCGT CCTTCTTCAA GTTCTAGTTA TAATGCAAAT	1620
CCAGCTCAAC CAAGATTGTC AGAGAACCAC AATCTGACTG TCACTCCAAC TTATCATCAA	1680
AATCAAGGGG AAAACATTTC AAGCCTTTTA CGTGAATTGT ATGCTAAACC CTTATCAGAA	1740
CGCCATGTGG AATCTGATGG CCTTATTTTC GACCCAGCGC AAATCACAAG TCGAACC GCC	1800
AGAGGTGTAG CTGTCCCTCA TGGTAACCAT TACCACCTTA TCCCTTATGA ACAAATGTCT	1860
GAATTGGAAA AACGAATTGC TCGTATTATT CCCCTTCGTT ATCGTTCAAA CCATTGGGTA	1920
CCAGATTCAA GACCAGAAGA ACCAAGTCCA CAACCGACTC CAGAACCTAG TCCAAGTCCG	1980
CAACCAGCTC CAAGCAATCC AATTGATGAG AAATTGGTCA AAGAAGCTGT TCGAAAAGTA	2040
GGCGATGGTT ATGTCTTTGA GGAGAATGGA GTTTCTCGTT ATATCCCAGC CAAGGATCTT	2100
TCAGCAGAAA CAGCAGCAGG CATTGATAGC AAAGTGGCCA AGCAGGAAAG TTTATCTCAT	2160
AAGCTAGGAA CTAAGAAAAC TGACCTCCCA TCTAGTGATC GAGAATTTTA CAATAAGGCT	2220
TATGACTTAC TAGCAAGAAT TCACCAAGAT TTAAGTGATA ATAAAGGTCG ACAAGTTGAT	2280
TTTGAGGCTT TGGATAACCT GTTGAACGA CTCAAGGATG TCTCAAGTGA TAAAGTCAAG	2340
TTAGTGGAAG ATATTCTTG	2359

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TTCTTTCTGC TATAATCGTA TAAAATACTT ACTTTAGGAG TTCTTATGAA AGTTGTAAAA	60
TTTGGAGGTA GTTCTCTTGC CTCTGCTAGT CAATTAGAAA AAGTTTTAAA CATCGTCAAA	120
AGCGATTGAG AGCGTCGTTT TGTAGTCGTT TCTGCGCCTG GTAAACGCAA TGCTGAAGAT	180

1267

ACTAAGGTTA CGGATGCCCT GATTAAATAC TACCGCGACT ATGTTGCGGG TAACGATATT	240
AGCAAGAACC AAAGCTGGAT TATCGACCGC TATGCTGCTA TGGTTAGTGA ATTGGGACTA	300
AAACCAGCTG TGCTAGAAAA AATTTCTAAA AGCATTACAG CCTTGGCCAC TCTTCTTATT	360
GAAGAAAATG AATTTCTCTA CGATACTTTC CTAGCAGCCG GTGAAAATAA CAATGCCAAA	420
TTGATTGCTG CCTACTTTAA CCAAAATGGT ATCGATGCAC GCTATATGCA CCCTAGAGAA	480
GCTGGGATTG TGGTCACAAG TGAACCTGGT CACGCTCGCA TCATTCCATC AAGTTATGAC	540
AAGATTGAAG AATTGACAAA CACCAATGAA GTCCTTGTC TTCCTGGTTT CTTTGGTGTC	600
ACTAAGGAAA ATCAAATCTG TACTTTCTCA CGTGGAGGTT CTGATATTAC AGGTTCTATC	660
ATTGCTGCTG GTGTCAAAGC TGACCTCTAT GAAAACCTTA CGGACGTTGA TGGTATCTTT	720
GCAGCCCACC CTGGTATTAT CCACCAACCA CACTCGATTG CTGAGTTGAC CTACCGTGAA	780
ATGCGCGAGT TGGCCTATGC AGGCTTCTCA GTCCTTCATG ACGAGGCTCT TCTTCTGCC	840
TACCGTGGA AAATCTCTCT GGTATCAAG AATACCAACA ACCCTGACCA TCCAGGTACT	900
CGTATCGTTC TAAAACACAG TAATGATGAA TTTCCAGTTG TGGGAATTGC TGGTGACTCA	960
GGCTTTGTCA GCATTAACAT GTCGAAATAC CTCATGAACC GTGAGGTTGG ATTTGGCCGC	1020
AAGGTTCTGC AAATCCTGGA AGAACTTAAC AT	1052

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

CCCTCGAAAA CTAAGCCGAT GAAGTCAGAA CACTTCAATC CTGTTCTGTA CTGGTGGGAA	60
AATCGTGAAG AGATTCTGGA AGGTAAGTTC TACAAATCTA AATCATTTAC ACCTAGTGAA	120
TTGGCTGAGT TGAATTATAA TTTAGACCAG TGTGACTTTC CAAAAGAGGA AGAGGAAATC	180
TTAAATCCCT TTGACTTGAT TCAGAAATTAT CAAGCGGAAA GAGCAACTTT AAATCATAAG	240
ATTGATAATG TATTAGCTGA TATTTTGCAG TTGTTGGAGG ACAAATAATG ACACCAGAAC	300
AACTTAAAGC AAGTATTCTC CAAAGAGCGA TGGAAAGGAA ATTAGTGCCG CAAAATCCCA	360
ATGACGAACC TGCAAGTGAA TTATTAAAGA GAATTAAAGC TGAAAAAGAA AAACCTATCA	420
GTGAAGGAAA AATCAAACGA GATAAAAAGG AAACCTGAGAT ATTTCTGGGT GATGATGGGA	480

1268

AACATTATGG GAAGTTTGCT GATGGAAGCA CTCAGAAAT TGATGTTCTT TATGATATTC	540
CTGATACTTG GGAGTGGGTG AGGATAAAAT CAATTTATTG GAATTTTGGG CAAAAAAGC	600
CAGAGAAATC CTTTAGGTAT ATAGATACGT CTAGTATTGA TAGAAAAAG AACATAATCA	660
ACTACAAAA TCTACAATAT CTTTCACCTG AACAGCGCC TTCCCGTGCT AGAAAAATTAG	720
TTTCGCAGAA TAGTGTCTTA TTTTCAACAG TTAGACCATA TCTAAAAAT ATTGCTGTAG	780
TTAGAGAACT TAAAGAGTAT TTGATAGCTA GTACAGCATT TAATGTTTTG GGATACTTTA	840
CTTAACGAAA CATAT	855

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TTTAGGAAGG CTATCCGTAA TTTTACAAAG GATTTAGATA TTACAGAGGA ACATTTAGAT	60
ATTATCAAAA GAGAGATGTT TGGCGAATTT TTCAGTAGCA TGAAGTCTCT TGAATTTATT	120
GCAACGCAAT ATGATGCTTT TGAAATGGT GAGATAATTT TTGATTTGCC GAAATTTTA	180
CAGGAAATTA CTTTAGAGGA TGTCTTGAT GCTGGACATC ATTTAATAGA TGATGGTGAC	240
ATAGTTGATT TTACAATATT CCCATCGTAG TAACCTATTA TAATAGACAC TAGAAAGAAG	300
GGATGACAAG TATGAGAAAA AAAACAATTG GAGAGGTTTT ACGATTAGCT AGAATCAATC	360
AGGGATTGAG TTTAGATGAA TTGCAGAAAA AGACAGAAAT CCAGTTAGAT ATGTTGGAAG	420
CAATGGAAGC AGACGATTTT GATCAACTTC CAAGTCCTTT TTACACGCGT TCTTTCTTGA	480
AAAAATATGC ATGGGCTGTT GAGTTAGATG ACCAAATTGT TTTGGATGCT TATGATTCTG	540
GGAGTATGAT TACTTATGAG GAAGTAGATG TTGATGAAGA TGAGTTGACA GGTGCTAGAC	600
GTTCAGTAA GAAAAAGAAG AAAAAACAT CATTTTTACC TTTATTTTAT TTTATCCTGG	660

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1805 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

1269

CCGGTTGCAC AGGATCGTGC ATAGTCAACT CTTCAAGTAT AGCATATCTC CTATTTTCTT	60
ACAAGTAATA ACACCTAAAA TGAAGCTTTT TCTTTTACTT TTTTCTGCCA AGAGGCCAAAA	120
AGCATGCTGA GGTAAAAAC GCTCATCATA ATAGGAACAC CAAGAATGGT CTTTTCATGA	180
TAGAAAATCG TCAAATAGGC TGAAAAGACA ACGCCAAGGA CAAACTACT AAGCAGGCTA	240
ACAAATATGA ATCCTTCACG CAAAAAGGA GTGTGCTTGG TTCGGAAATA ATCTCCAAAA	300
GCCAGCATGG TCCGTTTGAT ATTCCCTGTC ATAAAAGCGT TATTATAGGC AATACCCGAC	360
ACTTCTCCAA AAGCAGTTGT CACCAGTCCC ATACAGAAGG CCAAGGGCGG CACTAGATAG	420
ATATTATCCA CAGTTTGCGG CACAAAAGCA ATAATGATTG ATAAGATTGC CAAGGGAATC	480
AAGGACAGAA TAGGTTTTTT CACAATTCTC AATTTTTCCT TATAAATCGT TAATAAAAAG	540
ACTCCCATCA TAAACGCTAG CAAGGTGAGA ACCTTGTCCT TAACATCCGA AACATTATTT	600
TTAATTAATT CTACTGAAAG AAAGACAACA TTTCAGTTT GTCCAGCTAC AAGGGTATTC	660
CCGCGAACAA TAAAAGTGTA AGCATCCACA TATCCAGCAC AAAACGTCAA AAAAAGTGCT	720
AACCTTTTAG ACTGACGTGA TATTTTCTT ATAGGTAATA ACCTCATTTT ACCTCCCATT	780
GTATTTTCTC TTAGAAATAT TGTACCATT TCTTTCTAAA AAATCGTAGG CTACCATTTA	840
GATTTTACTA TTAGCATAAA AATAATAATA GACAACTATT TATCCAAAA TAGATAGATG	900
TAACATGTTT GCAAACAAAG CATACGAACC TTTAGTAAAA TCATTTCAT GAAACTAGAA	960
TAGAGCCCTC TTAGCAAAAA TCATTATTTT AATTTATTTT TAATCACTCC TTGACATAAA	1020
TAACCTCTAC CAATAAAGA CTATGTCTTA AAAAAATGGT ATAATAAAT CAATACTTGG	1080
GCTTGATGGC TATGCTACTA ATAACAATTA GGAGAGAAAA TCAGGCACTT GTTAACAACA	1140
AGGATTATCC CCTGAGATG AAAGGAACTT TAGAAATCTT ATGATGAACA TGCAAAACAT	1200
GATGCGTCAA GCACAAAAAC TTCAAAAACA AATGGAACAA AGCCAAGCTG AACTTGCTGC	1260
TATGCAATTT GTTGGCAAAT CTGCTCAAGA TCTTGCCAA GCGACCTTAA CTGGCGATAA	1320
GAAAGTTGTC AGCATTGATT TCAATCCAGC TGTCGTTGAC CCAGAGGACC TTGAGACTCT	1380
TTCTGATATG ACCGTTCAAG CCATCAACTC TGCTCTTGAA CAAATCGATG AACTACCAA	1440
GAAAAAAGT GGTGCTTTCG CTGGGAAATT ACCTTTCTAA AAACAAGGAG CTAGAACAAT	1500
GCTTGTGCGAT AACAAAGGCT AAGAAAGGTG CAAAAATGAC TCTATAATAT TTGTAGTGGG	1560
TAAATCCCCT ATGGATATTA TGGAGCCTAT TTTTGTGTAG AAAAAAGTCC CATATGACCT	1620
ATAATGAAAA GCGACAAAAC AACTCATTAG AAAGAATCAT ATGGAACAAT TACATTTTAT	1680
CACAAAATTA CTAGACATTA AAGACCCTAA TATCCAGATT TTAGACATCG TCAATAAGGA	1740

1270

TACACACAAG GwaATCATCG CCAAAGTGGr CTATGAAGCT CCATCTTGTC CTGAGTGC GG 1800
AAGTC 1805

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CTGCATCTAG TTTGTTTCTC CCTACAGTTT TAGCTAGACA GATTGGAGAT TATGATTTAA 60
CGTCGCCGCG TTGGGGTTCG GATACAATA GTGAGCTTGA GAAAGAAAAC TCCTCTGCTG 120
GAATTAATAA TAATGACAGC ACTGGTGGCG GTAAAAGGTT AAATACCTCT ATTCGTAGCG 180
CCTATAGTGG GTCAGATATT ACCCCGGTAT ATTCATTGGG GTCTGGCTCT AGGATTGTCA 240
TGTACTATAA TGGAGGTGGT GACAATTATA TTGGTTCTGG TACTAGATTA GCTATGGCGC 300
CACAATTTGG AAATCATGTA AGAATTCATA CTTCAGGTTT TTGGAATCCA GATTCTTATT 360
AACTTACTTG TCAGAGTAAG CCTTAAAGAT GGTGATTGT GGGGTAGCA TGAAAAAAGA 420
ATGCTACACC CTATTTTAT TATAAGGAGG AGTAAGGATG GAATTTTCA TTTGTAATCT 480
TGTACGAGTC GTTCAATCAC CTCGATTTTA TATGTCTTTA TTTTGTACCC TTCTTTGCAT 540
GAGTTTAGGA AATTTCTTG CTTTCAATGG TATTTATAAA ATTGAAGGTT TATCGATTTT 600
TTTTGCCGCT TCTTCTATTC GAGGATTTTC ACCGATTAGC CTAGTAGCTG CACTTATCTG 660
TACACTGCCC TATTCTAGTC AGATAATAGA GGATGCTGAG AGTCATTTTC TAACAGCACA 720
ATTGTGTCGA ATTTCTAAAA AGAAGTATCT GGCTATTGTG GGTAGTACTG TAATTATTTT 780
TTCTTTTCTA GTCTTTTTC TCCCCTATTT ATTATTATTA GGAATTAATC TTTTAGTGAC 840
TCCTTATCAG GAAATTTATA TTGGAGATTA TAGTGGTGCC TTAAGAAGAT TATTTGATTC 900
CAATCAGTTT CTCTATAGTC TTGTAACGAC TCTCTGGTAT GGAGTTTGGG GCGCTGTGTT 960
CTCTATTTT GGACTAGCTA GTGCTTTGCT AGTGAAGAAA AAAATAGGAG CTATTTTCAT 1020
CCCAGTTGCC TATATGATGG TTGGTGGTAT TTTTGGGCT ATTTAGGGC TATCTTACTT 1080
AGAACCTGTG ACAACGCTAG CTTTGGGATA TCAGAAAGAT ATCAGTCTTT CCTAGTTAG 1140
TGCTCATCTT GCTTTTATTT TATTTGTTAG TTGTTTGGTT GTTTATGGTA CATTTTTCTT 1200
ACATTCAGAG GACTATGTAT AATGAAACAA TTTGTTCAAT TTTATAAAAA AGATTCTTAA 1260
GCAGTATTGG TTTATTTTAT ATTACTGCTA TCCTGTGTTT TATCTAGTAC AGTATATTTA 1320

1271

TTGCGCtGTC GCCAATATTC AATCCATCCA AATGTATTAG AATGGATCTT AGTTTTACTT	1380
CAAGATATGA CGACTGGAGT ATATTGCTTT CCGTTCACAT ATATATTGTT CTTTTTTTAT	1440
TTGATGAATA ACTATTTTAA TAGGTTGGAG TGTCGCATTC GTCTGAAATC AATTAAGCAC	1500
TTTACCAGTT TTAGTTTCAA ATTAGCAGCT CTTAGTACGG GGATTGGAC GCGGACTTTA	1560
TTTTTATTGA TTTTCTAAT TGCATTTAGT AATGGTTTTA GCTTCTCTTT GGAGATAAAG	1620
GAGGTTGATT TTTTAAGAGA ATTTTATGGT ATAAGTATTG CAAACAATGC TAGTTTCTTT	1680
ATAGGATTTT TTTTCTCTTA TATAGCATAC TATTTCTTTT TATCCTTACT TACTATTAGC	1740
AGTTTTTCTT GGTTTAAAA ATCAAACATG AGCTTAGTAT TTCTGTTTAC TTTTTTATTT	1800
GTAGAATCCT TATTCTGGAT TTATCAGTTG GACAATGGGA TAATTGGATT ATTGCCAATT	1860
TTTCAGTATA TGGTAAATTC CAATCCGTAT GCATTGATTT ATTGGCTTAC ATTACTATCT	1920
ATCATAATTC CATTGACTGT ATTTTCTGTT CATAGAACT GGAGGAGAGT GTAAAAGTTG	1980
GAAATGGGAA AGTTAAGTAG TCACATGTGG AGGTTGAATC AGATAATCTA TACCAAGTAC	2040
TTTTGGGGTT ATGTTCTTTT TTGGATATTG ATTTGTTTAG GATTATGGTA TTGGTTAGAA	2100
GGAAATGATA GACTTGTTAT AGAAATTTTA AAAGGGCCTA ATCTGAGTCA AAACCTTTTT	2160
TTAGTCTTAT CTATATGGTT GCTTCATTGG TTTATTATTC ATACATTTTT TCTAGCAGTT	2220
GTATATCGTA GAAGAGCATC CGATTTCTTT ATGGAAGTGA TTCGATTTTC TTCTATTAAG	2280
CTCTGGATTA GGTATCAGAT TTGGACCTGT TTTCTTTATG GACTCATTTT AATCATGGTA	2340
AAAGTTCTAG TGATTCAATT TATGTTACAG TTACCAAACT GGGATATAGG AGTTTTGTTT	2400
ATAGTTGATT CTTTGAATGC TTGTGTGTTA GTCTTGTTTT GCTTTATGTT ATACGCACTA	2460
GGAGCGAATG TACAAATGAA CTTTGCTTGC GTTAGTTTCT TTTTACTCAT GATTGG	2516

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CGGTGTTTTT TTGTAAATTT TCTAGCACTT GTATGGTAAA ATAGATACAG GTGTTTATTA	60
AACTAGACTA AAAACCTATT TAAGCAGGCA AAATGAAGAA ATACCAACAA TTATTTAAGC	120
AAATCCAAGA AACCATTCAA AACGAGACTT ACGCTGTCGG AGATTTCCTT CCTAGCGAGC	180

1272

ACGACCTTAT GGAGCAATAT CAAGTGAGTC GTGATACCGT CCGAAAGcCC TGTCTCTCCT	240
CCAAGAGGAA GGATTGATCA AAAAGATAAG AGGGCAAGGT TCTCAAGTCG TCAAAGAAGA	300
AACCGTCAAT TTCCCTGTAT CCAACCTAAC CAGCTACCAA GAACTAGTTA AAGAACTTGG	360
ACTGCGCTCT AAAACCAACG TGGTCAGTCT GGACAAGATT ATTATTGATA AAAAATCCTC	420
ACTGATAACC GGTTCCTCAG AGTTTCGGAT GGTTCGGAAG GTGGTCCGCC AGCGTGTGGT	480
GGATGATCTG GTATCCGTTT TGGATACGGA CTATCTGGAT ATGGAAGTCA TCCCAAATCT	540
CACTCGCCAA ATTGCTGAGC AGTCTATCTA TTCTTATATA GAAAATGGCC TCAAACCTCT	600
TATTGATTAT GCTCAGAAGG AAATCACCAT TGACCACTCA AGCGACCGAG ACAAGATTCT	660
CATGGACATT GGCAAAGACC CTTATGTCGT TTCGATTAAA TCAAAAGTCT ATCTCCAAGA	720
CGGACGCCAA TTTCAGTTTA CCGAAAGTCG CCATAAGTTA GAGAAATTTA GATTTGTAGA	780
TTTTGCAGAA CGCAAGAAAT AAAAGACTGA GACACCAGAT CTCAGCCTTT TTCGGCTCTA	840
TAATATTTGT AGTGGGTAAC CCCCTATGG ATATTATGGA GCCTATTTTG TGTAGAAAAA	900
AAGTCCATA TGACCTATAA TGAAAAGCGA CAAAACAACT CATTAGAAAG ATTCATATGG	960
AACAATTACA TTTTATCACA AAATGCTCG ATATTAAAGA CCCAAACATC AAGATTCTAG	1020
ACATCATCAA TATGGATACC CACAAGAAA TTATCGCTAA GCTGGATTAT GAGGCTCCAT	1080
CTTGCCCTGA TTGTGGAAGT CTAATGAAGA AATATGACTT TCAAAAACCG TCTAAGATCC	1140
CTTACCTCGA ACAAATGGT ATGCCTACTA GAATTCTCCT TAGAAAGCGT CGTTTCAAGT	1200
GCTATCATTG TTCTAAATG ATGGTCGCTG AAACCTCTAT CGTCAAGAAG AATCATCAAA	1260
TTCCTCGTAT TATCAACCAA AAAATTGCGC AAAAGTTGAT TGAGAAGATT TCTATGACCG	1320
ATATTGCTCA TCAGCTGGCC ATTTCAACTT CAACTGTCAT TCGG	1364

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CCATGAAGAC CGCTTGGAAT TGGAATGGCA CAAGTCTTTG TTGAATGGTC TATTTCCATT	60
GACAATCGGT GGAGGAATTG GACAATCTCG TATGGCCATG TTCCTACTTC GCAAGAGACA	120
CATCGGAGAA GTGCAACAA GTGTTTGGCC TCAAGAAGTC CGCGATACTT ACGAAAATAT	180
TTTGTAGAGA ATCGAACCGC AAGGTCGGT TTTCTTTCTC TTTTGTCTA TAATTTGGTA	240

1273

TAATAAACAG TATGAAAATC GTATCAGGAA TCTATGGGGG ACGTCCCCTC AAGACACTAG	300
AAGGCAAGAC GACAAGACCT ACTTCGGATA AGGTTAGGGG AGCCATTTTT AACATGATTG	360
GTCCCTACTT TGAAGTGGGA CGAGTCTTGG ACCTTTATGC AGGTAGTGGT GGTTTATCTA	420
TCGAAGCAGT ATCGCGTGGC ATGTCCAGTG CTGTTTGGT GGAGCGAGAC CGTAAGcTCA	480
GACCATCGTG GCTGAAAATA TCCAGATGAC CAAGGAAGTT GGAAAATTTC AACTCCTCAA	540
GATGGATGCA GAAAGGGCAT TGGAACAGGT ATCTGGGGAA TTTGACCTCG TTTTCTTAGA	600
CCCTCCCTAT GCCAAGGAAC AAATCGTAGC AGATATTGAA AAAATGGCTG AGAGAGAGCT	660
TTTTTCTGAA GATGTTATGG TTGTGTGCGA GACGGATAAA GCCGTTGAAC TTCCAGAAGA	720
AATTGCCTGT CTGGGTATCT GGAAGGAAAA GATTTATGGA ATTAGTAAGG TGACAGTCTA	780
TGTCAGATAA GATTGGCTTA TTCACAGGCT CATTTGATCC GATGACAAAT GGGCATCTGG	840
ATATCATTGA ACGGGCGAGC AGACTTTTTG ATAAGCTTTA TGTGGGTATT TTTMTAATC	900
CCCACAAACA AGGATTTCTC CCTCTTGAAA ATCGTAAACG GGGGTTAGAA AAGGCTGTGA	960
AACATTTGGG AAATGTTAAA GTCGTGTCTT CTCATGATAA ATTGGTGGTC GATGTCGCAA	1020
AAAGACTGGG GGCTACTTGC CTAGTGCAGG GTTTGAGAAA TGCCTCGGAT TTGCAATATG	1080
AAGCCAGTTT TGATTACTAC AATCATCAGC TGTCTTCTGA TATAGAGACT ATTTATTTAC	1140
ATAGTCGACC TGAACATCTC TATATCAGTT CATCAGGCGT TAGAGAGCTT TTGAAGTTG	1200
GTCAGGATAT TGCCTGCTAT GTTCCCG	1227

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCGGTCAAGT TAAAAACGCT ATTTCTTCCC ATTTTATTTA TTTTITAGGA GTGGTAACGT	60
ATCAAAATAG CCCAAGCGTT CTCACCCGTG TGAGTTTGAA TAATGGAACC CGTTTCCAAA	120
ACAGAAATTG GCTTTTCAAC ATAAGCTTGT AAGCTTTCTT TCATCTCTTT TGCCCAATCA	180
TCACTACCAG AATATGAAAT TCCAATCTCT GCTACAGCAC GTTCAGAAAG CGATGTTATC	240
AACTCATCTA ACCATTTTMT AAATGTTTTA GTTCCACGAC CTTTAACCAT TGGCTGCAAT	300
TCATGGTCTT TCATTTGCAT GACAGCACGG ATATTGAGAA GAGAGCTCAA CAAGCCAGTT	360

1274

ACACGGCTAA	TTCGTCCACC	TTTGACAAGA	TTTTCCAAAG	TTGAAACACC	AATATAAAGC	420
TCTGTATGGT	TTTAAACCTC	TTCTACATGA	GATAAAATTG	CCTCCATATC	TTTACCTTCT	480
TGAGCTAACT	TCGCAGCCTC	AACAACCTGG	AATTTCAAGG	CTTGGTCAGT	GAAGGAACTA	540
TCAACAACAG	TCACATCTGC	AGTAGATAGG	CTAGCACCTT	GGCGTGCTGC	TTCTACCGTA	600
CCCGAAAGAG	CATGGGACAT	ATGAATAGCA	AGAATCTGGC	CACCATCTTT	GCATAGGTCT	660
TCAAAAATCT	CAGCAAAGAC	ACCTACAGGT	GGCTGACTTG	TTTTCGGAAG	ATTCTTACTT	720
TCTTGCATCA	ACTGAAGAAA	TTTACCTTCT	TCTTTCAAAT	CCGCATCAGA	ATAAACAACA	780
TTATCAATCA	TTACAGATAA	TGGAACAATT	GTAATATCTA	ATTGCTTTAC	TAGTTACGGT	840
TCAATAGTAA	CAGATGAATC	GGTTACAATC	TTAATTTTTG	TCATAGTATC	AATCTTTCTA	900
TTTTAGGATT	CAGATTGGTT	TCCTTACTTC	TAATTATATC	AAAAAAAAGA	TTAAAAATCC	960
TAATGGAGTC	AATCAAATTT	TCCGTAAAAT	TTGATATAAT	CAACTTATAA	GAAAAGAGGT	1020
GTCCTATGAT	TAAAAAATTT	TACCCCATTT	TTACCATTTT	ACTAGGTGCT	GCTATTTATG	1080
CTTTTGGAAT	GACTTATTTT	GTAGTTCCTC	ATCATCTCTT	TGAAGGAGGG	GCGACAGGCA	1140
TTACCCCTCAT	CACCTTTTAT	CTTTTAAAAA	TCCCTGTGTT	CCTCATGAAC	CTGCTGATTA	1200
ATATTTCCCT	TTTCATCCTA	GCTTGAAGA	TTTTTGGAGC	CAAATCCCTC	TATTCTAGTT	1260
TACTAGGAAC	CTTAGCTTTG	TCCGGCTGGT	TAGCTTTTTT	TGAGCATATT	CCCCTTCATA	1320
TTGATCTTCA	AGGTGATTTA	CTAATCACAG	CCCTTATAGC	GGGAATCCTA	TTGGGAATTG	1380
GCCTTGGAAAT	TATTTTAAAT	GCTGGAGGTA	CAACTGGCGG	AACTGATATT	CTAGCTCGTA	1440
TTCTCAACAA	ATACACTCAT	ATATCCATAG	GAAAACGCT	CTTTATCTTA	GATTTTGTGA	1500
TTCTCATGTT	GATTCTCCTA	ATCTTCAAGG	ATTTGAGATT	GGTTTCCTAC	ACGCTTTTGT	1560
TTGATTTTAT	TGTTTCTCGT	GTTATTGATT	TGATTGGTGA	AGGAGGATAT	GCCGGCAAAG	1620
GCTTTATGAT	TATCACAAAA	CGTCTGACC	AACTTGCTAA	GGCGATTAAT	GATGACCTCG	1680
GAAGAGGTGT	TACTTTTATT	TCTGGTCAAG	GCTACTATAG	TAAAGAAAAAT	TTGAAAAATCA	1740
TCTACTGTAT	TGTCGGAAGA	AATGAAATTG	TGAAAACGAA	GGAAATGATT	CATCGAATCG	1800
ATCCTCAAGC	CTTTATAACT	ATTACAGAAG	CCCATGAAAT	CCTAGGAGAA	GGCTTCACCT	1860
TTGAAAAAGA	ATAAAAAGAG	GTAATGTCGT	GACCTCAAAA	GTTAGACTAA	ATCATCTATC	1920
TTTTGGGTTA	CAGACAACCT	CTTTTATTAT	TTATTTACTC	AAGCTCTTAA	GACCAATTCC	1980
GAGTTACTTC	TTTCATCAGC	TTTAACTGAT	CCACTAATTG	GTCAACTGAG	TCAAATTTGG	2040
TCATATCTCG	AATGCGATCA	AGCCAATAAA	CCATGACGGT	TTCCCATAAA	ATATCTTGAT	2100
TAAAATCAAA	AATATTGACT	TCAAAACGTG	CTTCTTCTCC	ATCAAAGGTC	ACATTTTTC	2160

1275

CGACACTAGC CATAGCACGA TACTTCTGTC TTTGAATCTC AACATCAACA ACATAAACGC	2220
CATCTGCTGG CATATAAGTA CGGTCTAAAA GCACTAAATT CGCTGTCGGA TAACCAATTG	2280
TACGACCACG AGCATTACCA TGAACCACCA TACCTCTTGA TGGAAAGCGGT GCCCCAAAA	2340
GTTTTCTGTC TTCTTTCACA TTTCCATCTA AAATAGCTTG ACGGATACGA GTTGAACATA	2400
TCTTTCTTTT CTCATCTTCT ACAGGTGGAA CAATGATAAC TTCTCCATCA AAGTAATTCT	2460
TTAAATCTTC TGCTGTTTTT TTGTCAGAAC CAAATGTATA ATCAAAACCT GCAACAATAA	2520
TTTTGGCATT CATAGCCTTG ATATAAGTTG CAAAGAATTC TTGTGCAGTG AACTAGCGA	2580
ATTGACTACT AAAATCAAGG AGATATAATT CTCTACACC TTCGCGCTTT AATTTCTTTT	2640
CACGTTCAAG AGGGTTCAAA ATATGCAAAA ACAAATCTGG ATGATAAGGC TCTAAAGCGA	2700
TCTTTGGAGA TTCATTAAAG GTCATAACGA CGATAGGCAA CAAATCCTTT CTCGCAGCCT	2760
TGTTGGCAAC ACGAAATAAT TCTTGATGCC CCTTATGTAT GCCATCAAAA TAGCCGAGAA	2820
CAACGACTGA ATCAGATGGT GTGCCAATAT CTTTTTGGTT TTTTATAGGA ATAGTAATAA	2880
TCATAAAATA ATTATATCAT AGCGATAGCT ATTTCTGGAA CAGAAAATCT GAAATGTTGT	2940
TTTTTTCACA TGAAGTGTAC CTGTTTCAA AAAGCACTTT ATTCTATCGT TGCTTAACTA	3000
TGAACTTTGC AATATCTTC TCAAAAACCT GTAGGACATC TTCAAAATTT TGCAAGGAGT	3060
GATTAGACTT GTTCGGTAAC CATAAAGTGT CATACTATGC TTATGTATGA AAAAGCAATG	3120
CAACTAATC CTGAGAACTT TAAATTACTA ATTGGTGCCG AAAAGGTAGA ATTTAGAATC	3180
GAGGTACACC TATGGCTGTA AAATTTACAA AATGAGACAA CTTGGGCAAG ATGTTTGAAG	3240
AATTTCTTAA ACTCCCTGAT TTGAAGCAAG TCACTTTCCC TAATGACAAA GAAAAAAGCC	3300
AAAACAGCAA AGAAAACTA GATGACTGCT TTCCAACAAC TCCCATCTAG TGTGCTTCAG	3360
ACTGGGCTAT TTTTCTCTCC ATCTGTTAGC TTGGATTCTC AGACCGTTTC AGCTAAAGAA	3420
TATCTTTTCC CTTATCAGAA GGAACGGCTC AAGCCATTCA GACAAGTGAA GGGACGACAA	3480
GCCAATATTT GAAACCAGAT AGCAGTTCTT ATAGTCAATT GAAATAAAT CTGAAGAAAT	3540
CGAGTAGGAA ACTCATATCA ATGTTTAAAC GTGTTCTATT CCAGATTCAT ACTCAATGaw	3600
AATTAAAGTG CAAACTAGGA AGTTAGCCGC AGGTGATACT TTGGGTACGG CA	3652

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 743 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GTACCGTGGT GCCAAAGTAC AGCAAGGTTG GCTTTTGGAC AAACAATACC AATCTTGGTT	60
TTACATCAAA GAAATGGA ACTATGCTGA TAAAGAATGG ATTTTCGAGA ATGGTCACTA	120
TTATTATCTA AAATCCGGTG GCTACATGGC AGCCAATGAA TGGATTGGG ATAAGGAATC	180
TTGGTTTAT CTCAAATTG ATGGGAAAAT GGCTGAAAA GAATGGGTCT ACGATTCTCA	240
TAGTCAAGCT TGGTACTACT TCAAATCCGG TGTTTACATG ACAGCCAATG AATGGATTG	300
GGATAAGGAA TCTTGGTTTT ATCTCAAATC TGATGGGAAA ATAGCTGAAA AAGAATGGGT	360
CTACGATTCT CATAGTCAAG CTGGTACTA CTTCAAATCC GGTGGTTACA TGACAGCCAA	420
TGAATGGATT TGGGATAAGG AATCTTGGTT TTACCTCAA TCTGATGGGA AAATAGCTGA	480
AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC TACTCAAAT CTGGTGGCTA	540
CATGGCGAAA AATGAGACAG TAGATGGTTA TCAGCTTGGG AGCGATGGTA AATGGCTTGG	600
AGGAAAACT ACAATGAAA ATGCTGCTTA CTATCAAGTA GTCCCTGTTA CAGCCAATGT	660
TTATGATTCA GATGGTGAAA AGCTTTCCTA TATATCGCAA AGTAGTGTG TATGGCTAGA	720
TAAGGATAGA AAAAGTGATG ACA	743

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TTTTGGTTGA TGATACGAGG GATTGGTGA TTCTTCTTGA CGATAGAAGT TTCAGCGACC	60
ATCATTTTTG AACAGTGATA GCACTTGAAT CGACGCTTTC TAAGGAGAAT TCTAGTAGGC	120
ATACCACTCG TTCAAGATA AGGAATTTTA GAAGTTTTT GAAAGTCATA TTTCTTCAAT	180
TGGTTTCCGC ACTCAGGCA AGATGGGCG TCGTAGTCCA GTTGGCGAT GATTTCCTTG	240
TGTGTATCCT TATTGATGAT GTCTAAAATC TGGATATTAG GGTCTTAAAT GTCTAGTAAT	300
TTTGTGATAA AATGTAATTG TTCCATATGA TTCTTCTTAA TGAGTTGTTT TGTCGCTTTT	360
CATTATAGGT CATATGGGAC TTTTTTCTA CAATAAATA GGCTCCATAA TATCTATAGT	420
GGATTTACCC ACTACAAATA TTATAGAACC GAATTAATTT AATTAGAGAG CCAACTTTCT	480
AATATAGTAA TCGCGTCATA ACAAGGTATC TATCATTCAT GGAGTTCCTC CTGTATACTA	540

1277

TTAGTAAAGT AAAACTATTG GAGGATATTT TAATGCCACA ACCTATTGTT CCTGTAGAGA	600
TTCCACAATC TCGTCGTTTT GATTCTAAAA AGAGAAATGA TATTCTGCTT AAAATTCGTA	660
TTGGCAAGCT TGAAGTAAGT TTTTTCAT CTCTCAATCT CGAAATGGTA GAACAGCTTT	720
TGGATAAAGT GTTGCTCTAT GACAATTCAT CTATCTAGCC TAGGGCAGGT CTATCTCGTA	780
TGTGGGAAAA CGGATATGAG GCAAGGCATT GATTCATTGG CTTATCTGGT TAAACCCAC	840
TTTGAATTAG ATCCTTTCCTC CGGTCAAGTT TTTCTCTTTT GTGGTGGACG TAAAGACCGC	900
TTTAAAGCCC TTTACTGGGA TGGTCAAGGA TTTTGGCTAC TATATAAACG CTTTGAGAAC	960
GGAAAATGA CTTGGCCCAG TACAGAAAAG GATGTCAAAG CTCTCACACC TGAACAAGTA	1020
GATTGGCTTA TGAAGGGCTT TTCTATCACT CCAAAAATAA ATTTATCAGA AAGTCGTGAT	1080
TTCTATTGAA ATGAGGACTT TCTTTTGTAGT TATAATAAAG TTAGGAAATA AGGAGAGGAA	1140
GCCCATGGAA GAAGATTGAA AATCATTCOA CAACAGAGTG CTACAATTGA TAGTCTCACC	1200
AATGAACTTG CCTTCTTCG TGAACAAGTG GCTTATCTAA CGCAAAGCT CTATGGAAAA	1260
TCCTCTGAGA AAAGTGTTCG CCCATCTGGA CAACTCAGTC TTTTGAAGA GGAACAAAAT	1320
ATGGAAGAAG ACTCTGACTT ACCCAGTTGA AAGAGAAGAA ATCACCTATA AACGTAAGAA	1380
AGCTAAAGGG AAACGTCAAG CTCTTCTTGC CCAATTGAT TCAGAAGAAG TTCATCATCA	1440
AGTAGAAGAG AGCATTTGCC CTGATTGTCA GGGAGATCTA AAAGAGATTG GAGCAACCTT	1500
TCAACGACAA GAATTAGTCT TTATTCCTGC GCAATTAAAA CGAATAGATC ATATCCAACA	1560
CGCTTATAAG TGCCAAGCAT GCAGTGATAA AAATCCGAGT GATAAAATCG TGAAAGCTCC	1620
TATTCCTAAA GCCCCTTTGG CGCATAGCCT TGGCTCAGCT TCTATTATCG CTCACACCAT	1680
CCATCAGAAG TTTAATCTGA AGGTACCCAA TTATCGCCAA GAAGAAGATT GGGCTAAGAT	1740
GGGTTTACCA ATCACACGTA AGGAAATTGC TAATTGGCAT ATCAAGGCCA GTCAATACTA	1800
TTTGGAGCCC CTTTATAATC TTTTACGAGA AAAGTTGTTA GAACAAGCTC TTCTTCATGC	1860
GGATGAAACC TCTTATCGGG TTCTAGAGAG TGATAGTCAG TTGCCTTACT ATTGGACTTT	1920
TTTGTCTGGG AAAGCTGAGA ATCAAGCAAT CACGCTGTAC CACCATGATC AGCGTCGGAG	1980
TGGTTTAGTA GTACAAGAAT TCCTAGGAGA TTATTCTGGC TATGTTTATT GTGACATGTT	2040
GCGGCAGTAA CTTAGGACTT TAGTCCTCTA GTTCTGCCTA TGCGATAGCA GTCCAAGGTT	2100
TAGGAGTAAG GCGACGCTAA GCTTGGTAAA CTGCGAACAG CTAGAAGCTT ATCGTCAACT	2160
GGAAGAAGCT GCACTTGTTG GATGTTGGGC GCATGTGAGA AGGAAGTTT TTGAAGTGCC	2220
CCCCAAGCAA GCAGATAAAT CATCCTTAGG AGCTAAAGGT TTAGCTTATT GTGATCAGTT	2280

1278

ATTTTCCTTG GAAAGAGACT GGGAGGCTTT GCCAGCTGAT GAACGACTAC AGAAACGTCA	2340
AGAACATCTC CAGCCCCTAA TGGAAGACTT CTTTGCTTGG TGCCGCCGTC AGTCAGTTT	2400
AGCAGGTTCA AACTAGGAA GGGCAATTGA ATACAGCCTC AAGTATGAAG AAACCTTTAA	2460
GACTATTTTG AAAGACGGAC ATCTGGTCCT TTCCAATAAT CTAGCTGAAC GCGCCATTAA	2520
ATCATTTGGT ATGGGACGGA GTAAAAGAGT CCAGTGGACT CTTTAGCCT GAGCTCAGTT	2580
TAAAAAAGCG AGGGTGTTA TTTTCTCAA GTTTTGAAG AGCTAAAGCA AGAGCTATTG	2640
TTATGAGCTT GTTGGAAACA GCTAAACGTC ATCAATTATA GTGCGTTGAA TCTATAACAG	2700
TACGCATCGA CTGCTAAAAC ATTTCTATA ATCAATTTC CTTTCCTAAT CGATTGTTC	2760
ATATCTTATT TCAATCCATT ATAAATAGCG AGAAATATCT ATCCTATCTT CTAGAATGTC	2820
TTCCAAACGA GGAACTCTC GTAAACAAAG AGGTTTTAGA GGCCTATTTA CCGTGGACTA	2880
AAGTTGTACA AGAAAAGTGC AAATAAGAAA TCTCCAGATT AGGAACTATC CGTGAGTTCT	2940
CTAGTCTGGA GATTTTCAA TAGACTTCGT TATTGGACGG TTACAATTTA TTATATGAAA	3000
ATCCCATATT ATTCTCCAAT TCTATATTTT ACCTTTCTAA ATGTATAGAT TAACTACCTA	3060
ATTATAGCAT ATAACGCAGA TTCCTTTCAA TCGTATGATT TACTGCATTA AATTAAGTAA	3120
AAAAATAAAG GCAGTCCGAA GACTGCCGAT ATTTATCTCT CATCTCTTTA ATTATGGTAA	3180
GTAAATAAAT AATTTCCTA AAGATATGGA AATTATTAAT ACTATAAATA CATATTATAA	3240
AGTTTATAAA TACTGTAAAA ATCCTGAAGT TAATTTTCTA ATAAATATCA ATATGTGTTA	3300
GTATCTTTTA AATTTTGA CAATTTACTA GTTCTATAGA CATGTTTAAC AGACTCTATT	3360
TTACAATTCA AAAATTTTAT CTGCCACTTC ATTTAAAAAT TCTATATCAT GGGAAACAAT	3420
AAAAATTATT TTATCCATGG TTTTATACTT ATTAATCAGT TCAGATATTT TTATCATATT	3480
GGAATAATCC ATACCACTTG AAGGTCGTC AAAAAAGACA AATGGAGAAT TCTTGCACAT	3540
AACAGATGCT ATTGCAAGCC TTTGCTTTTG CCCTCCTGAT AAACCTCATG GATGCCTTTC	3600
AATAAATTCG TCCAGGCATA AATCTTTTAA CCCAAATCAT TCATACCTCT CTCAACTAGA	3660
TGTAACCTAC AAAACCCCTG ACCTCATGAG CCACTTTCTT CCTCCTCATG AGGTCAGTTT	3720
TACTTTCTGC TGTCCAGTA TCGTTTTC TCGCTAGATT TCCTCAAAG GGCAGACTCC	3780
TCCCTTGTT CGTCACACGA TTTTTCATC TCGACTGTTC TTTAATGCAT CATTAACGAC	3840
GCTTTTCTTC TAGGTGGTTC ATAAGGAACA GGAAGATTCA GGTGACTTT TCTAATCCTA	3900
GAATAAAGTG CTGAAAACA TTCGGAATAG GCATAGAGAC TAGACAATT GAGGAGCTGC	3960
TTGCGTCCTG TTCGAACACA TTTCCACC ACGTGAAGAA AAAGATGGCG	4010

(2) INFORMATION FOR SEQ ID NO: 254:

1279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

ATGCATCCGT TTGTCAAGCC TAAATTGTAA TTTTTTTCAA TTAAAAACAG AAAAACCCAG	60
GAAAAATGACA TAAAAATATC ATTCCTAGGC CTATTATATGC TATTTCTCTC TGAAAAATAT	120
GAGTATTCAG TCGGTCAAAT GAAGCTGAAC GAACTCATTT TCCCTCGCCT AATTCATGA	180
TTCGATGACA TTGTTGGGCT ACATAAGCAT CGTGGGTCAC GATAATGACT GTTTTCCCCT	240
CTCGATTTCAT CTCTAAGAGA AACTTCAAGA CCAAATCTCT ATTTTCAGGA TCCAGAGAAC	300
CTGTCCGGTTC ATCGGCTAAA ATCAGCTGGC TGGGTTTTAA GATGGCTCTA GCAACTGCAA	360
TTCGTTGTTG TTCGCCCCA GACAACTCGG AGACCCTTTG ATGCAAAGTA GCTGATAAAC	420
CTACTCTCTC TAAAATCTCT TCCACCTTTT TGAGCTTGTC TTTCTTAGGC AATTTACAT	480
ATTTTCAGCGC CACATGAGAT TGTACTCGAC CGTTTCATCA TCAATCAGGG CAAAATTTTG	540
AAACAGATAA GAGATATGTT CACGGATTAT TGTTTGCGAC TTAGCAGAAT TAACCGCTAG	600
ATTTGTCTGA CCAAAATCT CATACCGTCC GCTATAATCA CCATCTATCA AACCCAATAA	660
ATTTAACAAG GTCGACTTCC CACTACCACT CTTACCAACA ATAGCTACCA AATCCCCCTG	720
ATCAATCCTG AGAGATAAGT TATCCAAAAT CACTTTTCCC CCAATGGTTT TGGTAATATT	780
TTTCAACTCA ATCATAAGAT GCCCCCTTTC AATAACTCTA CTAGACTTCT TTTCTCCATC	840
CTAGAAGCTA AGCCTAGCAC AAATAGTATA TCCAGACATG TAAAACCTGC AAACAGTAGA	900
AGTGGTAAGA ACGCATGGGC AAAGAAAATC AAGACTAGAA GAGGGAAACT ATAGCCCAGC	960
AAGAGCAGAA CGAGGAGAGG ACGGTAGCGA TCGACCAGTT TCCACCCCAT AAACCTCTTG	1020
GTAATGATAT CCCTGCGCTT CAATAAGAAA GTTGTTACTA GTAAGAAGTA GGAAATCATC	1080
ATGCTAAGGA GACCAAACAA AGCAAAGAGT AGGTAAAAAT TCCGAACAGC ATCTCGATAA	1140
GAATCCACTT TCTCTTGTG AATGGCTTGA ATAGATGAAA ATTTTAAATA ATTTCCATCT	1200
GACAAATTCT CAACTAATC TGTAATCTCT TTTTGATGTT GAACCGTATT TTCAATTTTA	1260
ATCGGATTAT TTAAGCCAGT TGTGACAGG GAGGCTTTCT CATCCCACAT CATATCAGAA	1320
TCATTGACCA AGCTAATAAT TGGATTGGAG AGATTTTCCT TTCGCTTATC ACTATATGGG	1380
AAAAATGACC AATCTCCTTC ATAATAGGCA ATCTCGACAT CCATCTCCTC TATCGTTCGT	1440

1280

TTTTGCTGCT	CTTCATACTT	CATCGAATGA	AAGGCAATTA	ACTTCCCCAA	GAGCTGATTT	1500
TTATCTTCTT	CACCTTTCGT	ACTTGCTGGC	ATCAAAATAA	CTTTTTTAAT	ACCGGTATTT	1560
GGTAGCTTGA	ATCCCTTGCT	CTTTAGAAAA	TGCGGATTGG	CATAGTAAAC	ATCCACCGTA	1620
TCTGTAACT	GATATTGCTG	AATCTGTTCT	GATTGGACAA	AATTTTTTAC	AGGAAGACTG	1680
CTACTCTGCA	CATAGCCCGC	CTGCGTTTTT	TCTACCAAAT	CCTGATAAAA	TCGATAGAAA	1740
TAATCTGTAG	ATTTCCCTGA	CCCTGCTAGC	TCTTCTTGCC	ACAGATTATC	ATTGAGTTTG	1800
AAGGTTTCTA	AGGTCAGGTA	ATTACCTTGA	CTTACCCACT	GTTGCTGATA	AGCAAGTTCT	1860
TTGTTTTCTT	GTTCTAAACT	TCTGCCCACC	CCAATCAGTA	AGGCCGTCAG	TAAAATAGTT	1920
GTCCTTATTT	TCATCACATA	ATTGAAGATA	AGACCAAAT	TGAAAGATGA	AAAACCTTTC	1980
AGCAGAGAGC	TGATTGTCAT	TTTTTGGATT	AAGAGGTAAG	TCAACCAACT	GATAAAGAGA	2040
TAAAGCTGCA	ACAGCAAAAA	ATGAGACAAC	CACAGCATAG	GAAACAAATC	TTTTGGCTTA	2100
TAATCAAGCA	AGAAAAACAC	GCCTAGATTG	ATCACAAGAG	CCCCACCTAG	GAGGAGGTAA	2160
AGGTTGCCTT	TTACAACATC	AGCTAAAACA	GCCCTATCTT	GAAAACCAAG	TAATTTTTGT	2220
ACCCCAACTC	TTTTCATCTC	CATCATCGGT	TGATACACTG	TCACTAACAC	AAGAAGCAAA	2280
ATAGCCAAGA	CAAAAACAAT	GGCAGATAAA	AGCAAATCTC	GATTTATGAC	TTCCACTGCA	2340
CTTTTGTAGG	TCGGCTCTAG	CAAGGTAGCC	TGGTCTATCT	TGAAAAAATC	GCTCCATTTT	2400
TGTACAATCC	TATCCTTGTC	CATCTCTTGT	GTAGAAGTTA	TCGTATAGCG	ACCATTTAAA	2460
CTACGAGATG	TATCCTTGAT	ATAGGTTTGA	AAAGTCATAA	GCTGAATAGG	TTTGGCTTTT	2520
AGAAAGGTCG	GAATCGTACC	AAGTTTATTG	GAAATTTCTT	TATTACTATA	GACTCCTTCA	2580
CCATCTGTGG	TAAAATCAAG	AGAAGAAATC	CCAAACTCTT	GGTAGGGGAA	GGTATCTTTA	2640
TCAAAAACAC	CAGACTTGAC	CACCTCATCA	CCACTGTCTG	TTTTGATGAT	GGAGACTTTA	2700
TACTCCTTTG	ATACATCCTC	AAAAAATCGA	AGAACAGACG	CTGCAGGTTC	GTTAATATCT	2760
TTCAAATACA	AATCCAAAGA	ATCTACAGG				2789

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CTGCGAATTT	TATTAAAGAT	AATGTGTTAA	TTACAGCGGC	TCACAACTAC	TACAGACATG	60
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1281

ACTATGGGAA AGAAGCGGAT GATATTTATG TTCTTCCGGC TGTTAGTCCA AGTCAAGAAC	120
CATTTGGAAA GATCAAAGTA AAGGAAGTTC GTTATTTGAA GGAATTTAGA AATTTAAATT	180
CTAAGGATGC AAGGGAATAT GACTTGGCTT TATTAATTCT AGAAGAGCCC ATTGGTGCAA	240
AATTAGGGAC TTTGGGTCTT CCTACTAGTC AAAAAAATTT GACAGGAATA ACTGTGACTA	300
TCACAGGCTA TCCATCATAT AATTTTAAAA TTCATCAAAT GTATACAGAT AAGAAACAAG	360
TTTAAAGTGA TGATGGCATG TTCTTGGATT ACCAAGTTGA TACTTTAGAG GGGTCTAGTG	420
GATCTACAGT TTATGATGCT AGTCACCGTG TAGTAGGAGT GCATACTTTA GGAGATGGAG	480
CTAATCAAAT TAACAGTGCA GTTAAATTAA ATGAACGAAA TTTGCCATTT ATTTAwTCGG	540
TTCTTAAAGG TTACTCTCTT GAAGGATGGA AGAAAATAAA TGGTAGTTGG TACCATTATA	600
GACAACATGA TAAACAAACG GGTGGCAGG AGATAAATGA TACCTGGTAT TATTTAGACA	660
GTTCCGGTAA GATGCTTACA GATTGGCAAA AAGTCCATGG AAAATGGTAT TATCTCAATT	720
CAAATGGAGC AATGGTTACA GGTAGCCAAA CTATCGATGG TAAAGTTTAT AACTTCGCTT	780
CATCTGGTGA GTGGATTAA TGTGGAGGA TATATAAAAT GAAGCTTTTG AAAAAATGA	840
TGCAAATCGC ACTAGCCACA TTTTCTTCG GTTTGTTAGC GACAAATACA GTATTGTCAG	900
ATGATTCTGA AGGATGGCAG TTTGTCCAAG AAAATGGTAG AACCTACTAC AAAAAGGGGG	960
ATCTAAAAGA AACCTACTGG AGAGTGATAG ATGGGAAGTA CTATTATTTT GATCCTTTAT	1020
CCGGAGAGAT GGTGTGCGC TGGCAATATA TACCTGCTCC ACACAAGGGG GTTACGATTG	1080
GTCCTTCTCC AAGAATAGAG ATTGCTCTTA GACCAGATTG GTTTATTTT GGTCAAGATG	1140
GTGTATTACA AGAATTTGTT GGCAAGCAAG TTTTAGAAGC AAAAACTGCT ACGAATACCA	1200
ACAAACATCA TGGGAAGAA TATGATAGCC AAGCAGAGAA ACGAGTCTAT TATTTGAAG	1260
ATCAGCGTAG TTATCATACT TAAAAACTG GTTGGATTTA TGAAGAGGGT CATTTGGTATT	1320
ATTTACAGAA GGATGGTGGC TTTGATTGCG GCATCAACAG ATTGACGGTT GGAGAGCTAG	1380
CACGTGGTTG GGTAAAGGAT TACCCTCTTA CGTATGATGA AGAGAAGCTA AAAGCAGCTC	1440
CATGGTACTA TCTAAATCCA GCAACTGGCA TTATGCAAAC AGGTGGCAA TATCTAGGTA	1500
ATAGATGGTA CTACCTCCAT TCGTCAGGAG CTATGGCAAC TGGCTGGTAT AAGGAAGGCT	1560
CAACTTGGTA CTATCTAGAT GCTGAAAATG GTGATATGAG AACTGGCTGG CAAAACCTTG	1620
GGAACAAATG GACTATCTC CGTTCATCAG GAGCTATGGC AACTGGTTGG TATCAGGAAA	1680
GTTCGACTTG GACTATCTA AATGCAAGTA ATGGAGATAT GAAAACAGGC TGGTTCCAAG	1740
TCAATGGTAA CTGGTACTAT GCCTATGATT CAGGTGCTTT AGCTGTAAAT ACCACAGTAG	1800

1282

GTGGTTACTA CTAACTAT AATGGTGAAT GGGTTAAGTA ATGAAGGCTA ATTGTAAACT	1860
GTGATGGATA CTAACTTTG TATAATAGGT GGATAAAAGT CTTACAATC AAAAAACGCA	1920
TAGTATCAAG GTTTTCTGT ACTGCCCTCA AACAGTTAGA CAATTAATTT ATCCGAAGgA	1980
TTTAGTTCTG TATTGCACAG GGCTAAGTCC TTTTAGTTTT ACCTTAATTC GTTTATTGTT	2040
GTAGTAATCA ATATAGTCTA TAATGGCTTG TTCCAATTGC TTAAGCGACT GAAACGACTT	2100
CTCATAACCG TAAACATTT CCGATTTTCTAG AATCCCAAAG AAGGACTCCA TCATACTATT	2160
GTCTGGGCTG TTTCCCTTAC GTGACATGGA TGCTTGAATT CCCTTACTCT CTAGGAACCG	2220
ATGATAAGAA TCGTGTGGT ATTGCCAGCC TTGGTCACTA TGGAGAATCG TATTCTCGTA	2280
GTGCTTCTCT GTGAATGCCT GTTCCAACAT TGTTTGTACT TGTCTAAGT TGGGTGAAGT	2340
TGAAAGATTA TAGGCGATAA TTTCGCTATT AAAGCCATCT AAAACTGGTG ATAAGTAAAG	2400
CTTTTGAGTA CTTGCTGGAA TGGCAAATTC TGTCACATCT GTGTAGCACT TTTCCATTGT	2460
TTTAGAGCCT TCAAATTGGC CTGAATGAG ATTCG	2495

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TACCACCGTA TTCATCCAGC AAGATTGCCA TTTGTCTTTG GGTATTTTCGC AGTTCCTTTTA	60
GCAAGTCATC CACAAAATA GTTTCAGGTA CAAAAGTGG ATCTTGTAAG ATTCTCTTCC	120
AAACAATATT GTCAAAACCG TCCACAAAGC CTGCCTTAAG GAGACTCTTG GTGTGAATGA	180
TTCCAATTAC ATTGTCCTTA TCCCCATCAT AAACCGGGAT ACGAGAATAA TTTTGTTTTA	240
AAATACTTTG GATAATGGCT TGACTATCAT CCTGAATATC CACCATAAAG GCATCCGTTT	300
GAGGAACCAT AACCTCTCGT GCCATCAGTT CATCGAGCGA AAAGACACCT TGTAGCATCT	360
CAATCTCATC AGCATCCAAT GTTCTTTCAC TATTTGTCAG CATATAGGCA ATTTTCATCAC	420
GGGTCATCTT TTCATCCGCA TCATCGAATG ACATAGGAGT CAAATGGCTC AAGAAATTGG	480
TCGAAGCAGC TAAAGCCAA ACAAAAGGAC TGACTAGTTT TCCGATCCCA ATGATAATCG	540
GCGCTGTACG AATTGCCAAG GCATCCTTTA GATTAAAGAGC GATTCTCTTA GGATATAATT	600
CCCCAAAAC GATGGAAATA TAGGTCAAAA ATGCCAAGGA TAGAAAAGTT GCCACGGCTT	660
GTGCTGTTTC GCCATTCCCA AGCCAAGAGG CAATCACACG TCCTAGAGTA TCAGTTAAAC	720

1283

TCGCCCCTGA TAAGATTGTA ATCAGGGTGA TTCCTACCTG GATGGTTGAT AAAAAGTGGT 780
TAGGATTTTC TAGTACCTTC AGCAGGCGGA TGTAGCGTCT GTCTCCTTCT TCCGCCTTTT 840
GTTCAACTCG GGCACGATTA AGAGAAACGG 870

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CGTTCCTCAGA AGCCCGCATT CTCATCGCCA ATGTCGTGAT TGATTGGCC CTTTCTCCAA 60
AATCCAATC AGCCTATGTA GCTATGGATA AGGCACTGCG TGACCTCAA ACATCAGGGC 120
ACTTGCCTAT TCCGCGACAC CTGCGTGATG GGCACCTACAG TGGAAGCAAG GAACTGGGGA 180
ATGCCCAAGA CTATCTCTAT CCACACAAT ATCCTGGAAA TTGGGTCAAG CAAGACTATC 240
TGCCAGAAAA AATTCGTAAT CATCACTATT TCCAAGCAGA AGATACTGGT AAATATGAAC 300
GGGCTTTGGC TCAAAGAAAG GAAGCTATCG ACCGTTTGCG AAAAATCTGA AATCCTTTTC 360
AAAAAATGCG ACTTTCCTCT TGATTTTTTT TGAAAAAGTG GTATCATATA AATATAGAAA 420
CGCTGTGGTG TACGACTTCA CACTTAAGTG TTGACCGACT ATTTTTTGTA TTATTAGGGA 480
AACAAAAGTC TTCTAACAGC ATGTAGGCCG TCTCACACGG AACAGCTTC AGTTAGAGCG 540
AGTTGCCAC CTGCTTAATT GCGCGGGTTC AATACAAACC GTGAAGTTTC GGCACCAATA 600
CAGCTTTTTT CTTTGCCTCC TTAGCTCAGC TGGCAGAGCA GCGGACTCTT AATCCGTGGG 660
TCACAGGTTC GATCCCTGTA GGGGCGATAT AAATACAACA GGAAAAGCCT TATAATATAG 720
GGCTTTTTTT GCTTTCCTTT TAAAAATTGT CGTGCAATTT GCCGTGTTTT TACAACAAAC 780
TTTTACAGC CATAAACTCC TCACTAATTT TTTCTCCAA GGTATGCCCA TAAACGTCAA 840
TCAACATGGA GATATCTTTA TGTCTAAAA TTTGGCTCTT TGTCAACTGT AGTGGGTGA 900
AGTCAGCTAA GCTCGAGAAA GGACAAATTT TGTCTTTCT TTTTGTATAT TCAGAGCGAT 960
AAAAATCCGT TTTTGAAGT TTTCAAAGT CCGAAAACCA AAGGCATTGC GCTTGATAAG 1020
TTTGATGAGA TTATTGGTCG CTTCCAATTT GGCCTTAGAA TAGTGTAGTT GAAGGGCGTT 1080
GACGATTTTC TCTTGTCTT TTAGAAAGGT TTTAAAGACA GTCTGAAAAA GAGGAGGAAC 1140
CTGCTTTAGA TTGCTCTCAA TGAGTCCGAA AAATTTCTCC GGTGCCTTAT TCTGAAAGTG 1200

1284
AAACAGCAAG AGTTGATAGA GCTGATAGTG ATGTTTCAAG TCTTG 1245

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

ATGCCTATGT AACTCCACAT ATGACCCATA GCCACTGGAT TAAAAAAGAT AGTTTGTCTG 60
AAGCTGAGAG AGCGGCACCC AGGCTTATGC TAAAGAGAAA GGTTCGACCC CTCCTTCGAC 120
AGACCATCAG GATTCAGGAA ATACTGAGGC AAAAGGAGCA GAAGCTATCT ACAACCGCGT 180
GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCCTTAC AATCTTCAAT ATACTGTAGA 240
AGTCAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT TACCATAACA TCAAATTGA 300
GTGGTTTGAC GAAGGCCTTT ATGAGGCACC TAAGGGGTAT ACTCTTGAGG ATCTTTTGGC 360
GACTGTCAAG TACTATGTCG AACATCCAAA CGAACGTCCG CATTCAGATA ATGGTTTGG 420
TAACGCTAGC GACCATGTTT AAAGAAACAA AAATGGTCAA GCTGATACCA ATCAAACGGA 480
AAAACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG GAAGAAACCC CTCGAGAAGA 540
GAAACCGCAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA GAGGAACCAG AAGAATCACC 600
AGAGGAATCA GAAGAACCTC AGGTCGAGAC TGAAGAGGTT GAAGAAAAAC TGAGAGAGGC 660
TGAAGATTTA CTTGGAAAAA TCCAGGATCC AATTATCAAG TCCAATGCCA AAGAGACTCT 720
CACAGGATTA AAAAATAATT TACTATTTGG CACCCAGGAC AACAATACTA TTATGCGAGA 780
AGCTGAAAAA CTATTGGCTT TATTAAAGGA GAGTAAGTAA AGGTAGCAGC ATTTTCTAAC 840
TCCTAAAAAC AGGATAGGAG AACGGGAAAA CGAAAAATGA GAGCAGAATG TGAGTTCTAG 900
TTCTCATTTT TTTCATGAAA ATGTGCAAAA TATAGTAGAT TGAAACTAGA ATAGTATACC 960
TCTACTTCTA AAACATTGTT AGAAATCGAT TTGACTGTCC TGTTCCTATT TCATTTTACT 1020
ATATCTTAAC AGATAGTGTA AATAAAGATA AACTATTTAC TGGCTAATTA ATCAGTTAAA 1080
CACTAGTTAA GGAGTAATGA TGAAAAAAG AACAATACTA TTATTGATGG CCAGTCTGTT 1140
AGCTCTTGTC TTAGGAGCAT GTGGTTTCTT GGACATATTG ATCCTGGATC ATTCTCATCA 1200
GGATTACTCT TTACTGCTAT TTTAGAACT GGGGTGGTTT GATGGAAAGT ATTGGTCTTG 1260
TTATCGTTTC ACATTCCAAA CACATTGCAG AAGGTGTTGT TGAAGTGATT AGTAAAGTAG 1320
CTAAAGATGT TCCGATTACT TATGTAAGAG GAACCGAGGG CGGAGGAATT GGAACGAGTT 1380

1285

TTGAACAAGT AGATAGGGTT GTTTCGAAA ATCCAGCAGA TACTTTACTT GCCTTTTGTG	1440
ACCTAGGTTT TGCTAAAATG AACTTAAAA TGGTGAAGA TTTCAGTGAT AAAAGTATCA	1500
TCATCAACAG GGTTCCAATT GTAGAAGTG CCTATAATGC AGCTGCTCTT CTTCAGGCTG	1560
GTGCAGAACT GTCAGTTATT CAAACACAGT TaGCGGAgCt TGAAATCAAT AAATAAGGAA	1620
TTTTACTATA ACTCTTTTTA TAGATAAGCT ATTGaTTATC TCAACTATAA TAATGTTAAG	1680
TnAA	1684

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 970 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGGAGTGGAG AnATATGAAG ACACAAATT TCACATTATT GAAAATCGTT GCTGAGATTA	60
TTATTATTTT GCCATTCTTA ACTAATCTAT AAGTTCTTTA TATTGCTGAA AACGCAATTC	120
AAAAAGGGCT ATTAATTGTG GATTTTCTAA TACCTGCAGA GATTGGATAA AGCGTTCAAT	180
CTCTTTTGA TTGCTTCCCT TTGTTTGAAG AAAGACACTC ATCTTCTTTA AAAATGCCA	240
CGATACTTTT TCAAAAACAT CATACGGTCG TAACATCCTC TCCAACCTCG CTTCGAAGAT	300
TGGGATGTAG GAGAAAAGTT TCGCTCCAT GAGTTCTGAT AAGATATTTA AGAGTCCTTG	360
CTTCATATAC AATCGATTGT GTACTAACTC TTAAATTTCT TTGGATTTT CGAGTAAGGA	420
GGTTGATAAA AAAATCAGAT CTTGATTGCT CAAGAAGGGC ATGGTATTGC AAAAGAGATA	480
GAGTTCAAAC CAGGTCCAAG ACTCGATAGC ATAGAGATAG GTGGTCAAAA ACTCGCTATC	540
CTCCTCTGCT AGTGGGTAGC TTTTATTTAG TGAATGGATG GCATCTTTAA TCACGATGGC	600
ATTCAAACGA CGATAGGTCT GCGCCATCTG TTCTTGATCG ACTTCCTCCA ATAGCTGCTC	660
TAAAGCAGCT ATATCCTGAT GGGCAAAGCG ATTCACAACC TTTGACCGA TTCGCATATG	720
TGGAGATTCT TGATAGTTGT TGAGCTTGTG CCCAACTCA TCAAAGGTCA CATTTATACC	780
TTGGATAGCT AGAATCAACT TATCCGAGA CAGCATAGAC TGCCCTAGTT CAACTTGGA	840
CAACTGAGAA GCTGTTAGAC CCTCACAAGC CACATCTGAC TGCTTGAGCT TTCTGCCAA	900
ACGTAATTCC TTGTAAAATT CCCCAGTTC CATTCTCTCA ATCATCTGAC CACCTCCTAG	960
CTTTTGCAGG	970

1286

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GTGACCACG GGTAAACTA CCCTAACTGC AGCTATCACA ACTGTTTGG CACGTCGCTT	60
GCCTTCATCA GTTAACCAAC CTAAGACTA TGCCTCTATC GATGCTGCTC CAGAAGAACG	120
CGAACGCGGT ATCACTATCA AACTGCGCA CGTTGAGTAC GAACTGAAA AACGTCCTA	180
CGCTCACATC GACGCTCCAG GACACGCGGA CTACGTAAAA AACATGATCA CTGGTGCTGC	240
TCAAATGGAC GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CACAACTCG	300
TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTAAACAC CTTATCGTCT TCATGAACAA	360
AGTTGACTTG GTTGACGACG AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT	420
ATTGTCAGAA TACGACTTCC CAGGTGACGA TCTTCCAGTT ATCCAAGGTT CAGCACTTAA	480
AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATTGATGA ACACAGTTGA	540
TGAGTATATC CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTCGAGGA	600
CGTATTCTCA ATCACTGGAC GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTATCGT	660
TAAAGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTCAAA AAGCAGTTGT	720
TACTGGTGTT GAAATGTTCC GTAAACAACT TGACGAAGGT CTTGCTGGAG ATAACGTAGG	780
TGTCCTTCTT CGTGGTGTTT AACGTGATGA AATCGAACGT GGACAAGTTA TCGCTAAACC	840
AGGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTC TACATCCTTA CTAAAGAAGA	900
AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACTAC	960
TGACGTTACA GGTTCAATCG AACTTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA	1020
CGTGACAATC GACGTTGAGT TGATTCACCC AATCGCCGTA GAACAAGGTA CTACATTCTC	1080
TATCCGTGAG GGTGGACGTA CTGTTGGTTC AGGTATGGTT ACAGAAATCG AAGCTTAATT	1140
CGATTTAGTT CCCAGAAGAA CAATTATTTA AGTTAGACAC TAAAAGAATC TTGCTTGCA	1200
AGGTTCTTTT TTTAGATATT GAACTAATAC TCAATGAAAA TCAAAGAGCA AACTATAATA	1260
TATTGAAACT AGAATAGTAC ACATCTACTT CTAAACATT GTTAGAAATC GATTGACTG	1320
TCCTGATCGA TTTGTCTTGT TCTTATTTCA TTTTACTATA GAAAGTTAGC TACAGACTGC	1380
TCAAAACATT GTTTTAGGT TGTAGATAGA ACTGACGAAG TCAGTAACAT CTATACGACA	1440

1287

AGGCGAAGCT GACGCGGTTT GAAGAGATTT TCGAAGAGTA TAATACTAGA CTAAAATCAA	1500
AAAGCATTAT ACAATAGTAA TATGAAATCA ATTAAAGAAG AAATCCAAAC CATCAAAACA	1560
CTTTTAAAAG ACTCTCGTAC AGCTAAATAT CATAAACGCC TTCAAATCGT TCTATTTCTGT	1620
CTGATGGGCA AATCTTATAA AGAGATTATA GAACTTTTAT AGTGGTTTGA AATAAGATGT	1680
GAACAACTCT ATCAGGAAAG TCAAATAAT TTATAGAAAT ATTTTAGCAG CCAAGGTGTA	1740
CTGTTATAGA TTCAATACAC TTTAGACTGT AATCAAACAA CGATTGGCG AAATGTAAAA	1800
AATATGAGGA GTTCGGACTC GACTCTCTCC TTCAAGAAAC ACGTGGTGGT CGTAACCATG	1860
CTTATATGAC GGTGAGCAA GAGAAAGTCT TTCTTGCCCG CCATTTGAAG GCTACAGAGG	1920
CAGGAGAATT TGTACAATT GATGCCTTAT TTCAGGCTTA TAAAAAGGAG TTAGTCTGTT	1980
CCTACACACG TGATGCCTTC TATCAACTGT TGAAGCGCCA TGGTTGGCGA AATATTACGC	2040
CACGTCCAGA ACATCCTAAG AAAGCAGATG CTCAAAACCAT TGTCGCGTCT AAAAAATAAG	2100
TCTCAATTCA AGAAGACAAG TGAAGTGCAC CCCAAAAGTT AGACAGAAAA AATCTAACTT	2160
TTGGGGTGTT TTTATTATGA AATTAACCTA TGATGATAAA GTTCAGATCT ATGAACTTAG	2220
AAAACAAGGA TATAGCTTAG AGAAGCTTTC AAATAAATTT GGGATAAACA ATTCTAATCT	2280
TAGGTACATG ATTAAATGA TTGATCGTTA CGGAATAGAG TTCGTCAAAA AAGGAAAAAA	2340
TCGTTACTAT TCTCTGATT TAAAACAAGA AATGATTCAT AAAGTCTGAC ATGAAGGCTG	2400
GACTAAAGAT AGAGTTTCTC TTGAATACTG TCTCCCAAGT CGTACGATAC TTCTTAACTG	2460
GCTAGCACAA TACAGGAAAA ACGGGTATAC TATTGTTGAG AAAACAAGAG GGAGAGTACC	2520
TGAGAGCGGA GAATGCCATC CTAAAAAGT TAAGAGAACT CCGATTGAAG GAGGAAAAG	2580
AGAAAGAAGA AAGACAGAAA TTATTCAAGA ATTAATGACT GAGTTTTCGT TAGATATTCT	2640
TCTAAAAGCC ATTAACTAG CTCGTTTGAC TTAATACTAT CACTTGAAAC AGCTAGATAA	2700
ACCAGATAAG GACCAAGAGC TTAAAGCTGA AATTCAATCC ATTTTATATCG AACACAAGGG	2760
AAATTATGCT TATCGTCGGA TTTATTTAGA ACTAAGAAAT CGTGGTTATC TGGTAAATCA	2820
TAAAAGAGTT CAAGGCTTGA TAAAAGTACT CAATTACAA GCTAAAATGC GACAGAAACG	2880
AAAATATTCT TCTCATAAAG GAGACGTTGG CAAGAAGGCA GAGAATCTCA TTCAAGGACA	2940
ATTTGAAGGC TCTAAAACAA TGGAAAAGTG CTACACAGAT GTGACAGAAT TTGCCG	2996

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 837 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

1288

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTTATCAACT CCCGACATGG CTCTCAGACC AATCCAAATC CCTAAAAAAA TCAGAACAAG	60
GATGGTGGTC AAGATCAAAC TCTCGAAATA TAAAGAAAAT AGTTGCAGTA GCATGATTTT	120
TCTCATTTCT ATCTTTTSTA AAGAGTAAAC TCAGCTAGTC CAACTAACTG AGTTTTCCTT	180
TATCTATTAT ATCAAATATA AGTCCGTTTG TAACTAGCGA AGAATTCCTT TGTCCGCTCT	240
TCTTTAGGGG TGTGGATAAT CTCATCCGGA GTTCCAGACT CGATGATTTT CCCCTTATCT	300
AAGAAGAGAA TTTTATCCGC AACTTGGGCT ACAAAGGACA TGTCACTGACT GACCAAAATC	360
ATGGTCTGAC CTGACTTAGC AGCATCTGCA ATAGACTTTT CTACTTCACC GACCAATTCT	420
GGGTCAAGGG CTGAAGTTGG TTCGTCTAAG AGCAAAACAT CTGGTTTCAT AGCAAGCGCA	480
CGCGCTAGGG CAACCCGTTG CTTCTGTCCA CCTGATAAAT GGCGAGGATA ATGGTTTTCA	540
CGGTCCGAAA GCCCAACCTT AGCCAACCTT TCCTTGGCAA TCTTAGTCGC TTCTTGGTCA	600
GATAATTTCT TGACAACAAC CAAGCCTTCT TTCACATTAT CAAGTGCTGT TCGGCGTTCA	660
AACAAATTAA ACTGTTGGAA AACCATAGAC AACTTACGAC GTAGGGCAAG GATTTCTTCT	720
TGAGTGATTT TAGAAAAATC AACTGAAAAA CCATCAATCT GAATAGAGCC ACTGTCAGGT	780
GTTTCTAGAT AATTGAGACT GCGAGAAAGG TTGATTTTCA GCTCTGAAGA CCAATCA	837

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CCGAACAAAA TGGGCTAATT AGATTATAGT AAGAAAGGTA AGTTAAAAAT GAGAATTGCA	60
ATTGGATGTG ACCACATCGT AACTGATGAA AAAATGGCGG TTTCAGAATT TTGAAATCA	120
AAAGGATATG AAGTCATTGA CTTTGGTACC TATGACCATA CACGGACTCA CTACCCAATC	180
TTTGGTAAAA AAGTAGGGGA AGCTGTAACT AGCGGTCAAG CTGATCTTGG AGTATGTATC	240
TGTGGTACTG GTGTTGGTAT CAACAACGCT GTAAATAAAG TTCCAGGTGT TCGTTCGTCC	300
TTGGTTCGTG ATATGACAAC AGCCCTTTAT GCTAAAGAAC AATTGAACGC TAACGTTATT	360
GGTTTTGGTG GTAAATTAC TGGTGAATTG CTTATGTGTG ATATCATCGA AGCTTTCATC	420

1289

CATGCTGAAT ACAAACCAAC TGAAGAAAAC AAAAAATTGA TTGCGAAAAT TGAACATGTT	480
GAAAGTCACA ATGCTCAACA AACAGACGCA AACTTCTTTA CAGAATTCCT TGAGAAATGG	540
GATCGTGGAG AATACCACGA CTAAGAGGTG ACCTATGATT TTAACAGTCA CAATGAACCC	600
ATCCATCGAT ATTTCTATC CCTTGGATGA GTTGAAGATT GATACTGTCA ATCGTGTGGT	660
GGATGTAACC AAAACGGCTG GTGGTAAGGG ACTCAATGTT ACCCGAGTAC TTTCAGAATT	720
TGGCGATTCT GTTCTTGCTA CTGGTTTAGT GGGTGGCAA CTTGGTGAGT TTTTGGTTGA	780
ACATATCGAT AATCAAGTAA AGAAAGATTT CTCTCAATT AAGGGAGAAA CTCGTAAC TG	840
TATCGCTATT CTCCACGGAG ACAACCAA	868

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CCGTTCAAAG TCTTCATAAG ACTCGAAAGT CACAGTTCTT TCGTTCCTGC TGGCATCTAT	60
ATAGGTAAAT TCAATCATGT TAAAACTCC TTTGTTTAAT GCTAACTTTA TTTTACTCCT	120
TATAAAAGAG AATGTCAAGA AAAATGATTG CGCAGCAAC TTTTTTTAAA ATCATCTTAA	180
ATCAAGAAAT CCAAACCTGC TTCCAAGCTT TCTTCGACAG TCTTTTGTAG CGAGGCCAGT	240
GTCTTTTGCC CATCATTTGT CAGGCAGATA AAAC TAGAGC GTCTATCTTG ATGGCAACAC	300
ATGCGACTGA GTAGACCGCA ATTTTAGCT TCCAAGCGAG CCACCATCCT AGAAACTGCG	360
CTCGGGCTCA GATGAAGCTT ATCTGGCAGG TCAATCTGGC GTAGAGATTT TTCTTCAGCC	420
AAGTCCAGAT AGTAGAGCAG GTAGAACTCT TTCAAGGTCA GACTTTGCTC GCTCTGTTGG	480
GCAATGGTCT CTCCAAGAG ACTTTCAATT TCTTCTGAC GCCGATTGAA GTCAAACCAT	540
TTTTCCAAAT AGGTCATAGT GTCTCCTTTC TTTT TAGAGT CATAAATAGA AGAAAGTCCA	600
TTAACGGGCA GTCTCTGCGT CACAAGATGA TTGCGCATGC AATAATTATA CTACTTTTCA	660
AGAATGCTGG CAAGCTCTGT TTTT TAGTG TTTTATTTT GTGTGAATAA TGGGGGAATC	720
CTATTGTTTC AATTCTAAC TCCTTATCAC ATTCGAATTC AGATTTTATT TCATTTCTCT	780
ATCTATAGTT GCTTAGTTTA AAATAAGCAT GGTCTAATAA AGCTATGCAT ATAGTACTGA	840
TTTTAAACAA GGAGCATTAG ATTCCATTAA AGGAGGGCAC AGACATGTCG AGGCGGCCAA	900

1290

AGTTTTTGAT	GTCGGCGTCA	GAAGCTCTCTT	CACGTGGGAA	AAGAAAGACG	TAAACAAGGG	960
AACTTAGAGC	GGAAAAAGCG	AGTCGTCAAA	AAGCGTAAGA	TCCCTTTAGA	AGAATTGAAA	1020
GCCTTTGTAG	AGGCTCATCC	AGACGCTTTT	TTACGGGAAA	TTGCGGCCCG	TTTTGATTGT	1080
GCTTTGCCCT	CCGTATGGGC	AGTTTTAAAG	CAGATTAAGG	TCATTTTAAA	AAAGACGACC	1140
AGTTTTAGGG	AACAAAAGCC	TGAGAAAGTT	TCTGAGTTTC	TTGATATTTT	GGATAACCTA	1200
AAAGATTAC	CAGTCCTATA	TATTGACGAA	ACGGGAATCG	ACCGCTACCT	CTATCGTCCT	1260
TATGCAGGGG	CTCCTAGAGG	GGAGAAAGTC	TATGGCAAGA	TTAGCGGACG	GCGTTTTGAG	1320
CGGACTAATG	AGGTGGAGCA	AAAACCTCAAT	GGTAGTTTTC	TAATCAGATA	TATTGATTCA	1380
CAAATTAGAG	AATGAAAGAA	TAATTATGCA	TAAAAATAGG	AATATAAACC	AAAAATTAGC	1440
TGATTTATAC	TCATTTGCGT	GTCTTTATAA	AAAACCTATC	TTATAATATA	TATATATATA	1500
TATACAAAAT	AGTAAAATGC	TTTTTTTTTT	TAGCAAAAAT	ACCTCAAGTT	TCTTGCTATT	1560
TTGGGTTCCT	TATCTATATA	TTATAGTATG	GTAATTTATT	TATATCCATA	CATGAAAATA	1620
ATACTCGAAA	GGAAATTTCA	AAATATTTTT	TAGACGTCAG	AAGGGTGAAT	ATAGAGAAAC	1680
AGACCGAGTA	ACTCGGTTCA	AATTAATCAA	ATCAGGGAAG	CATTGGCTAC	GGGCCTCGAC	1740
TTCTCTTTTT	GGCTTGTTTA	AGGTCTTGCG	AGGTGGTGTT	GATACTACTC	AGGTCATGAC	1800
CGAAACGGTA	GAAGATAAAG	TAAGTCATTC	AATTACTGGG	CTTGATATCC	TCAAGGGGAT	1860
AGTTGCTGCG	GGAGCTGTCA	TAAGTGGAAC	CGTTGCAACT	CAAACGAAGG	TATTTACAAA	1920
TGAGTCAGCA	GTACTTGAAA	AAACTGTAGA	GAAAACGGAT	GCTTTGGCAA	CAAATGATAC	1980
AGTAGTTCTA	GGTACGATAT	CTACAAGTAA	TTACAGCGAGT	TCAACTAGTT	TGTCAGCTTC	2040
AGAGTCGGCA	AGTACATCTG	CATCTGAGTC	AGCCTCAACC	AGCGCTTCGA	CCTCAGCAAG	2100
TACAAGTGCA	TCAGAATCAG	CAAGTACATC	GGCTTCGACA	AGTATTTCTG	CATCATCTAC	2160
TGTGGTAGGT	TCACAAACAG	CTGCCGCTAC	AGAAGCAACT	GCTAAGAAGG	TCGAAGAAGA	2220
TCGTAAGAAA	CCAGCTAGTG	ATTATGTAGC	ATCAGTTACA	AATGTCAATC	TCCAATCTTA	2280
TGCTAAGCGA	CGCAAGCGTT	CAGTGGATTC	CATCGAGCAA	TTGCTGGCTT	CTATAAAAAA	2340
TGCTGCTGTT	TTTTCTGGCA	ATACGATTGT	AAATGGCGCC	CCTGCAATTA	ATGCAAGTCT	2400
AAACATTGCT	AAAAGTGAGA	CAAAAGTTTA	TACAGGTGAA	GGTGTAGATT	CGGTATATCG	2460
TGTTCCAATT	TACTATAAAT	TGAAAGTGAC	AAATGATGGT	TCAAAATTGA	CCTTTACCTA	2520
TACGGTTACG	TATGTGAATC	CTAAAACAAA	TGATCTTGGT	AATATATCAA	GTATGCGTCC	2580
TGGATATTCT	ATCTATAAAT	CAGGTACTTC	AACACAAACA	ATGTTAACCC	TTGGCAGTGA	2640
TCTTGGTAAA	CCTTCAGGTG	TAAAGAACTA	CATTACTGAC	AAAAATGGTA	GACAGGTTCT	2700

1291

ATCCTATAAT ACATCTACAA TGACGACGCA GGGTAGTGGG TATACTTGGG GAAATGGTGC	2760
CCAAATGAAT GGTTCCTTTG CTAAGAAAGG ATATGGATTA ACATCATCTT GGACTGTACC	2820
AATTACTGGA ACGGATACAT CCTTTACATT TACCCCTTAC GCTGCTAGAA CAGATAGAAT	2880
TGGAATTAAC TACTTCAATG GTGGAGGAAA GGTAGTTGAA TCTAGCACGA CCAGTCAGTC	2940
ACTTTCACAG TCTAAGTCAC TCTCAGTAAG TGCTAGTCAA AGCGCCTCAG CTTCAGCATC	3000
AACAAGTGCG TCGGCTTCAG CATCAACCAG TGCCTCGGCT TCAGCGTCAA CCAGTGCGTC	3060
AGCTTCAGCA AGTACCAGTG CTTCAGTCTC AGCATCAACA AGTGCTTCAG CCTCAGCATC	3120
GACAAGTGCC TCGGCTTCAG CAAGCACATC AGCATCTGAA TCAGCGTCAA CCAGTGCTTC	3180
GGCTTCAGCA AGTACCAGTG CTTCAGCTTC AGCATCAACC AGCGCCTCGG CCTCAGCAAG	3240
CACCTCAGCT TCTGAATCGG CCTCAACCAG CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC	3300
TGAATCGGCC TCAACCAGCG CCTCAGCCTC AGCATCAACG AGTGCTTCGG CTTCAGCAAG	3360
CACAAGCGCC TCGGGTTCAG CATCAACGAG TACGTCAGCT TCAGCGTCAA CCAGTGCTTC	3420
AGCCTCAGCA TCAACAAGTG CGTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA	3480
ACGAGTGCGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT CAGCAAGCAC CTCAGCTTCT	3540
GAATCGGCCT CAACCAGTGC GTCACCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA	3600
CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG	3660
CATCAACCAG TGCCTCAGCC TCAGCAAGTA CTAGTGCATC GGCTTCAGCA TCAACCAGTG	3720
CCTCGGCTTC AGCGTCAAAC AGTG	3744

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CGATAAGAG GCCTTGAGTA ATCTCAATTT GCAGATTGAA AATGGAGAGA TTATGGGCTT	60
GATTGGTCAT AATGGGGCTG GAAAATCGAC CACTATAAAA TCCCTAGTCA GTATCATTTT	120
ACCCAGCAGT GGTCTGATTT TGGTAGACGG TCAGGAGTTA TCGGAAAATC GCTTGGCTAT	180
TAAACGAAAG ATTGGCTACG TAGCAGACTC GCCTGACTTA TTTTACGCT TAACGGCCAA	240
TGAATTTTGG GAATTGATCG CCTCATCCTA TGATCTGAGT AGATCTGACT TGGAGGCTAG	300

1292

TCTAGCTAGG CTATTGAACG TTTTGTGATT	TGCTGAAAAT CGCTATCAGG TTATTGAAAC	360
TCTTTCTCAC GGAATGCGTC AGAAAGTCTT	TGTCATCGGA GCACTCTTGT CTGATCCCGA	420
TATTTGGGTC TTGGATGAAC CCTTGACTGG	TTTGGATCCC CAGGCTGCCT TTGATTTGAA	480
ACAGATGATG AAGGAACATG CACAAAAAGG	GAAGACAGTC TTGTTTTCAT CTCATGTCCT	540
AGAGGTGGCA GAGCAAGTCT GTGATCGGAT	TGCCATTTTG AAAAAGGGGC ATTTGATTTA	600
TTGTGGTAGT GTAGAGGACT TGAGAAAAGA	TTACCCAGAC CAGTCTTTGG AAAGTATCTA	660
CCTTAGTCTT GCTGGTAGAA AAGAGGAGGT	TGCGGATGCG TCTCAAGGTC ATTAATAAAT	720
TAGTTGATAT CAATATCCTT TATTCATCTC	AAGAAGCTAA TCTGGCTAAT CTACGAAAGA	780
AGCAGGCTAA GAATC		795

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGGTAATGTG CTTGGCAGCw TCCTTGACAC	TGCTACTACC ATTTCCCATATA GCGACCGACA	60
TACCAACGCC AGCCAGCATT TCAAGATCAT	TATCTGAGTC ACCAAAAGCC ATGACTTGGT	120
TGAGGTCAAA GCCATATTCT TTCCCAACTC	GGCGAATGCC TTCTAATTTA GAATTTCCCT	180
GATTGATGAC ATCCGATGCA AAAGGATTGC	TACGTGTCAA TTCTCAAGTCT TCAAAATCAG	240
CTGCCGCCCTT CTCAGATTCT TCTGGTGTC	TCAGCATCAA AACTTGGTAG ATAGGCTGAT	300
TCATCAGGTG AAGCAGGTCC TCTTCCTTTT	GGGGAACAAC CTGCTGACC ATGCGATTAA	360
AAGACTGACT CACCGTCCGA GTTAAACAG	AGGGAACGAA GCGACTAATT CGTTGGGAAA	420
AAGAACCAG ACCAAAGGAC ATGATTTTAG	AACCCAACAT GGCATCCTTG GTCCCTAGAG	480
CAATCTCCGT GCCCTCTTTT TTAGCATAGC	TAATTAGATG GCGCAAATGT AACTTGGAAG	540
TAGGGCTCGT GAACAAGACT CTGTCTTTAC	TAAAGATATA CTGGCCATTA TAGGTTACCG	600
CAAAATCCAG ATCCAAATCG TCCATCAATT	CCTTAACAAA AAAAGGTCCT CGCCCTGTCTG	660
CTACGCCAAC TAGTACCCCT TGTTCCTTGA	CAATCTTAAT CGCATCCTTA GTGGATTTCA	720
AAACACTCTT GCGATTGTTG ACCAAGGTTT	CATCGATATC AAAAAAACA GCTTTGACTT	780
CCATCCTATC CCAATCTCCC CTTTTGTGAT	ACAATGATTA TACCACATTT CAGAAAGAGT	840
GAGTAAATCA TGCCTAAGAA AATCCTTGTT	TTACATACGG GTGGAATAT TTCCATGCAG	900

1293

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GCCGATGCTT CTGGCGCTGT TGTGACGAGT TCAGATAATC CCATGAACCA TGTGTCCAAC      960
CCACTTGAAG GAATCCAAGT CCACGCCTTG GACTTTTTTTA ACCTTCCAAG TCCCCATATC      1020
AAACCCAAAC ATATGCTGGT CCTCTACCAG AAAATTAAAG AGGAAGCAGA TAACTACGAT      1080
GGAGTGGTGA TCACACACGG AACCGATACT TTAGAGGAAA CAGCCTATTT CCTTGATACC      1140
ATGGAAGTTC CCCATATGCC TATCGTTCTA ACAGGAGCCA TCGGTAClCC AATGAGCTCG      1200
GTAGTGATGG TGTTTATAAT TACCTAAGTG CTTTACGAGT GGCCAGCGAT GACAGGGCTG      1260
CTGACAAAGG AGTTTGGTC GTTATGAACG ATGAAATCCA CGCTGCCAAG TATGTCACCA      1320
AACACATAC GACTAATGTC AGCACCTTCC AGACTCCAAC ACATGGCCCC CTGGTCTCA      1380
TCATGAAACA GGAAATCCTC TACTTCAAAA CAGCTGAACC TCGTGTTCGC TTTGACCTTG      1440
ATCACATACA AGGTTTAGTC CCTATCATCT CGGCTTATGC TGGTATGACA GATGAGCTGA      1500
TTGATATGCT GGATTTAGAA CACTTGGACG GTTTGATTAT CCAAGCCTTC GGAGCTGGTA      1560
ATATTTCCCA AGAAACGGCT CAAAAATTAG AAAGCCTTCT GCAAAAAGGA ATTCCAGTCG      1620
CTCTGGTATC ACGATGCTTT AACGGTATTG CCGAGCCTGT TTATGCATAC CAGGGTGGGG      1680
GCGTACAGTT GCAAAAAGCA GGCCTTTTCT TTGTTAAAGA ACTCAACGCC CAAAAGCTC      1740
GCTTGAAACT CCTCATCGCC CTCAATGCCG GACTAACAGG ACAGGCTTTG AAAGACTATA      1800
TGGAAGGCTA ATACTCTTCG AAAATCTCTG CAAACCACGT CACGTCGCCT TACCGTATGT      1860
ATGGtACTGA CTTCGTCAGT TTCATCTACA ACCTCAAAAA CATGTTTTGA GCTGACTTCG      1920
TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTCGTCAGT TCTATCTACA      1980
ACCTCAAAAA CATGTTTTGA GCTGACTTCG TCAGTTCTAT CTACAACCTC AAAAACATGT      2040
TTTGAGCTGA CTTCGTCAGT TCTATCTACA ACCTCAAAAA CATGTTTTGA GCTGACTTCG      2100
TCAGTTCTAT CTACAACCTC AAAAACATGT TTTGAGCTGA CTTCGTCAGk TCTATCTACA      2160
ACCTCAAAAA CATGTTTTGA GCTGACTTCG TTAGTTTCAT CTACAACCTC AAAAACATGT      2220
TTTGAGCTGA C                                     2231

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(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

1294

GAGTCAAAGG CTCCGAGGTT GACTTTTAC AAGGGGACAG GTGAATATTA TCTAGACCTG	60
TCAGAAATTC TCTTCTTTGA AACAGAAGGG AGCAAGATCT ACGCTCATAA CCAGAAGGAA	120
GCTTATGAGG TTCGCCTCAA GCTCTATGAG TTGGAGTCTA TCTTGCCTCG CTATTTTAAT	180
CGAGTTTCCA AGTCAACGAT CGCAAACATC CGTCAGATTT ACTCAGTGGG CAAGTCCTTT	240
TCAGGAACGG GCACCATTTC CTTTATCAG ACGCACAAGG AGGTTTCATGT CTCACGGCAT	300
TACCAATCCC TCCTAAAAGA AAATCTAAGA AACATGAGGT AAAAAACATG AAAAAGAAAG	360
CATTGATGAT TGTATTATG GTTTTAGCAG CTTGGATCTT GCTGCAAGGG AATTTTGGA	420
TTCTTCTTT GGATGGTAAA ATATGGCCTT TACTAGGTAT TGTTTTTTTT GCTTATAAGT	480
CCATTGAGTC CATCCTTAGA CGTCATCTCA CTTGGCAGT TTTTACAGGT TTACTGGCGC	540
TCATCATGTC AAATTACGCT TATGACTTGT TACCAGTTAC CAATCATTCT CTATTTTGGG	600
CTAGCATCTT GGTGGTACTT GGTGTTGGTT ATCTGACGCA TTCAAGTAAG TTCTGGAATG	660
AAAAAAATG GTGTACAAT GGGAAAAAA CAGTCGTCAC GGATAAGGAA GTCGCTTTTG	720
GTAGCGGGAC CTTCTATAAG CAAGATCAAG ATCTCGTAGA TGACCAAGTG GAAGTCGCTT	780
TTGGGGATGC TAAATCTAC TATGATAATG CAGAGATGCT AGGTGATTTT GCAACTTTAA	840
ATATTGAAGT GGCCTTCGGG AATGCAACCG TCTATGTTCC ACAACACTGG CGTGTAGATT	900
TGAAAGTAGA AACCTCCTTT GGTGCAGCTA AGGCTGACGC TCCTGTAGCC CCAACCAGCA	960
AAACCTTGAT TATCCGTGGA GATGTGGCTT TTGGGAAGTT GGAAATTGTC TACGTAAAT	1020
AAAAAATCT TCACTTCAAC CATCAAAATA GACGTACTAA GAGTAGGAAA TTGATGCCTT	1080
GCTCTGATTT CAGTTCTATG GTTGTAGAC TTTAAAAAAT GAAATGCTGC CTTTAAAGT	1140
TGTATATTTT TCGATATTTT GGCTTTTACG TTTGATGTAT CTATGTACTA CAGCGTAGAT	1200
GATGTAGTGT CAAATGCTTT TAAAAACGG ATGATATTGG ACAGTTTTTT TGCCTTTAAT	1260
TGCTCAGGAA CCATGAAAGT CAGTACCTGG GTTTATGACA AGGGAGAATG	1310

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

ACTCTGATTT GATTGGAACG ACAGTCGGTG CCATTGCAGT TACTTCAAAC GTAACGACTT	60
ATGTTGAGTC TGCTGCTGGT ATCGGTGCAG GTGGACGTAC TGCTTTGACA GCCTTGCTTG	120

1295

TAGCTATCTG TTTTGCGATT TCAAGCTTCT TTAGCCCACT TCTAGCGATC GTACCAACAG	180
CGGCTACAGC TCCAATCTTG ATTATCGTTG GGATTATGAT GCTTGGTAGC TTGAAAAATA	240
TCCATTGGGA TGATATGTCT GAAGCAGTTC CTGCCCTTCTT CACATCTATC TTTATGGGAT	300
TCAGCTACTC TATCACTCAA GGGATTGCAG TTGGTTTCTT GACTTACACT TTGACTAAGC	360
TTGTTAAAGG TCAAGTTAAA GATGTTTCATG TCATGATTTG GATTTTGGAT GCCTTGTTTA	420
TCCTTAAC TA CATCAGCATG GCCTTATAAT AGAATGACCC AGGGGGATT CCCCCCTTTT	480
TTAATACAaG GAGATAGGTG ATGAAAGAGA AAAATATGTG GAAAGAATTG TTGAATCGTG	540
CAGGCTGGAT TTTGGTCTTT TACTTGCCG TCCTTTTATA TCAGGTTCCT CTAGTGGTTA	600
CCTCTATTTT GACTTTAAAA GAAGTAGCCC TGCTACAGTC AGGGCTGATA GTTGCTGGCC	660
TTTCAATTGT GGTCTGGCT CTATTTATTA TGGGAGCTCG TAAACCAAG TTAGCTAGTT	720
TTAATTTTTC TTTTPTTAGA GCTAAAGATT TGGCACGTTT GGGCTTGAGT TATCTAGTTA	780
TTGTCCGGTC AAATATACTT GGTTCATT TATTGCAACT GTCAAATGAG ACGACAACAG	840
CTAACCAGTC TCAGATTAAT GATATGGTTC AAAATAGTTC GTTGATTTC AGTTTCTTCT	900
TGCTAGCCTT GCTTGCTCCG ATTTGTGAGG AAATCTTGTG TCGTGGGATT GTTCCTAAAA	960
AGATTTTCCG AGGCAAGGAG AACTTGGGAT TTGTAGTCGG TACGATTGTG TTTGCTTTAT	1020
TGCATCAACC AAGTAATTTA CCTTCTTTAT TGATTATGG AGGTATGTCG ACAGTTCTAT	1080
CTTGACAGC CTACAAGACC CAACGTTTGG AAATGTCGAT CTGCTTCAC ATGATTGTTA	1140
ATGGGATTGC TTTCTGTTTG TTGGCTCTTG TGGTATTAT GAGTCGGACA TTAGGAATTT	1200
CTGTTTAAAA GTTTTATGT AGGAACCGAC CTCTTCTAC CAGGGAAAGA TGAATGCAAT	1260
CGTGTCCATC TTTTCTTTT TATGGTAAAA TAGAAAAATA ATATGATGAA AATCCTTGAG	1320
GGAGTGACCG ATATGTCAAG TAAAGCCAAT CATGCAAAGA CAGTTATTTG CGGAATTATC	1380
AATGTAACCC CAGACTCCTT TTCGGACGGT GGTCAATTTT TTGCTCTTGA GCAGGCGCTC	1440
CAGCAGGCTC GTAAATTGAT AGCAGAAGGA GCCAGTATGC TAGATATCGG CGGAGAATCG	1500
ACTCGGCCGG GAAGTAGCTA TGTTGAGATA GAAGAGGAAA TCCAGCGTGT TGTTCAGTG	1560
ATCAAAGCGA TTCGCAAGGA AAGTGATGTC CTCATCTCTA TTGATACTTG GAAGAGTCAA	1620
GTAGCAGAGG CTGCTTTGGC TGCTGGTGCC GATCTAGTCA ATGATATCAC TGGTCTTATG	1680
GGTGATGAGA AAATGGCTTA TGTGGTAGCT GAAGCGAGag CGAAAGTGGT CATCATGTTT	1740
AACCCAGTTA TGGCTCGACC TCAGCATCCT AGTTCGCTTA TCTCCCTCA TTTGGTTT	1800
GGTCAAACCT TTACAGAAAA AGAGTTAGCT GACTTTGAAA CATTGCCAAT CGAAGACTTG	1860

1296

ATGGTGGCTT TCTTTGAACG AGCACTAGCG AGAGCGGCAG AAGCTGGTAT TGCACCAGAA	1920
AATATCCTGT TGGATCCAGG AATTGGCTTT GGTCTGACCA AGAAAGAAAA TCTGCTTCTT	1980
TTACGGGACC TGGATAAACT ACATCAGAAG GGCTATCCAA TCTTTCTCGG AGTGTGCGGC	2040
AAGCgATTTG TCATCAATAT CCTAGAGGAG AATGGTTTGG AAGTCAATCC TGAGACAGAG	2100
CTTGGTTTCC GAAATCGGGA CACGGCTTCG GCTCATGTAA CTAGTATCGC TGCGAGACAG	2160
GGTGTAGAAG TGGTGC GCGT GCATGACGTA GCTAGTCACA GGATGGCAGT TGAAATTGCC	2220
TCTGCCATTC GTCTGGCTGA TGAAGCGGAA AATTTAGATT TAAACAATA TAAATAAGAT	2280
GAAAGAAATT GAAACAATC AGTGGATTGC TAACTACCGG ACGGATCAAC CGCATTTTGG	2340
CTTGGAACGA ATGGTGGAAC TGTTAGCTTT GCGTGGCAAT CCCCATCTCA AACTCAAGGT	2400
CCTCCATATC GGAGGGACTA ACGGCAAGGG CTCGACTATT GCTTTTGTGA AAAAGATGCT	2460
AGAAAAGCTA GGGTTGAGAG TTGGCGTGT TAGCTCGCCC TATCTCATTC ATTACACAGA	2520
CCAGATTAGC ATCAATGGGG AATCGATCTC AGAAGCGAGG CTAGAAGCTC TCATGGCAGA	2580
CTATCAGTCT TTGCTGGAGG GAGAAGCGGT CGCCAATTTA CAGGGCACAA CCGAGTTTGA	2640
GATTATCACA GCCCTGGCCT ATGACTACTT TGCCCTCAGAG CAAGTAGATG TGGCCATCAT	2700
GGAAGTTGGC ATGGGTGGAC TTTTGGATAG TACCAATGTC TGTCAGCCCA TTTTGACAGG	2760
AATTACAAC TTTGGCTTGG ATCATGTGGC TCTACTTGGT GACACCTTGG AGGTCATAGC	2820
AGAGCAGAAG GCAGGTATTA TCAACAAGG GATGCCCTTG GTAACAGGGC GTATTGCTCC	2880
AGAAGCCTTG GCTGTGATTG ACCGCATTGC GGAAGGAAAA GATGCGCCGA GACTTGCCCTA	2940
CGGGACAGAT TATCAGGTTT GTCATCAAGA AAGTGTGGTG ACAGGGGAAG TCTTTGACTA	3000
TACAAGTGCT GTCAGACAAG GTCGCTTCCA GACTAGCCTG CTTGGTTTGT ACCAAATAGA	3060
GAATGCTGGG ATGGCCATAG CTTTACTTGA TACTTTTGT CAAGAAGATG GTCGAGAGCT	3120
AGCAAGCAAT GATTTTCTTG GTCAAGCCTT GGAAGAAACA AGTTGGCCAG GCGTTTGGG	3180
AATCGTGTC AGAGATCCCT TGATGATTTT GGATGGAGCC CACAATCCCC ATGCTATCAA	3240
GGCCTTGTG GTAACCTTGC AAGAACGTTT TGCGGATTAT CATAAGGAAA TCCTCTTCAC	3300
TTGTATCAAA ACCAAGGCCT TGGAGGATAT GTTGGACTTG CTGGGAGCCA TGCCAGTTAC	3360
CGAGCTTACT CTAACACATT TTGCGGATAG TCGGGCGACG GATGAAAACG TGCTGAAAGA	3420
GGCAGCTAAG TCTAGAAATC TCAGCTACCA AGATTGGCAT GATTTTCTAG AGCAGAATTT	3480
GACAGATAAA AAAGAAGAGA AACAAACAGT TAGGATTGTC ACAGGTTCCT TGTATTTCTT	3540
GAGCCAAGTG AGGGCCTATC TGATGGAGAG GAAGAACGAG AATGGATACA CAAAAGATTG	3600
AAGCGGCTGT AAAAATGATT ATCGAGGCTG TAGGAGAGGA CGCTAATCGC GAGGGCTTGC	3660

1297

AGGAAACACC	TGCTCGTGTA	GCCCGTATGT	ATCAAGAGAT	TTTTTCAGGT	CTTGGTCAAA	3720
CAGCAGAGGA	ACATTGTGCA	AAATCCTTTG	AAATTATTGA	CGATAATATG	GTGGTAGAAA	3780
AGGATATCTT	TTTCCATACC	ATGTGTGAAC	ACCACTTCTT	GCCATTTTAT	GGTAGAGCGC	3840
ACATTGCCTA	CATTCCAGAT	GGTCGTGTGG	CAGGCTTGTC	TAAGCTAGCC	CGTACGGTTG	3900
AAGTTTATTC	GAAAAAACCA	CAAATTCAAG	AACGTTTGAA	TATCGAAGTG	GCCGATGCCT	3960
TGATGGACTA	TCTAGGTGCT	AAAGGAGCCT	TGTTGTGCAT	TGAGGCGGAA	CATATGTGTA	4020
TGAGTATGCG	TGGTGTTAGA	AAACCAGGCA	CTGCAACCTT	GACGACAGTA	GCTCGTGGTC	4080
TATTTGAAAC	AGATAAGGAT	CTCCGTGACC	AAGCTTATCG	TTTAATGGGG	CTATAAAAAG	4140
AATCCGCTTC	AAGCGGATTT	TTCTAGAAAAG	GAATCATTAT	GGATCAACTG	CAGATTAAGG	4200
ATTTGGAAAT	GTTTGCCTAT	CATGGTCTTT	TTCTTAGTGA	GAAAGAATTG	GGGCAGAAAT	4260
TTGTCGTTTC	AGCCATCCTA	TCCTATGATA	TGACCAAGGC	AGCTACAGAC	TTGGATTTAA	4320
CAGCCTCTGT	CCATTACGGA	GAATTGTGTC	AGCAGTGGAC	GACTTGGTTT	CAGGAAACGA	4380
GTGAAGATTT	GATTGAAACG	GTAGCCTATA	AACTGGTGGA	ACGTACCTTT	GAGTTTATC	4440
CTCTTGTCCTA	AGAAATGAAG	TTGGAACCTGA	AAAAACCTTG	GGCACC GG TG	CATTTGTCAC	4500
TAGATACTTG	CTCGGTAACC	ATTTCATCGCC	GCAAGCAACG	AGCCTTTATC	GCCCTAGGAA	4560
GCAATATGGG	AGATAAACAA	GCAAACCTGA	AGCAAGCCAT	TGACAAACTG	CGAGCTCGTG	4620
GCATCCATAT	TCTCAAAGAG	TCCAGTGTCT	TAGCGACGGA	GCCTTGGGGT	GGAGTGAGC	4680
AGGATAGCTT	TGCCAATCAA	GTGGTTGAGG	TGGAACCTTG	GCTACCAGCA	CAAGACTTGT	4740
TAGAAACCTT	GTTAGCCATT	GAGTCAGAGC	TGGGACGGGT	GAGAGAAGTG	CATTGGGGAC	4800
CTCGTTTGAT	TGATTGGAC	TTGCTCTTTG	TGGAGGACCA	GATCCTTTAT	ACAGACGACC	4860
TCATATTGCC	TCATCCTTAC	ATAGCGGAAC	GCCTTTTGT	CCTTGAGTCT	TACAGGAAAT	4920
TGCGCCTCAT	TTTATCCATC	CGATATTAAA	ACAACCGATC	CGCAACTTGT	ATGATGCTTT	4980
GAAAAAATAG	AAAAACTCTA	GTTTTCAGTT	ACTTGCAACT	GAAGGCTAGA	GTTTTTATAC	5040
TCTTCGAAAA	TCTCTTCAAA	CCACGTCAGC	GTCGCCTTAC	CGTACTCAAG	TACAGCTTGC	5100
GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	TAAAATAGGT	CATTTTCTTC	5160
TGGGAGGAGG	ATAGTTTCTC	TACCGTCCAT	GTCTAAAACC	AGTACTCTTG	GGGGATAACG	5220
AGGGTCGAAA	GGATGGTTAA	AGTCAAAATC	AATGGCTGTA	GGGAGGTGTT	GACTTGAAAA	5280
GTGGAAGGTA	ATCTTTCCTT	GGTTATTAAG	CAATTGAAAC	TCGAGTCTTT	CTTCCAATTC	5340
AAAGACATTT	TTTAAGAAAT	GGTCGATGAT	ATACCAAAAA	GAGTCAATGA	TGTCATCAGG	5400

1298

CAAGCTGGTA ACAATACCAA AACTAGCAGA TCGCATGTGG GTATTGGTAA AAGCCATATC	5460
TCTGTCCCCT TTCTTTTCCC TTATCATACA GCAAATAGGA TTAAAAATCA AGAAAAGGTG	5520
ATTTTTTGAA AAGGATTTTA GTTACAGGGA GAAATAGGGA AAAAATTCCT AAAAATCTAC	5580
CGAAGTTAAT AGGTAAATTC CCAAATTAAC TTGATTATAT AACTTTCAGT TACTTTGAGA	5640
AGTTACCGAA AAATATTTTT CATATCTATT GACTTTTAGG GGTAAAATTT GGTATGATAG	5700
TAGGCGGTAT TGTTTACCCC ATTTGAAAGG CCCCAGAAC TTCCAAATAC TTTTCGATGG	5760
GAAGGAACAC CCATCACCGT AAACAAAAAT CGAACTATAT ATAGGAGAAA TCATGAACAA	5820
AACAACATTT ATGGCTAAAC CAGGCCAAGT TGAACGTAAA TGGTACGTAG TTGACGCAAC	5880
TGATGTACCA CTGGACGTC TTTCTGCAGT AGTTGCTAGC GT	5922

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1988 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TAACATCTA CGATGAGCTG TTGTGATTCT CATTAGTTCC CCTTCCCAA GAGGCATAGG	60
GGTGCGCATA ATAGATGTGC TCCTCAGAAA ATATATCAAA CAAGCGATTG AATCCGTTCT	120
CATTATCTGC CGTGATGGAA AGAATCTTGT GTTGTTTTAA GATGAGTTTT AGAGCCTGAT	180
TGACCACCTC AGCACTTTTA TTTGGAATCA ATCGGATGAT CTGATGTCTA CTCTTTCGAT	240
CCGTCAAGAC AATCAAGCAG TAGTTTTTCG ATCTCGTAAG TAGAACCGTA TCAATCTCAT	300
AATGCCCAT CTCCAAGCGA AGATTGATAG CTTCAGGCCG CTGTTTCGATG GATTGACCAG	360
CAGGTTTAAA GTTGGTGCTA GCCTGTTTCT TAAGCGCTTT TCCTTTTCTA GGGTAAAGCA	420
AATCCTGCTT GCTTAACCCC AATTTTCCAT GATGAATCCA ATAGTAAATG GTTGAAATTC	480
CCACGTTAAC CCCTTTAGCC ATAACCATCA TTTCAGGCGA AAATTTTGG TTATGATAGT	540
GGAGAATCTT TTCCTTTAGT TCCTTGGTCA AGCTTGATTT CTGACCGAG CGCTTGCGAT	600
TGTTTTCATA AGACTGTTGA GCGTAGTCGG CAGAATAAAC CTCTTTGAAG CGCCCTTTTC	660
CAAGACATTG TCGGACTGTC CCACGCTTGA TTTCAGTGTG ATAGTTTGAG GAGCTTTTCC	720
AAGTAGAGAG GCAATTTCTC TATTTGATTT TCCTTCTTTT TTCCATCTTT CGATTAAGCG	780
ACGGCTATCG ATTTGTCAAAT GTTTGGCTTT TGTAATATAA TTGTCTTGCA TCTCTGTGCC	840
TTTCTTGTGT TTGTGGTTGA ACAACAAGTA TAACACAGAG GTGCTTTCTT ATGCTACAA	900

1299

GAGCTTTCAT TATTTCCATT TTCTTTTGGG TTTCACCTCTA TTCTGAAAAA CTGTGTGTATA	960
TTTACTGAAG CTAGCAAGTC TTACCTGTAA ATTTAATGAA AGCAACACAA AATCCGAGAG	1020
GGGAATCTCG GATTAATAGA TAGAGAGTTT TTAGTTTAAA TAAATTGTTT AAAATATCAA	1080
CAACATCACT TCTTTTCTTA ACCTGATAAG TCTTGATTCC TAATTTTGGG GCTACGATTA	1140
TATTGTCTC AATATCGTCT AGAAAGACAC AATTTCTAGG TTATAACTGG TATTTATCGA	1200
.TAGTTACTCA TATACATCAG TCCACCTCCA TACTTATGTG CGAGCCTCTC TTTGTATTAT	1260
ACCTCCATAC TCACCTTACA GATTCTTTTG GTAATAATAT CTTTGCCTAA TGTAGAGACA	1320
GTCTTGCAAA GAAAAAAGT CTTGTAGCC ATGTTTCTGA TAAAAGTCCG GTGCCTGGAA	1380
CTGGTAAGTA TTGACAAAGG CAAACAACA ATTCGATTG TTAGCTTCAC TTTCTGCCTG	1440
TTGCAATAGT TTTGAACCGA TTCCTTGCCC TCGCAGTTCC TCTTTTACAA ACAAATACTC	1500
GATTTCTAGC CAATTTCCAA AAGTCTCTGC TATCAACCT GCCAGGAGAT TGCCCTTTTC	1560
ATCTTCGACA TAAAGATTAA GTGGCTCACT TTCAGCCTCT TCTCTTTTTC AACGGTATA	1620
AACACGAATC AGATTCCCTA TTTCTTGCGA TTTATGTGAT TCCTTATTTT CCAATCTAAA	1680
GTATAGTGAA ATGAAATAAA ACATGCGCAA ATCGATTAAG GAATTTAATC TAATTTCTAA	1740
CAATGTCTTA GAAATCAAAG TGTACTATTT TAACTCAAT GCACTATACA TCTAATACTC	1800
AATAAAAATC AAAGAGCAA CTAGGAACT AGCCGAGGT TGCTCAAAAC ACTGTTTGA	1860
GGTTGTAGAT AGAACTGACG AAGTCAGCTC AAAACATAGT TTTGAGGTG TAGATGAAAC	1920
TGACGAAGTC GGCTCAAAAC ATGGTTTGA GGTGTAGAT GAACTGACG AAGTCAGCTC	1980
AAAACAGG	1988

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CCGGATATTT GTTTATGTA ATTTCTTGC AAGTTTCTTC TTAGTAGCTT GTCAGTCAGG	60
TTCTAATGGT TCTCAGTCTG CTGTGGATGC TATCAACAA AAAGGGAAAT TAGTTGTGGC	120
AACCAGTCCT GACTATGCAC CCTTTGAAT TCAATCATTG GTTGATGGAA AGAACCAGGT	180
AGTCGGTGCA GACATCGACA TGGCTCAGGC TATCGCTGAT GAACTTGGGG TTAAGTTGGA	240

1300

AATCTCAAGC ATGAGTTTGT ACAATGTTTT GACCAGTCTT CAAACTGGTA AGGCTGACCT	300
AGCAGTTGCA GGAATTAGTG CTA CTGACGA GAGAAAAGAA GTCTTTGATT TTTCAATCCC	360
ATACTATGAA AACAAGATTA GTTTCTTGGT TCGTAAGGCT GATGTGAAA AATACAAGGA	420
TTTAACTAGC CTAGAAAGTG CTAATATTGC AGCCCCAAAA GGGACTGTTC CAGAATCAAT	480
GGTCAAGGAA CAATTGCCAA AAGTTCAATT AACTTCCCTA ACTAATATGG GTGAAGCAGT	540
CAATGAATTG CAGGCTGGAA AAATAGATGC TGTTCATATG GATGAGCCTG TTGCACCTAG	600
TTATGCTGCT AAAAACGCTG GCTTAGCTGT CGCAACTGTC AGCTTGAAGA TGAAGGACGG	660
CGACGCCAAT GCCGyTGCTC TTAGAAaATA GTGATGATTT GAAAGAAGT	709

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

TATAAAATGT TAAGTTAAAT GATTTCAAAA TTCAGAAAGG GATTGCTTTA TGCAGTTCCT	60
TTTTATTTTA ACAGGAGTGA AACTATAGTG TTTCTAAATT GTGAATCAAT CAAAAGTAT	120
TGTGATGGGG CTATTCTAGC TTTAGAAACC TTCAAAAATT AAAATTTAAG GCAATCAATT	180
ACTTGGAAGA GTATGAAAGC ATTTAGTTTA TAGGAATTCT AGGTCTAGAA TTACATATAT	240
ATATTTATGA AGACGGGGTG TTCGATAGTT AGTATTGTTC TATTCTGAAA GATTTGAGCT	300
GTCAGTTGTA TAGAAAGTGT TCGAATTTTT TTAAGTGATT AAATTAGTTA ATTGTATGAG	360
GTGCTTTATG ATATAATGTT CTTAATGAAT TTCAGAAAG GAAAACCTCA AATTGTTCTA	420
CAAATTTCTA CTCTTCGACC TCGACCACAC TCTTCTTGAT TTTGATGCTG CTGAGGATGT	480
GGCTTTGACC CAACTTCTAA AAGAAGAAGG AGTTGCGGAT ATTCAGGCTT ATAAAGATTA	540
TTACGTTCCCT ATGAACAAGG CTCTCTGGAA AGACTTGAG CTGAAGAAAA TCAGTAAACA	600
AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT TTTGGACAGG AAAAAGACGG	660
TAGTTTTCTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG CAGGGACAAA CACTATCGGG	720
CGCTCATGAT CTCTTGACA GCCTCATTGA GCGTGATTAT AACTTGTATG CTGCGACAAA	780
TGGCATTACT GCCATTGAGA CAGGACGTTT GGCTCAATCT GGTCTAGCAC CTTATTTCAA	840
TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG GATGCTCTTT TTTATGAAAA	900
GATTGGCCAG CAAATGCTG GATTTAGTAA AGAAAAGACG CTGATGATTG GAGATTCTCT	960

1301

AACCGCCGAC ATTCAAGGTG GCAATAATGC GGGGATTGAC ACTATCTGGT ATAATCCTCA	1020
TCACCTCGAA AATCACACAC AAGCCCAGCC GACTTACGAA GTCTATTCTT ACCAAGACTT	1080
GCTGGATTGT TTAGATAAAA ATATTCTTGA AAAGATCACA TTTTAAAGGA GACGAGCTAA	1140
TGACTACAAA AAAGCTAATA TTAATTATTGA AGAGTACATT GAAATGTCTG AAGTTGATTT	1200
TAATGAAGCT GTTAATTATG AATTTACATC TGACACTTGT CAATTAGCAA ATAGTATTTA	1260
TCAATCTCTT TTTAAGTTT TTGATAAGAA AAATTTCTCT GCGGATTTAA TTTTACTTG	1320
GAAATCTCCA TCATTAGTCA AAGAAGGGGA TTATATTGGG AGAAGGGATT CACAAGTAGA	1380
TAATCTTAGA GTAATAGGAA ATATATTTCC GAATTATCTT ACTAATCGAA AATATAGCCT	1440
CAATATGAAT CGTAATGGCT GTATGGGAGA TTTTCCTCAT GACTTTTTTG ATATATACCT	1500
AGATCATGTA GCAAAATATG CCTACGAACA AAAAGTTAAT AATATTAAAG AGTATTATCC	1560
TTTAAAAAGA GCGATTTTAC ACCAAGAGAA TGCATTGTAT TTTGATTTT TTTCTAATTT	1620
TGACGACTTT TTAGAAAAAA ATTATTTAAA GACTATATGG CAAGTTTCTA AAGAACTCC	1680

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGCTCGGTAC GTAGTATnTG TGGTGCATAA ATGAGTGAAA AGAGGATAGA GAGGATGAGG	60
CCGATAAGAA CACCGGTAGC TGCATCGTGA AATACTTGTT TTTTCATAGT TCTAATTCT	120
CCTTGATGGT TTTTAGATAA CGGCGTGAAG AGTAGGTGAA GCTTTCGTTT TTCAAGAAAA	180
TTTCTACCAG ACCGTTTGGC GTGAgCTTGA GGTGAGAGAT GGAATCGATA TTGATGATTT	240
CTGATTGGGA AATTGAGATA AAATTGGTTG GCAAGAGTTT AAGAACCTGA TAGAGTCGCA	300
AATCAATGCT GTAGGTCTGA CTCGCGGTTT CTGCTAGAAC CTTCCGATTC TCGATATAGA	360
AGCGCTGAAT CTTGCCAATC TCAACTAGAT AGACCTGATC ATCGATTTTT CCTTTGATTT	420
TTTCTCTTTG GTCCAGATTT TCTGCGAACT CGATGACTTT CTGGACTTTT TCGGTTTCTT	480
GAGGTGCTTG GACAATCAGC TTTTCCTCCT CGTAAGTCTC ACTAATCTGT AGTTCTACTT	540
TCATAGTTTT CTCTCCTTTT CAGTTATACA AGTTTGTGAT CACTTCCTGT ATATCCGG	598

(2) INFORMATION FOR SEQ ID NO: 272:

1302

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1099 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CCAGCAAATC AATAACTGCA ATTGCTATAA AATGGATTCT ATAGAGTTT TTCATGACAA	60
GACCTCCCTC TTTTATCTAA CTTCATTCTA CTCCAAAAGA ATGGGAGTTA CAACTAAAT	120
GATAAAAATA GCAGAAGGA GATTCTCTTA AGTTGGCTAG TATCTTTAT TTGAGTTTC	180
TTCTATTATC TAACTTCTTC ATCATTCAG ACAAATAAG CTCGATTGC ATTGAGGATA	240
TAAAAGATGT ATTTACCGAT ATTGGCGAAG TTTCCTTGAA TACCAGCTTT TGTCAGCTGA	300
ACGAAATTGT AAATCAACCA AAAGCCCCAC TGAGTTGTTA GTTTAATGC ATTCAAAGCA	360
TTGGCAATGA GGGACAGTGC AAAGGCAATA GTTGTTACGT AGGCAAGGAG ATTCATCTTG	420
CCCCCATATC CGATATAGTT GGTACAAAG GCAAAGAGGA AGGCGATGAT GGAAATGATG	480
ATGGCCGCCA ATTTTACCTG TTTTGGCTC ATTTGGTTGG GTCTGCCTTC TTGCGAAGCT	540
TCCCACTTCT TTATAGCAA GGTATAATG AGGAAGGTGA CGGGATAGGT AATGATGGCC	600
GCCTTATTTC CAAGGATATA ATCAATAGCA CCGGACAAA TGGTATTAA AATACCAAAG	660
TAATTTCCCC ATTTGCTTAA TTTCCCGTG AAACGAGTGG ACAACATGA AATCCCAACG	720
TTGGTTACGG AAATCAATCC AAAGGGTACA AGAGCTGTCC ATGATCCCCA GTCTACAAAT	780
TTATCGAGGT GTGAGTTGAG GTAACCAGAT GCAATCGCAA TCCCAACGAC CAAAGCAACC	840
CCGAAGAGGT CAACTATTT AGATGTAGCA AAAATTTTGA GTGATTTTTT CATAGGTTAA	900
ACTACCTTTC TTTTTTCAA ATATTCTCCC ACCAAATGAA AGTAAATAA AATGATAGAA	960
ATAAAACCCT GAAAATAAAG GTTCTATAAT ATTTGTAGTG GGTAAATCCA CTATAGATAT	1020
TATGGAGCCT ATTTTATTGT AGAAAAAAG TCCCATATGA CCTATAATGA AAAGCGACAA	1080
AACAACTCAT TAGAAAGAT	1099

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

1303

CTGGGATTCA	CGTGAAAAGG	AAGCCCAGAG	AGTAGCCAGG	TGTACTGCTA	GAACAGTGAG	60
TGAAATTGAA	TATTACCATA	GAGAGTCAAC	CCAGATAGCT	CAGGCTTTAG	TTGAAAATCA	120
AGCTCGTATC	GAGGGAATCT	ATAAATACTT	TAGCCTTAGC	ATGCCAGACT	ATTTTACTG	180
GCAATTAGAG	CGGAAAGCTT	CGCCTTATAT	ATCAGTCTCT	CTGTATGAAA	ATGTTGATGA	240
CCTCTATGTT	CGAAATGATT	TTGTAACTGG	GGTGGCCATT	GCTTTTCAAG	ATTACAAGGA	300
AGTCTATGTT	TCTACTAAAG	ACAAACGTAG	GKkAGAAAAA	ATCAGGGCTG	AGGATTTCAA	360
ACCAGCAGGA	AATAGTTTGG	CCATTCCAGT	GTCAGATCCA	GTGTCAGATC	AAGACTTAGG	420
AGTGATTTAC	ATCTCCTTGG	ATCCTGCTGT	TTTATACCAT	GCCATTGATA	ATACTAGAGG	480
TCATACTCCG	ATGGCAGTAA	CAGTGACCTC	ACCTTTTGAT	ACGGAGATTT	TTCATATGGG	540
TGAGACAGTT	GATAAGGAGA	GTGAAAATTG	GCTAGTTGGC	TTAACTTCTC	ATGGATATCA	600
GGTTCAGGTG	GCAGTTCCTA	AAAACCTTGT	TTTACAAGGA	ACAGTGACTA	GCTCTGCTTT	660
GATTGTGGGT	TTGAGCCTTC	TCTTTATTGT	CATTCTTTAT	CTGACTTTGA	GGCAGACTTT	720
TGCTAATTAC	CAAAGCAGG	TAGTGGATTT	AGTAGAATCC	ATTCAAGTCA	TTGCTCAAGG	780
CGAAGAGGGG	CGTCGGATTG	ACATTTCCGA	GAAAGATCAG	GAATTACTCC	TAATCGCGGA	840
GACGACCAAT	GATATGTTGG	ATCGATTGGA	AAAGAATATC	CATGATATTT	ACCAGTTAGA	900
GCTTAGTCAA	AAAGATGCCA	ATATGCGAGC	CTTGCAGGCG	CAAATCAATC	CTCATTTTAT	960
GTATAATACG	CTGGAGTTCT	TGCGCATGTA	TGCAGTTATG	CAGAGTCAAG	ATGAGTTGGC	1020
AGATATCATT	TATGAATTCA	GTAGTCTCTT	GCGTAACAAT	ATTTCCGACG	AAAGAGAGAC	1080
CCTCCTCAAA	CAGGAATTAG	AATTTTGCCG	TAAATACAGC	TATCTCTGCA	TGGTTCGCTA	1140
TCCCAAGTCC	ATTGCCTATG	GTTTCAAGAT	AGATCCAGAG	TTAGAGAATA	TGAAGATTCC	1200
CAAGTTTACC	TTGCAACCGC	TGGTAGAAAA	CTATTTGCGG	CATGGTGTG	ACCACAGGCG	1260
GACAGATAAT	GTGATTAGCA	TCAAGGCTCT	TAAACAGGAT	GGTTTTGTGG	AAATTTTGGT	1320
GGTCGATAAT	GGTAGAGGAA	TGTCGGCTGA	AAAGTTGGCA	AATATCCGAG	AAAAATTAAG	1380
TCAGAGATAT	TTTGAACACC	AAGCCAGCTA	CAGTGATCAA	AGGCAGTCTA	TCGGGATTGT	1440
CAATGTACAC	GAGCGTTTTG	TGCTCTATTT	TGGAGACCGC	TATGCCATTA	CTATAGAGTC	1500
TGCAGAGCAA	GCCGGTGTTT	AGTATCGTAT	TACAATTCAA	GATGAGTAGA	AAGGGAGAAA	1560
ATGTATAAAG	TATTATTAGT	AGATGATGAG	TACATGGTGA	CAGAAGGTCT	GAAGCGTTTG	1620
ATTCCCTTTG	ATAAGTGGGA	TATGGAGGTC	GTCGCAACAG	CCAGTCATGC	CGATGAAGCT	1680
CTAGAATATG	TTCAGGAAAA	TCCTGTCGAT	GTCATCATTT	CCGATGTCAA	TATGCCAGAC	1740

1304

AAAACAGGGC TTGATATGAT TCGGGAGATG AAAGAGATCT TACCAGATGC TGCCTATATC	1800
CTGCTCTCAG GTTATCAGGA GTTTGATTAT GTAAAAAGAG CAATGAACCT TAGTGTGGTG	1860
GACTATTTGG TCAAGCCTGT TGATAAGGTA GAGCTGGGAA ATCTGCTGGA GAAGATTGCA	1920
GGTCAGCTCG GCGAGAGAGG GAAGAAAAGT CAGACTCTTA GTCAAGAATT AGACGAGGCT	1980
GGATTGTGTA GTTATTTAGG GGATAAGGAG AATTGGTGGA TAGGTCTATC CAAGGAAAAA	2040
CAAGGTTCCT TCACCATTCCT CTACTATGTC TTGGGTCAAG ACTGGCAGAT TTTCATTTCCT	2100
GGCCACCCCC TAGATGGTTT AGTCGTTACA CCTTTTGAAG CTCCTTATCA AGAACACTTT	2160
GAACGCTGGA AGCTGAATGC TGAGAAAACC CTCTTTTACG GTTCTGTAAA TCTGCAGCAG	2220
TCTGAGAGTC TCTTGCCTA TTACGAACCG ATTTATAGGG TTATCATTCA GGGAAATCTC	2280
AATCAAAATCG TAGAAGAGTT AAATCTCTTG GAGAAGGTAG TTCTTGAAAA TACACCTCGT	2340
GTTTCGATTA CTAAACAGCT TTTTATCCAG TTTGTCATGG ATGTTTCCA TTTATTTGAA	2400
CATCTCAAAG CTGATGATAT GACGGACATT GTCAAAACCA TTCATGCTAT TCAATCCTTC	2460
GATGAATTGG TTTCTTATAT CAAGGAACT CTGATCAGCT TTTTCGGTCA ATACCGTATG	2520
AATGAAAATG TGGTCAGTGT GCTGGAAGTC ATTGGTCGTG ATTACCAAAA AGAGCTTTCC	2580
CTCAAGGATA TCAGTAAGGC CCTCTTTATC AATCCTGTCT ATCTAGGGCA GTTGATTAAG	2640
CGTGAAACCG ATTGACCTT TGCAGAGTTA CTAAACAAAC AACGTATTAA GGCTGCCCAG	2700
CAGCTCTTGC TTCAACTAG TGA	2723

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 836 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CCGCAGTTTT TTAAACCGT ATATAAGTAT AGCATAGTCA AAAAAAGAAT GCAAGATTTT	60
TGCAAACTTT TTAAAATTT TTCGTAATTT TTCTTTTAAA GTTCTACTGT CAGGACTTGA	120
CCTTGCTTAA CAACCTGTTT TCCGGCGATA TAAACATCAT CTACATCACT AGATTTAACT	180
GCATAAACCA GGTGAGACAG CATATTTTCC TGAGGTTGGA GATGAATTTT CCCTGTGGT	240
TGAATGACCA GAAAATCTGC TTGCTTGCCG ACTTCCAGAC TTCCTATCTG ATTTTCCATT	300
CCAAGGACCT TAGCCCCCTT GATTGTCAGT ACCTTGAGAG CTGTTTCGAT TGGAACTGG	360
CTGGCATCCC CACTTTTCAT CTTCTGAAGA AGAGCTGCAG TCCTTCCTTC CTCAACATA	420

1305

TCTAGATTGT TATTGGAAGC AACCGAGTCA GTCGCAATTC CGACTGCTAC TCCCGCTTTT	480
TGGAGCTGGA TAATTGGAGC AATTCCTGAT GCCAGTTTGA GGTACTGAT AGGATTGTGG	540
GCGATAGCnA CTTGAGAAGA TGCCAAGCGT TCAATTTCTC TCTCGTTTAA TTCGACCCCG	600
TGAGCAAATA CGGACGGATG ATCTAAATAA CCCAGTTCTT CAAGAAAAGC AAGGGGGCGT	660
TTGCCGTATC GTTTGAGGAT AATTCCTGAC TCCTCCTTGG TCTCCGCCAC ATGGACATGG	720
AGCGGAATAT TTAGCTCTTT TGCCATTTCC AAACCTCGCTT CCAGCAAGTC TCTACTGCAG	780
CTATACGGAG AATGAGGTGC TACCATAACC TTGAAATTG GATTTTATA TTTTAA	836

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ATTTTATTTC ACTTTTAGG TGGTCTGGGG CTATTCTTAT ATAGCnTCAA GACCATGGGA	60
GACGGTTTAC AACAAGCTGC TGGAGATCGC CTGGGTTTTT ACATTGACAA ATATACTAGT	120
AATCCTTTGT TTGGAGTTCT GGTGGTATT GGGATGACTG CTCTAATTCA GTCTAGTTCT	180
GGTGTAACAG TTATCACAGT CGGCCTGGTC AGTGCCGGTC TCTTAACCTT ACGTCAGGCT	240
ATCGGGATTG TCATGGGTGC TAATATTGGG ACAACTGTCA CATCCTTTCT CATCGGTTTT	300
AAATTAGGTA ACTATGCCCT ACCTATGCTC TTTATCGGTG CCGTCTGTCT TTTTTTTACG	360
AAAAATCGGA CAGTCAATAA TATCGGACGC ATCCTCTTTG GTGTCGGTGG TATCTTTTTT	420
GCCCTCAATC TCATGAGCGG CGCAATGGCT CCACTCAAGG ATTTACAGGT CTTTAAGGAC	480
TATATGATTG AGCTAAGTAA GAATCCTGTT TTGGGTGTCT TTGTCGGTAC TGGCTTGACC	540
TTGCTAATTC AAGCTTCTTC GGCTACCATT GGGATTTTAC AAAACCTCTA CGCCGGCAAT	600
CTAATTGATC TACAGGGAGC TTTGCCAGTT CTATTTGGTG ACAAATATCGG GACAACCATT	660
ACAGCCATCA TTGCCTCTTT AGGGGCTAAT ATTGCAGCTA AACGGGTAGC AGGAGCTCAT	720
GTTGCCTTCA ACGTTATCGG AACAGTTGTC TGCCTATTTT TTCTAGTTCC TTTTACTGTC	780
CTGATTCAAT GGTTTGAAGC TACGCTAAAT CTAGCACCGG AAATGACCAT CGCCTTTGCT	840
CACGGAACCT TTAATATTAC CAACACCAT GTCCAATTTC CATTTATCGG AGCTCTGGCT	900
TACTTTGTAA CCAAGATTAT TCCTGGAGAG GACGAGGTTG TCAAATACGA ACCCTTATAT	960

1306

CTTGATGAAC ATTTTCATCAA ACAGGCCCCA TCTATCGCTC TAGGAAATGC TAAGAAAGAG	1020
CTCTTGCACT TAGGAACTA CGCTGCTAAA GCCTTTGACC TTTCTATAA GTACATCATT	1080
GACTTGGATG AAAAAGTTGC TGAAAAAGGG CATAAACCG AAGAAGCAAT TAACACCATC	1140
GATGAGCAAT TAACACGTTA TCTCATTGCC CTTTCAAGCG AAGCTCTCAG CCAAAAAGAA	1200
AGTGAAGTGC TTACCAATAT CCTTGATTCC TCCCGTGATT TGGAACGGAT TGGAGACCAC	1260
ACGAGGCTC TACTCAATCT GACTGACTAT CTTCAACGGA AAAATGTTGA ATTTTCTGAT	1320
GCCGCCTGA AAGAATTAGA GGAAGTTTAC CGCCAACTA GTGACTTTAT CAAAGATGCT	1380
CTGGATAGTG TGGAAAACAA TGATATTGAA AAAGCACGCA GTCTTGTA TAGCATGAA	1440
GCAATCAATA AGATAGAACG TGTTCCTCAGA AAAACCCACA TCAACGCCT CAACAAAGGC	1500
GAATGTTCAA CACAAGCTGG GGTCAACTTT ATCGACATCA TCTCACACTA CACTCGTGTA	1560
TCAGACCACG CTATGAACCT TGCTGAAAAG GTTTTTCAG AACAAATCTA AGAACCAAGA	1620
AGCTATCCAT CATAATTGGA TGGCTTTTTA CTTTTTCCTA AGCAAGACTA GGATGAATGA	1680
AACTGAAAGA GTATCTGCA GATATATAGT CCCCAATTAT TCACCCCAA TCTAAAACC	1740
ATCCAGAATC CTTGCCTTAG CTTAGATCCT GGATGGTTC TTTTTCACC CAATGGGTGT	1800
TTTTTACTAG AAAAAAAGA GTTCCCTT TATGGTATAA GTGTAGAAAA AAACACAAAA	1860
AGAAAGGAAA CTCACATGAA CAGTTTACCA AATCATCACT TCCAAAACAA GTCTTTTAC	1920
CAACTATCTT TCGATGGAGG TCATTTAACC CAGTATGGTG GTCTTATCTT TTTTCAGGAA	1980
CTTTTTCCT AGTTGAACT AAAAGAGCGG ATTTCTAAGT ATTTAGTAAC GAATGACCAA	2040
CGCCGCTACT GTCGTTATTC GGATTCAGAT ATCCTTGTC AGTTCCTCTT TCAACTGTTA	2100
ACAGGTTATG GAACGACTA TGCTTGTAAG GAATTGTCAG CTGATGCCTA CTTTCCAAAA	2160
TTGTTGGAAG GAGGGCAGCT TGCTTCACAG CCAACCTTAT CCGTTTCTT TTCCAGAACT	2220
GACGAGGAAA CAGTCCATAG TTTGCGATGC CTCAACCTTG AATgGkCGAA TTCTTTTAc	2280
AGTTTCACCA GCTAAACCAA CTCATTGTAG ATATCGATTC TACCCATTTT ACAAC	2335

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CGGATTCACCT GTTGTGACT AATCAATAAC ACAGTAGAAA ATCTCACAGC AGTCTATTAG	60
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1307

TTGCTTTTCA TACTAGGCAA GTGACTGAGG CTTGTACTTG GGTACAGCAA GGGAGCTTAA	120
GGCCGTAGAA GAGAAAAATA GTAGACTGAA AACCCGCAAG ACTTCATCAT TTCGAGAAGT	180
GACGTGGGAG ATGAAAATCG ATTGAACCAC TTACAAGGAG AATAGAAAAT GGCTAAAAAA	240
AGCAAACAAC TTCGTGCTGC TCTTGAGAAA ATCGACAGCA CAAAAGCATA CAGTGTAGAA	300
GAAGCTGTAG CACTTGCAAA AGAACTAAC TTTGCAAAAT TTGATGCAAC TGTAAGATT	360
GCTTACAAC TGAACATCGA CGTTAAAAAA GCTGACCAAC AAATCCGTGG AGCAATGGTA	420
TTGCCAAACG GTACTGGTAA AACTTCACGT GTTCTTGTTC TCGCACGTGG TGCAAAAGCT	480
GAAGAAGCAA AAGCTGCTGG TGCAGACTTT GTTGGTGAAG ATGACCTTGT TGCTAAAATC	540
AACGACGGTT GGTGGACTT CGACGTAGT ATCGCTACAC CTGATATGAT GGCTCTTGT	600
GGACGTCTTG GACGTGTCCT TGGACCACGT AACTTGATGC CAAACCTAA AACTGGTACT	660
GTAACAATGG ATGTTGGCAA AGCGGTGAA GAGTCTAAG GTGGTAAAT CACTTACCGT	720
GCTGACCGTG CAGGTAACGT TCAAGCAATC AT	752

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GTCAACATTG ATTCAAGGC TGTGCTTT CTATCTCCCC TTTTTCATAA TGTATAATAA	60
AATGAAATAA TAACAGGACG AATTGATCGG GACAGTCAAA TCGATTCTA ACAATGTTTT	120
AGAAGTAGAG GTGTACTATT CTAGTTTCAA TCTACTATAT TTTCGTACAG GTGCTTCAAC	180
CATTGGAACG ATTTCAAATC CTTCCTTTTG GTAAAGATTC TGAGCTCTTT GATTGCTCTC	240
GAAGACATTT AGAGAAATAC TGTCTATATC TCTATTTTCA AATGCTAAAC TAACAAATTT	300
CCTTAAAGCC TTGCTACCTA AGCCTTGCTC CTGTTCTGG GGGTTGATAA AAAATCTCCC	360
GATATGAAGA TTGCTGTCTT CTAGCCTGAT TTTCTGGATA AATCCACAA ACTCTGTTC	420
ATCAAAGATT GAAAAGACTC CTCCAAGGC TTGAAGTGTG AGTAGAAAAG GAATCCTTGG	480
TCCCATCCAT TGTCTTGAA AGGATTTGCC TAGGGAGTGG GACCACTGGC ATACAAATTG	540
AGCGTTTCT GTGCTCACCT TTTCTTCAA ACGAATTGTC ATCTTTTCTT CACCACCTTA	600
TCTATGTTTC TCCATTATAC TATTTCTCCC ATTTTCTACG AATAGATAAG TATGATTGAT	660

	1308	
TTTTATTTTT TTCTCGTCGG GAGCATTCTA GCTTCCTTTC TTGGTTTGGT CATTGACCGT	720	
TTTCCAGAGC AATCCATTAT CAGTTCAGCC AGTCACTGCG ATTCCTGTCA GACTCCCTTG	780	
CGTCCCTTAG ATTTGATTCC GATTCTCTCA CAGGTCTTCA ATCGCTTTCG CTGTCGTAC	840	
TGCAAAGTTC GCTATCCTGT CTGGTATGCC CTCTTTGAAT TAAGCTTAGG ACTCCTCTTT	900	
CTGCTTTACT CTTGGGGATG GCTCTCCTTG GGGCAAGTCG TCCTAATCAC CGCTGGTTTG	960	
ACCTTGGGTA TCTACGACTT TCACCATCAG GAATATCCCT TACTGGTCTG GATGACTTTC	1020	
CAGCTAATCC TAATAGCTTC CTCTGGCTGG AATCTGGTCA TGGTCTCCTT CTCATACTT	1080	
GGAAATTTGG CTCATTTTAT CGATATCCGC ATGGGTGCAG GGGATTCCTT CTTTTAGCT	1140	
TCTTGTGCTC TCGTCTTTAG CGTAACGGAG TTACTGATCT TGATTCACTT CGCTTCTGCG	1200	
ACGGGTATCC TGGCCTTTCT CTGCAAAAG AAAAAGGAAA GACTTCCTTT CGTGCCTTTC	1260	
CTCTTACTTG CTAATTGTTT GATTATTTTT GGTAAGCTAC TGCTTGTCTG ATAAAATCCA	1320	
ATTTCTGCCA TATATCCTTC ATGAAATTAT TTCACAGTTA AATTATAAAT TATTTCTTTT	1380	
GTACAAAGGG ATGATGTTAT CAAATCGATC TGTCTTCTA TCTTCTTGAT ACTGATCAAA	1440	
AAATTTCAAT TCGACTGAAA ATATTTTCGCT TATAAACTGT AAACGAATAC TTTGTTTAGA	1500	
CATTATAGTC GCTAGACTGA CTAGATGATT ACTCAAAACG ACGTCCAGAA TACTCTTTAC	1560	
TTTGCTTGGT TTTTAAACAA AAATTTGATC ATCCAAGGGT TCAATCATTT TGTAACCTTT	1620	
TTGCGCAATT TGACGATAAA AGTAAGAATG TTGCTTTGGA GTCAATAATC CTAACCTAAA	1680	
AGCTCGATAC TCTAAAGCCT GTATCGAAAC ATTCAAATCC GACTTCAATA AAATATAACT	1740	
ATCAGGATTG CTGACACGCT TGCCAACCCT CTCTCAAAT TTGACTAAAA ACTCTTCTTT	1800	
TGGCAATAAA AAACATGATG CAAAATAATT TGCTTCTTGC TCCAAACGAT CGCCATCTTC	1860	
ATTCATATCT TTATATTTAT GTAAAAGAAT ATGTCCTAGC TCATGAGCTA AGTCAAAATT	1920	
TCGACGTACA GATGATTTAT TCGTTCCTAA CACAATATAA GGTCTTCCCA ATTTTGACCA	1980	
TGCGCTATAA GCATCAGCTT GGCCATTAAT TAATCGTTCC ACGATATAGA TGCCTGAACG	2040	
TTCTAATTTA TAAAGCAAAT CATGATTATC TTTTGAAATA CCTAATTTTT CCCTGGCATA	2100	
AAGAGCCAAT TCCTCAATGG ATTCTCCCTT ATGATAAGAT TCACTCACTA CATTACTTAG	2160	
GTCATGAATT ATAATATTAG GTATAATTAC AAAACTTTCA AAATAATCAA TCAAACATC	2220	
TACCTTATGT AAATACATAG TTGGAATATC TATTGTTTTT CGTGTGCTA GGTCTGCATT	2280	
TCTAAAGGCA ATTACAGAAG AATCAAATCG AATGCTCTCT TCTTCCTGTT CAAAATAAGT	2340	
TAAATCAACA TGAAATTGGT TGGCCAAATG CATTTTGGTT GATAATTTAG GTTTCGTTTC	2400	
GTGGACTCA AACTGCCAAA TGGCTTGTTT CGTTAAATTA ATTCTCTGAG CTAATTCTGC	2460	

1309

TCTACTTAAA CCATTTAACA GCCGTAATTC TTTCAATACC CGACCATTAA ACATTTACAT	2520
ACTCCTTACT ACTTTTGACC TTCTTGTTT TCTATTCTTG GAATAATTC AAAATCTTCT	2580
GTTTCCGATA ATTCTGAAAA ATTAGGAATA TCTTGATATT TAGCTTCTTC GAAATGGTAC	2640
GGG	2643

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TGACCAGTGG CAAATGGCT ATCCAAATGC AGATGTTATT ATCGATGATA TCATCTCAGG	60
GCAAGCCTAC GTAGCCTTGG AAGAGGGAGA ACTGCTAGCC TATGCTGCTG TGACCAAGAG	120
TCCAGAGGAG GCCTATGAAG CTATTTATGA GGGAACTGG CAAGCTGGAG AGTCAGAGTA	180
TCTAGTCTTT CACCGTATTG CTGTGGCAGC AGATGTGCAG GGAAAGGAG TTGCTCAAAC	240
CTTCTTAGAG GGCTTGATG AAGGTTTGA TTATCTTGAT TTTGCTCAG ATACGCATGC	300
TGAAAACAAG GTTATGCAAC ATATTTTGA AAACTTGGT TTAAACAAG TCGGTAAGAT	360
GCCAGTAGAT GGCGAACGCT TGGCCTATCA AAAATTAAAG AAATAATGCA AAAGAAGTAT	420
GTAAAAATCC TCTACTCCTC ACCAATTGGT ATTCTATCAC TTGTAGCTGA TGACCATTAT	480
TTGTATGGAA TTTGGGTTCA GGAGCAGAAG CATTTTGAGA GGGGACTAGG AGATGAAACG	540
ATAGAAGAAG TTGTWAGTCA TCCTATTTTA GACCCAGTTA TT	582

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CCCAAGCTAC TAAGAGACTA AACTTGCTA GAGAAGCAAG AGAAAGTGTG AATCTTTT	60
ATTTTCATGAT GAATTCCTT TCTGCTACCA ATTTAGAGAA ATTTTCTCTA ACCAGCAATT	120
CCCCTAGTAT AACAAGTCA AAAATGGAG TCAATTTATC TGCTCACGGT CCAGCAGGTA	180

1310

GCCCCGTACT TCTGAGATAA AATAGAGAGA CCCTGTAACG AACAGCAAGT CTTGAGCGTC	240
TGCCCTTTCT TCAAAATCGC TGATAAATTC TCGGTAAGAA GAAACTATAT CGTAACCTGT	300
CACATCCCTT TCGTCCAAAG CCCCCTGATA GTCAAAGCCG GTCACCTTGA GTTCCACCTG	360
AGGCAATTTT TCAGTCAGAT AACCCAACAT CCCTTGATAA TCCTTACGTT TCAAGGATCC	420
AAAGAGGATT TGAGGTCGAT AGCCTTCCTG CTCTTTTCT TTGATAAACT CAGCCAAGCG	480
AGTCAAGGCA GGGAGGTTAT GAGCACCATC CAAATAAATC TGTGGGCGAA TACGCTCCAA	540
GCGAsCAGCC CAAT	554

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CCGGTTTTTC AAATGAATTT CTTGGTTGTG GCTAAAAAAT ATGCTACACT ATCAATATGA	60
AAATTTTAAT CCCAACAGCA AAAGAAATGA ACACAGACTT CCCAAGTATC GAGGCAATTC	120
CTTTAAAACC AGAAAGTCAG GCCGTGCTTG ATGCCTTGGC TCTCTATCTT GCCAGTCAAT	180
TGGAGAGTTT CTACAAGGTA TCAGCTGAGA AAGCGGCGGA AGAATTTCAA AATATCCAAG	240
CTTTGAAAAG GCAAACTGCT CAACACTATC CAGCCTTGAA ACTTTTGTAT GGGCTTATGT	300
ACCGCAACAT TAAGAGAGAT AAGCTGACCG AGGCGGAACA AGATTATCTT GAAATCATG	360
TTTTCATTAC CTCGGCTTTG TACGGTGTG TTCCAGTCTT GTCACCCATG GCTCCTCACC	420
GTTTGGATTT TTTGATGAAA TTAAGAGTCG CTGGTAAGAC TTTGAAGAGC CATTGGAAGG	480
CAGCCTATGA TGAACTCTG AAGAAGGAAG AAGTGATTTT CTCTCTCTTG TCATCAGAGT	540
TTGAGACTGT ATTTTCTAAG GAAATCAGAG CAAAGATGGT GACCTTCAAA TTCATGGAGG	600
ATAGAGGCGG TCAGCTGAAG ATTCACTCAA CTATCTCCAA GAAAGCGCGC GGGGCCTTTC	660
TAAAGCTTTT AATAGAAAAT CAAGTACAAA CTGTGGGGGg AGCACGTCGC TTGAACCTTG	720
CTGGATTTGT TTACCGAGAA GATTTGTAC AACCACAGGG GGATGG	766

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 901 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

CCGGCCACGG TTCCATCCAA CTTACAGGT GTGCACTGA TTGTGTATGT AATTGTCACT	60
AACGGTAGAA TTTACCTAT CCCTCCTATC TGCTCGCAGT ACCCGCAGAC TTTCTGAAAG	120
AAGAAGATAA CCTACTTATC CGTTGCTATG ATTATACTAA AGTTTCTACT TTTTGCAAA	180
TAGATTTTAA AATTTTGGC TAATTGTCTG AATCAGGGTC GGAAGTTTGA CGACCTTGTC	240
ATTGCCTAGT TTTTCGCGTG CAATTTGAG AATGGCACCT GAGTCTTTTG AAGCAAAGAG	300
GAATTTTCCT TTGTCTGTAA AGACTTCGAA GTGGCGGCTG ATTTTGCCTC CAGTGACATT	360
GGCTCCAATC TGATTGATAT GGCTCCAAGG AATCTGGATA AATTGTTTGA CATTGACATC	420
TGGGTAAAT TCCAAAGCCT GATCTCCGAC AAGGAATTC CCAACTTTCC CAGCGATAGA	480
GAGGTAGGAA GTGCCTGTCTG TACTGAGGAG TACTGTTTTG TTAAGTGATT GGGCCATGCT	540
TAGTCTTCCT TACTTTCTCC AAAAAAGGCA TTGTAGAGGG CTTTAATTGC TGCTTTCTCT	600
TGGTCTTTAT TGACAACAAA CATAATAGAA ACTTCACTAG AACCTTGAGA CATCATCTGG	660
ATGTTGATTT TGTTTTGAGA TAGAGCGCGT GTCGCAGTAG CAGTCACTCC GATATGGCTC	720
TTCATTTTTT CACCAACAAT CATAATGATA GAAAGGTCGT GTTCGATTTT TGCATGATCT	780
ACTTTAGCCT TTTGAACCAA CTGACGCAGG ATTTCTTCTT CCTTGATGGG AGTTAGTTGG	840
CGAGAACGGA GAATGATAGA AAGAwCGTCG ATACCTGTTG GCATATGTTC CCAACCGATG	900
T	901

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

CCCTGTTACG TGGATAATAG GGTAAGACTG CTCAGGATTT CCTAACAAAT CCACCGCTTG	60
CTGCATTGGA CCCAAACCTG ATCGAAAATT CAAACCAATC CGACTATGGA GCCATTCTTC	120
TACTTCAAAC ATACACATCT CCTTGACAAA AGTCCAATCA ATTATCGCAT TAAAGTATGG	180
TTACTAATAA AAACAAGGCC AGGATTTTCG TCCCGACCTC TTACCTGGTT AGCTAATAAC	240
TAGCTACTAT GAATGTGAAT ATGGGCTAAA AACATCCACT GGACGTTCCA ACTCTCCCC	300

1312

ATTTCTGGGA GTTGGGGTAA AAATGTTTAC TGGACGTTCC AACTCTTTCCC CATTCTTGGG	360
AGTTGGGCTG ATACAGTCTC CCAGACTGTA TCACTCCTCC ATAAAGCTGT TGAAGACTTC	420
TTCAATCATG TTCCATTTCG CTCTCTGAGTC TTCTGGGATT GGTGCAATT CGCCTTCTGT	480
TCCATCTTCG TTTTCGATGA ATGAGTAAGC TTGGATTTC AACTGTCCGT CTTCGTCTTC	540
TTCTGCGTTA ACTGGTACTA GAAGAACATA GTTTTACCA AATCTTCTT TTCCATCAAT	600
TGTCAAAAGG ATTTCAAACA AGGTTTCATT TCCTTGCTCA TCTACTAGTG TGATTAGTTC	660
ACGTTCTTCG TGGTCGTGGT TATGATCGTG TGACATAGCC TCGCCTTTAT ATTAAAATTT	720
TCTATCTAAA TAATTTTGTA AAATCAGCTG AGCTGCTAAC TTATCAATGA CTTTCTTGCG	780
CTTATTGCGA CTGATATCTG CTTGTTCAAT CAACATGCCG TCAGCAGCCA CTGTTGTCAA	840
GCGTTCATCC TGATAGTCTA CTGGTAAACC AAAAACTCT TCTAGCTTTG CTCCGTAGCT	900
TGACTAGCTT CTACGCGCGG TCCACTTGTA TTGTTTATGT TTTTAGGCAA GCCCACTACA	960
AATCGTTCCA CCTTGTAAGT ATCAACCAAT TCCTTAACGC GGTCAAAACC AAATGGCCT	1020
TGTTCTTCAT TTATCTGGAT GATTTCAAGC CCTTGAGCTG TAAAACCAAG CGGATCGCTA	1080
ATCGCCACCC CTACCGTTT TGAACCGACG TCCAATCCCA TAATTCTCAT AGGTTATAGA	1140
TCGACTCCTT GTCCCTTGAG GTAGTAGCGA ACCAATTCCT CAACGATTTT ATCAGCTCA	1200
TACTTACGGA TTTGATTTCG TGCATTATTA TAACGAGGAA CGTAGGCAGG GTCTCCACTC	1260
AATACGTAAC CTACGATTTG GTTAATTGGG TTGTAAaCCCT TATCGTTCAA CGAAGCATAA	1320
ACATCTGTCA AAGTTTCGCT AATTTCTTTT TTATTGGAAT CGTCCAATTT AAAACGTACT	1380
GTTTCTTCAG TAAATCCCAT TCTAACACCC TCTTTCCTTA GAATAGTACC ATTATAGCAT	1440
AATTCCTTAC CTTCTACAAT TCAGGCAGTC TATTTATTTG GATTTTCTAT TGTCTGTCTG	1500
CGCCATTTGC CAATCTATCT GAAATATATT TGCTTGGTTC ATTTTTCAAA AGATTTTCCA	1560
AACCAATATT CTTCAGATGT TCCAACGGG AAGCCTTCTT GACATCCAGA ACTTGAAAAT	1620
CAAAACTAGT CGTTGTTTGA AGTTCCGTTG CGCTCAATAG TTTTGTTTCA AGTTTGAAAC	1680
CTGCCAATTT ACGAGCTTCA ATGATAGACT TATCCTTCTC CTCCGCTTCA AGAAGAGCTT	1740
TTTGAGTTTC CTCCACTCCA TGTG	1765

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

CTTATCCATT CACTTTCTTG TCTGTTATTC TATAAATCTT ACTCCTAAGT ATACCACATT	60
TGCCCCTAGA TGTGAACGAG AGAAACGCTC TAGACATTGC CAAGAAGGAA AAAAAAGGTT	120
ACAATGTAAC AAAATCAAGG GAGGTCTGGA ATGAAGAAAC AAAGCAAGTA CAAAGAGGTC	180
GTTTCTATC TGAAAAATGG TATCGAGTCT GGACGATTTC CGACGGGTAG TCGCCTGCCT	240
TCTATCCGTC AACTGAGCCT TGACTTTCAC TGCAGCAAGG ACACCATTCA ACGAGCCCTG	300
CTGGAATTAC GGCACGAACA ATACCTCTAT GCCAAGCCTC AGAGTGGCTA CTATGTATTA	360
GAACAAGGGC AACATCAAGA CCTAGAAATC GAGGTTACCG ACGAACATGC CAGTGCCTAT	420
GACGATTTC GACTCTGTGT CAATGAAACC TTGATTGGCC GAGAAACTA CCTCTTCAAC	480
TACTATGACA ATCAAGAAGG ATTAGAAGAC CTAAGACAGT CCATTCAAA ACTCCTCTTT	540
GAGCAAGCTC TCTACTGCAA GGCTAACCAA CTAGTACTGA CTTCTGGAAC CCAACAAGCC	600
TTGTTTATCC TCTCTCAAAT ATCCTTTCCT AGACAAGCCA AGGAAATCTT GGTGGAACAG	660
CCAACCTACC ATCGGATGAA TCGCCTCTTG ATTGCACAGG GGCTGGACTA TCAAACGATT	720
GAACGAGGCA TTGATGGGAT TGACTTGGAG GAGCTGGAAG GCCACTTCAA AACAGGAAAA	780
ATTAAGTTTT TCTACACCAT TCCCCGATTT CACTATCCCC TGGGACATTC CTATTCTGAG	840
CAAGACAAAC GATCTATTCT TAACTTAGCT GCCAAGTATG ATGTCTATAT CGTAGAGGAC	900
GATTATCTGG GTGATTGGA CTCCAAGAAG GGCCAAACCT TCCACTATCT TGATACAGAG	960
GAGCGTGTCA TTTATATCAA GTCCTTCTCG ACCAGCCTTT TTCCTGCCCT TCGTATTACA	1020
GCACTCATTC TTCCAAATGC TATCAAAGAA GCATTTGTGG CCTACAAAAA TATCCTAGAC	1080
TACGACAGCA ACCTCATTAT GCAAAAGGCC CTGTCACTCT ATATGACAG TCAATTGTTT	1140
GAAAAAATC GTTGGGCTCG CTTGACCAAT CATGAATCTT ACCAAAAACA AATCGAGGAA	1200
AGGATAACTA AAACACCTTG TCCCCTTCCT CATTATTCCC TACACGATGG yTTATTGCTA	1260
GACCTGAGAC AGTATCCTAA AATCGCCAGT CTCAAACACA GTCAACTGGG cTTGGACTTC	1320
TTTGAAGAGG CCTATTAAAG CACCTG	1346

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

CTATATTCAG AATATGCCAA AAATTCGGAA TGGTATAAAT TTGCGGAGGG TTCATTTGAC	60
ATATTTAGAA AACTCCCCCA AAGAATTAAT TTTAAGAAAG ATTTTCTAG AATTTGGCC	120
CCCTTTATTA TTAATTTGCT TAAATTAATC AATAATTATC TAGAGAATAA AGAATACGAG	180
TGGATTGACA AGAATGGAAG TATTTTTTCC TCTCTAGTAT TTTATTTAGA AGATTTAATC	240
TATCCTTGGA TTGTTAAACC TTGGTTTGA GAGATAAAT CATTGCGTGA AAAAGGTTTA	300
CTTGAAGGGG AATCGGAGCA GCAACGGTAC AAATATTTTA TAACATTGTT TGACAAGGAA	360
GAGAATATAT TAAATTTTGA TAACAAATAT CCCGTTTAC TGAGGCAAAAT ATCGGAGTCT	420
TGTCTTCGGT TCTATACTTA TTTTATAGAA ATTTTATCAA ATTTAGAAAA TGATTTTAGT	480
GTGCTAGAAG AAGAATTAGG GCTAAGGGG AAATTAAATG ATATAAAAT TGGAAGGGT	540
GATACACACA GCCAAGGAAA AACTGTTTG ATACTCTTCT TTGATGACGC GAAAATTGTT	600
TACAAGCCTA AAAATTTAAT AATCAATAAC TCACTAAATA CTATTGCTGA GTATATCCGA	660
AAGGTTGATG AAAAAATTAG GATAAGAATA CCTCGAACTA TTGCTTATTC GGATCACAGC	720
TATGAAGAAT TTATTGATTA TCTACCTCTA GAGCAAAAGA AAAATTTACC TGAATATTAT	780
TATAATTTTG GTGTGCTTTT AGCATTTATA TATTTATTTA ATGGGAGTGA TATACATTTT	840
GAAAATTTAA TTTCTATGG AGATATGCCT GTAATAATAG ACTTTGAAAC AATGTTACGG	900

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 862 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

TTATTTAGCA GAGGCAGTTT TAAATGTGAA GGATTTGGTC AGTCAAACAG TTTTATCA	60
GCAGATTATT GGTTTAGAAA TCCTATCTCA AACGGATACA GAGGTCGTTT TGGGACTTGG	120
AGGAAAAGCC TTGGTACACT TGATTCAAGC ACAAGAGGGT GGAGAAGTAA GGAACATTA	180
TGGTCTTTAC CATCTGGCTA TTCTTTTGCC GACACGAAAG GCTTTGGCGG ATGTCTTGAA	240
GCACCTGACG GATTACAGA TTCTCTTGT TGGCGGTGCA GATCACGGTT ACAGTGAGGC	300
CCTTTACTTA GAGGACTTGG AGGGAAATGG CATTTGAATC TATCGAGATA AGCCAGTTTC	360
CACATGGGAT ATTCGAGAAG ATGGACGTAT TATCGGGGTG ACTGAAGTCC TTGCGGCTCA	420
GGATATCTAT GAGTTGGGGG AAAGAGTAGA GCCTTTTATC CTAGCAGAGG GTACGAGAAT	480

1315

GGGGCATATT CATCTTTCTG TCAAGGATAG TCGAAAGTCC AGACAGTTT ATCAAACGGT	540
GTTAGGGCTC GAGGATAAAT TCAGTGTGCC TAGTGCTAGT TGGATCGCAG CTGGGGACTA	600
CCATCATCAT TTAGCAGTCA ACGAATGGGG AGGAAAAGGT CTGGATCCGC GTAAACAAGT	660
CCTACCAGGT TTAGCCTACT ATGTCATCGA AGTCGCACAT AAAGAAGAAC TGTTAACGAT	720
TGCCCCACGA GCACAAGAAG TTGACGCACC AATCAAATGG ATGACATCGA TCCAATTGGA	780
AATCACAGAC TCAGATGGCA TCGTGACCCG TATTCGTTTA GCTAGATAGA TGGTATGTGA	840
TGAAGGTAGA GCATCAATTG TA	862

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCGTTTACAA GATCGCTAAA ATGCATCTCA TGATCGCGAC CACGAATTCC AAGATAGCAC	60
GCGCTACCTC AATCATAGAT AGTTCACTTT TTTCTTGCCC AGCAAATACT TCTAATCCA	120
AAGCGTTTCT CCTCATTTAT ACTACTATCG CCAGAGCGAA CAGACTCTGA CCTCATTTTA	180
TCATTTACTC TTTATTTTAC GATAATTTTG CGGAATAGTC AAAGGTTAAG GGGGAGAAAG	240
TGGCAGGATT AGACTAATTC CAATATAAAA CTCATTCCCTT TTTCTGTTGC TCCATTTTCC	300
ACAAATCCAA GCGACTTGAA ACACCTCCTA GAAGCATGAT TGTAGGTGTA GATTTTCTTG	360
ACTCTCAATT CTTTCCATCC TTTTACTCGA GCCAATTCAA TCAAAGCACT TAGAATCTTT	420
TTTCCAAGTC CTCGATGTTG GTAAGCGGAA TTCCAATCA CAATGGGGAG ATTATCCTGA	480
GATAGTGTA TATCCCAAT TGGAAACCAT TCTCCCTTCT CCTTGACTTC AATCCAAAAA	540
AGCTCACCAT GCCGATyCa ATAGGAATAC ATGGCTTCCA AGGTCGcTtG ACTGTAAGGA	600
AGCTTCACCC CATCTACGAG GtAAcCAAGT TCACATCCGT GATACCAAGC	650

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GATAGCAATC CGCTTCAGAA ACTTCTCGCT TACCTCTAAC TCCGATCGCT AGTTTGGGAG	60
AAGATACTTC CATTCCTATA CTATCTGTTG GCTTTGCAGG CTGTAAAAAC AACTTTTCTC	120
TTGCTACTTC CTGAAAATCT GAATCTTGCA GTTCTTTGCT TTCAAAATAG TCCTGTACTC	180
GCTCCACATC AAAATTCCCA GCTAAAGACA GAGACATGTT TACAGGTTTG TAAAACTTTG	240
TAAAAATTTTC TTGCAAATTA GTTAGATTGA TTTGGGAAAT GGACTCCTCA CTCCCAACTA	300
TATCAGTTGC TAAAGGTGTA CCAGGATACA AATTCGCTAA AGTTGAAAAG AATAAACACG	360
AATCTGGATC ATCTTGGTAC ATTTCTCGTT CTGCTGAAT AATATCCTGC TCTGTCAGAA	420
TGGAAGCTTC AGTAAAGTGT GCTGATGTTA CCAATTCATC AAGTAAATCT AAATTTTCTA	480
AAAAATAATC CGTTGCTGAA AAAAGATAGT TTGTTTTTGT AAAGCTTGTA AAGGCATTAC	540
TATCTGCACC TAGACTCGTA AAAGCCGACA TCAAATCACT AGAATCTTCT CTCTCAAATA	600
ATTTATGTTC AAGAAAATGA GCAATTCCTC CAGGATATTG TTTTACATCT CCGTCAACTT	660
CTGTGACAAA CGTATCTACC GAACCAAAT GTACAGTGAC ACTCCCGTAA ACCTCTTTAA	720
ATTCCTTTTT AGGCAAAAGA GCAACTGTCA ATCCGTTGGC CAAACGAGTT CGATAAACCA	780
TTTCTTTTAC AGCTGGATAG TATTTTTCTT CAAAAACAAC CTTTGTCAAT CTATTCCTTC	840
CATAAAGTAA ATCGCTTGTA GTTTCACATT ATTAGCTACT CTACAAATAG CATCTTTGTC	900
AATTTGTTC AAGCTTTGCA TCCAACTTTT AAAGTCTGCT GAAGATTTTC CAAATAAGGC	960
ATTTTGATAA GCACGTTCAA TCAATGAAGA ATGATTATCT TGAGAAAGTA ACAACGACCA	1020
ACGAATCATT TCCTTGGTCT GATTTAACTC AAACCTGTGA AAAAAACCTT TTTTAAATC	1080
AAGCCGTTGA TTATTCATCA ATTTACGAGC CTGGTTACG	1119

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ACGCCCTCGC GGGGACATGA CGAATCCCC GTTCATCAG AAGGCCCGC AGGAGTGGGG	60
GGTGCCGTCC AAGTCAAAAG CGGCCCCACA TCGATTCACT TCCCCGACGA ACAGCCCTTT	120
CCCCCAGCGT TCCTGGCTTT GCAACCGTTT CACAACAGCC TCGTAAAGTA GGCCGGACAA	180
GGCAGACGGA CTCCAAAGGA GTTCTTCCAT CTGCAAGTGC GCCTGCGTTA TGTGATCCCG	240

1317

GTCTTTTGCA TGTGTGTGGC ATGAATGCTG TTCCCAATCC CACTCCAGAA CATTCCTCTC	300
AAAAGTGC GC AACGTCGCCC TGAATGAATC CTGCCTTGTA GTCGTGACCA TTCCTATGAA	360
GGGTGCGAGA GGATTTTCCC CGAGTGCAAG CGCATCCTCC GGCTCAAATC GGGTGCATTT	420
CACAGTCCCG CTCAACGCTA GCCCGATCCC TTTTGGCAT GGTGACTCAA GCGTCCTTTC	480
AAACAAAAGC TCCTCATCCG CTCCAACCGG CCCGACGTAG ACGCGTAGAC CGAAGTCGTC	540

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1949 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGAATTGC ACCAATTCAA GGTGAGGCA TCGCAAAC TAAGACTGTTC CCCCCTCAGT	60
TCTGGACAGA AAACGGGATA AGGTTGGCTG TGAAGCAAGC TGCCCTCCTA CCAACAATTT	120
TGGAAAGTAG GCATCAGCTG ACAATTCCTT ACAAGCATAG TCCGTTCCAT AACCTGTAA	180
CAGTTGAAAG AGGAAGTGA CAAGGATATC TGAATCCGAA TAACGACAGT AGCGGCGTTG	240
GTCATTCGTT ACTAAATACT TAGAAATCCG CTCTTTTAGT TTCAACTGGG AAAAAAGTTC	300
CTGAAAAAAG ATAAGACCAC CATACTGGGT TAAATGACCT CCATCGAAAG ATAGTTGGTA	360
AAAAGACTTG TTTTGGAAAGT GATGATTTGG TAAACTGTTC ATGTGAGTTT CCTTCTTTT	420
TGTGTTTTTT TCTACACTTA TACCATAAAG GGGAAACTCT TTTTGTCTA GTAAAAACA	480
CCCATTGGGT GAAAAAGAA ACCATCCAGG ATCTAAGCTA AGGCAAGGAT TCTGGATGGT	540
TTT TAGATT GGGGTGAATA ATTGGGGTTT TACAATATCA ACTCCCATGA TAGTCATGAG	600
ATGACTCTTC ACGAATTGAC GTGATGACTG TCCTTCCTTT TGCATAATTA CCTCCGAAAC	660
ACAAAAAAG GGGTAGACAA TCTAGTGTCT ACCCCGAAA GTTTATTAAA AAAAAATCC	720
TGCCAAAGAA TTTTGGCAG GAAACCAAT CAATTTATCA GTTCTATCA ATCGCTTATC	780
GCTCTCAAAG ACTGGTAAAT AGGGATTCCG CAATCAAATT GCGATACTCT ATTATTAAAG	840
AGTAACTGAA GCTCCAGCTT CTTCCAATT AGCTTTGATT TCTTCAGCTT CTGCAGTTGC	900
AACGCCTTCT TTAACAAGTG CTGGTGCACC GTCAACAAGT TCTTTAGCTT CTTTAAGACC	960
AAGACCAAGT ATTTACGTA CAATTTGAT AACGCCAAT TTTTGTGCG CTGCAGATGT	1020
CAATTCAACG TCGAATGAAT CTTTAGCAGC ACCAGCATCA GCTGCATCAG CTGCAGCAAC	1080

1318

AGCTACAGGA GCAGCTGCAG TTACACCAA	TTCTTCTTCG ATAGCTTTTA CAAGGTCGTT	1140
CAATTCAAGG ATTGAAGCTT CTTTAATTTC	AGCAATAATG TTTTCAATGT TCAATGCCAT	1200
TGTTATTTCC TCCAATAAG TTTTAAATTT	TATAATAGTT TTTTTCGTAG CTAGksTACG	1260
CTGTGTAGCT TAAGATTAAG CCGCGTCTTC	TTTGCTTTCT GCAACCGCTT TGA CTGCAAG	1320
AGCAACGTTG CGCACTGGCG CTTGAAGTAC	AGAAAGGAGC ATAGAAAGAA GTCCTTCGCG	1380
GTTTGGAAGA GTTGCAAGTG CAAGAATCTC	TTCTTTAGAT GCGACAGCGC CTTCGATTGC	1440
ACCACCTTTA ATTTCAAGTG CTTCAGCGTT	TTTAGAAAAG TCGTTCAAGA TTTTCGCTGG	1500
TGCGATAACA TCTTCATTAG AAAATGTAC	TGCAGATGGT CCAACAAATA CAGATGCAAG	1560
ATCTTCAAGA CCAGCTTTTT CAGCTGCACG	ACGCAAGATT GAGTTTTTAA TAACTTTATA	1620
CTCAACTTCG CTTCCACGAA GCTCACGACG	AAGAACTGTA TCTTGCTCAA CTGTCAAACC	1680
ACGAGCGTCT ACAACGACGA TAGATGCAGC	AGCTTTCATT TTTTCAGCTA TACGTCAACT	1740
AGTTCGCTT TTTTAGCAAT AATTGCTTCA	CTCATTAGTG TGTTCACCTC CGTAATTATT	1800
TTGCTTGGGG AATTTTTCAA AAAGAAAAC	GCGCCCAATC CTAGACACGA AAGTACAATA	1860
CGCTTCTTTT TACATGATAC GTTTTGTCT	CGGTAGGATA TTTATGAGTC GAGCTCCCCT	1920
ACTGTCTTAG GCAGTTTTTT TAGATACGG		1949

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1023 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGACTGTTTG ATCTTATACA GTAGCTGCTT	GATCCAAGCT TTCACCGATA GCGGCTAGGC	60
GCTCGATAAC TTCAGCTTGT GTCAATTCAT	TTTTTGAAAC ATAGCGGTTA CGTGGGTGAA	120
CACGGCACTC GTGTGAGCAT CCACGAAGGT	ACTTGTCTTC ATTTTCTTCT GATGTCAAGA	180
TACGACGGTT ACAGAAATGGA TTTCCACAGT	TGACATAACG TTCACATGGT GTTCCATCAA	240
ACCAGTCTTT CCTTACGATA GTTGGGTGGA	CATGGTTGAC ATCAACGGCA ATACGCTCGT	300
CAAAGACGTA CATTTTCCCA TCCCAAAGCT	CACCTTGAAC TTCTGGGTCT TTACCGTAAG	360
TTGCGATTCC TCCGTGCAAT TGGCCGACAT	CTTTGTAGCC TTCACGGACC ATCCAGCCTG	420
AGAATTTCTC ACAGCGAACG CCACCTGTAC	AGTAAACCAC GACACGCTTG TCCATGAATT	480
TTTCCTTGTT ATCACGGACC CATGTGGTA	ACTCACGGAA GTTGCGAATA TCTGGGCGAA	540

1319

TAGCTCCACG GAAATGTCCT AGGTCGTACT CATAATCGTT ACGTGTGTCA AGGACAACGG	600
TATCTTTATC AAGAAGCGCT TCTTTGAACT CTTTGGAGA CAAGTAAGCA CCTGTTGTTT	660
CAAGTGGGTT GATGTCATTG TCAAAGTCGT TGTCTTCCAA ACCAAGGTGG ACAATTTCTT	720
TCTTGTAGCG AACAAACATC TTCTTGAAGG CTTGTTTCATT TTCTTCGTCA ATCTTGAACC	780
AGAGTTCTTC CATTCCTGGA AGGCTGTGAA CGTAGTCCAT GTATTTTGA GTTGTTCAT	840
AGTCACCTGA AACTGTTCCG TTAATTCCT CGTCAGCGAC TAGGATACGG CCTTTAAGGn	900
CGATTGATTT ACAGAAAGCC AAGTGGTCTG CAGCAAATTG CTCTGCATTT TCAATTGGAG	960
TATAAAGGTA GTAAAGTAAG ACACGAATAT CTTTgkCaw AAGATTGTA TCTCTTTATC	1020
TAT	1023

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

ACTATGAACA AGACCCAGAA AAAGTAGCCT TATTTCTTAA GAATTTAAT AGTTTAAAGC	60
ACCTAGCACC TGTTTAGATT GACGAAACAG GATTCGATAC TTATTTTAT CGAGAATATG	120
GTCGCTCATT AAAAGGTCAA TTAATAAGAG GCAAAGTATC TGGAAGAAGA TATCAGAGGA	180
TTTCTTTGGT TGCAGGTCTA ACAAATGGTG AATTAATCGC TCCAATGACT TACGAAGAGA	240
CGATGACGAG CGACTTTTTT GAAGCTTGGT TTCAGAATTT TCTCTTACCA ACATTAAACA	300
CACCATCGGT TATTATTATG GATAATGTAA GATTCCATAG AATGGGGAAG CTAGAACTTT	360
TATGCGAAGA GTTTGGGCAT AAACTTTAC CTCTTCCTCC CTA CTGCTCCT GAGTACAATC	420
CTATTGAGAA AACATGGGCT CATATCAAAA AGCACCTCAA AAAGGTATTA CCAAGTTGCA	480
ATACCTTTTA CGAGGCTTTT TTATCCTGCT CTTGTTTCAA TTGACTATAT TAGAGGCGAG	540
ACATTTTTCG GTTCTTTGTC AACTGTAGTG GGTGAAGAA AGCGAAGATC TAGAAAGGAC	600
AAATTTTCGTC CTTTCTTTT TGAAGTTTTC AAAGTTCCTA AAACCAAAGG CATTGTGCTT	660
GATAAGTTTG ATGAGATTAT TGGTGGCTTC CAGTTTGGCG TTGGAATAAG GTAATTGAAG	720
GGCGTTGACG ATTTCTCTT TATCTTTGAG GAAGGTTTTA AACAAAGTCT GAAACAGAGG	780
TGGAAAAGCA AGAGCTGATA GAGATTATAG TGGTGTTTAA AGTCTTCGGA ATAGCTCAAA	840

1320

AGTTTATCTA GAATTCTTT ATTAGTCAAG TGCATACGAA AAGTAGGGCG ATAAAAATCGT	900
TTATCACTCA GTTCTGACT ATCTTGTTGA ATGAGCTTCC AGTAGCGCTT GATAGCCTTG	960
TATTCATGGG ATTTCCGATG ATGGCTTGTG TTCTGCTCTC AAGAACAGTT ATGATATTGA	1020
GTTTATCAAA GTCCTGAGCA ATAAAGCTCA TCTCCATCTC CCGATTGAAA CAGTCACTCC	1080
CCGGACTGTT TCAACsTCCT AGGACATAAT CTCAGGAAGA CCGGAAAAAT CATGCTCAAA	1140
GTGAAAATCA TTGTCTTGC GAATGACAGT TGAAGTTGAA ATAGACAACT GATGATCAAT	1200
GTCGGTCATA GAAGTCTTTT TAATTAGCTT CTGAGCAATC TTTTGGTTGA TGATACAAGG	1260
AATTTGATGA TTCTTCTTGA CGATAGAAGT CTCAGCGAGC TCCATTTTTG AGCAATGATA	1320
GCACTTAAAA CGGCCTTTTC TAAGAAGAAT TCTAGTTTGA ATTTTTTTAT ACTAGAAAA	1380
CAGAACCATA ATACCTATAT AAAAATATTA TAGTTCTAAT AGGATTTACC CAAAAGTTTT	1440
AAGGCGGTCT TTTTAGAACT TTAATTGTTT GAAATTTAGG TAGCAAATTT GTTCTATTTT	1500
TGTCAACTTT TCCTATTTTT ATCTTGTTGA GGCTGGTATT TTAACAATTC AGGAATTGAT	1560
ACTGAATGTG TAAAATTTTT TGTTAGAATA AGTTTATAAA AAAGAAAAGG AGTATTTGAT	1620
TATGTTACAA AAAATTTATG AGCAGATGGC TAATTTCTAT GATAGTATTG AAGAAGAGTA	1680
TGGTCCTACA TTTGGTGATA ATTTGACTG GGAACATGTT CATTTTAAAT TTTAATTTA	1740
TTATTTAGTG AGATATGGCA TTGGTTGTCG TAAGGATTTT ATTGTTTACC ATTATCGTGT	1800
TGCTTATCGT TTGTATCTTG AAAAATTGGT AATGAATCGG GGTTTTATTT CTGTGAGG	1860
TAATTTTAGT AAATTCCGA ACTAATTTAC TCTTTTATGG AAAGATGATA GTAAATAGCT	1920
AGTAATTTTT CTAAATCATT TTTTAATAGT TGGAAATAGC AAATCTTTCT ATTGTTTCTT	1980
CTTGATAAAA AGGCGATTTT TTATTATAAT AAATTGTAAG ATATAATTGC AGGTGAGAGT	2040
CCTGCCATGT ATGTGAGAAA GGAAGAGCCT GATGGCTCAG ACAAGATTAT GACTTCAGTT	2100
GTTGTTGTAG GTACCCAATG GGGTGATGAA GGTAAGGGA AGATTACAGA CTTCTTTCA	2160
GCGAATGCAG AAGTGATTGC ACGTTACCAA GGTGGTGATA ATGCTGGTCA CACGATTGTG	2220
ATTGACGGTA AGAAATTTAA GTTGCACTTG ATTCCATCTG GGATTTTCTT CCCTGAAAAA	2280
ATATCTGTCA TTGGGAATGG TATGGTTGTA AATCCTAAAT CTCTTGTAAG AGAGTTGAGC	2340
TATCTTCATG AGGAAGGTGT AACAACTGAT AACTTGCCTA TTTCTGATCG TGCGCATGTT	2400
ATTTTGCCTT ATCATATCGA GTTGGATCGC TTGCAAGAAG AAGCTAAGGG CGACAATAAG	2460
ATTGGTACGA CAATTAAGGG AATTGGTCCA GCTTATATGG ACAAGGCTGC TCGTGTGGA	2520
ATTCTGATTG CAGATCTTTT AGATAAAGAT ATTTTCCGTG AGCGTTTGA ACGTAACCTT	2580
GCTGAAAAGA ATCGTCTTTT TGAAAAATTG TATGACAGTA AAGCGATTGT TTTGATGAT	2640

1321

ATTTTGAAG AATATTACGA ATATGGTCAA CAAATCAAGA AATACGTGAT AGATACATCT	2700
GTTATCTTGA ATGATGCGCT TGATAATGGC AAACGTGTGC TTTTGAAGG TGCACAAGGT	2760
GTTATGCTAG ATATCGACCA AGGTACTTAT CCATTTGTTA CGTCATCAAA CCCTGTAGCT	2820
GGTGGTGTGA CAATTGGTTC TGGTGTCTGGT CCAAGCAAGA TTGACAAGGT TGTAGGTGTA	2880
TGTAAAGCTT ATACGAGTCG TGTAGGAGAT GGTCCCTTCC CAACTGAGTT GTTTGATGAA	2940
GTGGGAGAAC GTATCCGTGA AGTGGGTCAT GAATATGGTA CAACAACCTGG TCGTCCACGT	3000
CGTGTAGGTT GGTGACTC AGTTGTGATG CGTCATAGCC GTCGTGTTTC TGGTATTACT	3060
AACCTTCTT TGAACCTAT TGATGTTTGG AGCGGTTTGG ATACTGTGAA AATCTGTGTG	3120
GCCTATGATC TTGACGGTCA ACGTATTGAC TACTATCCAG CTAGTCTTGA ACAATTGAAA	3180
CGTTGCAAGC CTATCTATGA AGAGTTGCCA GGTGGTCAG AAGATATTAC CGGAGTTCGC	3240
AATTTGGAAG ATCTTCCTGA GAATGCGCGT AACTATGTTT GTCGTGTGAG TGAATTGGTT	3300
GGCGTTCGTA TTTCTACTTT CTCAGTAGGT CCTGGTCGTG AACAAACAAA TATTTTAGAA	3360
AGTGTGTTGGT CTAAGAGAT TTTTAAGATT TGTTAAGAT AGGTCGGSTA TACTATAGAC	3420
GGTTACAAGA AGACCTCCTA ACTTGTTGTA ACAAATATCC TAAACTTTTC TTTTTCATAA	3480
TAATCTCCCT ATAGAGTCAC CGCATTCGGT GGCTTTTTTT GTGTGGGAT TCATGATATA	3540
ATAATAAAAT CGATAAGTAG GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAAG	3600
AAGTCTTTAT GAGGGAGGCT TTGAGAGAGG CTGAGATTGC TCTTGAACAC GATGAAATTC	3660
CAATTGGTGTG TGTGATTGTC AAAGATGGGG AAATCATTGG TCGTGGGCAT AATGCGCGTG	3720
AGGAATTACA GCGAGCGGTT ATGCATGCGG AAATTATGGC TATAGAGGAT GCGAACTTGA	3780
GTGAGGAGAG TCGCCTTGCT GGATGACACA CTTTTGTGA CCATTGAACC G	3831

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CCGCTGTTC AACCGCAACA TACCATAGTC CGTACGGGAT TCGAACCCGT GTTACCGCCG	60
TGAAAAGGCG GATGACTTAA CCCCTTGACC AACGGACCTG AGTTGTTATT TTCAACTCTT	120
ACTATTATAC AGTCTTTTCA AACTTTGTCA ACTACTTTTT CTAATTTTGT TTTATTTTTT	180

1322

CAACTTATAG TAAAAAAGC CAGAATTATA CTGACTCTTC TATCGCTCAT TAACTTAGA	240
AGCACGTTCT TTTCCCCACC AATAAGGGAT TAGTTCGCG ACTTTAACTG TTTTCTTAT	300
ATTATAGTCC ATCATGAATT CTGCATCTTT ATTTTCAGCA TTAAGCTCTA AAAGGAATTC	360
TCTACAAGCA CCGCAAGGCA TGGCTGAACT TCCACCATAA GGTGGTTTGT CTCGAAAGGC	420
TAATACTTTC TTAACCTTAG TTTGTCCTGA AAATTGGTAC ATATTGAAGA GGGCCGCCCC	480
TTCTGCGCAG AGATGGAAAA CACCACAGGT TCCCTCCATA CAGAATCCTG TAAATATTTG	540
TCCATCTCCT GCTTCTACTG CAGCTACAAC ATGATTGGCA TAAACAAAGT CTGATACTTC	600
ATGTGGATTG TATAGTTTCT GTGCTTCTTC GTACATCTTT TCCCAGATGT CCATTATTGT	660
ATCCTCTTTA TTTAGAGATT TCTTTTAGCA TGTTCGAT ATGCTGAATT GATTTTCAC	720
GTCCAAGCAA GAAAATTGTA TCTGGTAATT CTGGCCCATG CATTCGCCT GAACTGCGA	780
TACGAATAGG CATGAAAAGA TTTTCCCTT TAATACCTGT TTCTTTTGG ACTGCTTAA	840
TTTGTGGGAA GATATTTTCT GTCACAAAT CATCATCTGT CATCGCTTCA AGTTTGTCT	900
TGAATGCTTC AAGAACTGTT GGAAGTGT CACCCGTCAT GACTTCGCGC TCTGCTTCTG	960
TCAATTCTGG GAAATCTGAG AAGAAAAGAT CTGTCAATGG GATAATCTCA TCTACTGATT	1020
TCATTTGTGG TTTATAGAGC TCAACTAATT TTTCAGCCTT GTCAGTCAA CGGCCTGCTT	1080
CCTCTAAGAA TGGTTTGGC ATTTCAAAGA TGGTTCAAG GTCTGCATTC TTGATATAAT	1140
CATTGCTCAT CCAGTCTAGT TTTTCTGAT CAAAGGCTGC TGGTGACTTG CTGAGGCGGT	1200
TTTCATCAA AAGTTTAATG AATCTTTCAC GAGAGAAAAT CTCATCCCCA CCACCTGGGT	1260
TCCAACCAAG AAGAGCAATA AAGTTAAAGA CTGCTTCTGG AAGGTAACCT TTCTTTCGGT	1320
AATCTTCGAT AAATTGAAGT GTATTAGTAT CACGTTTAGA TAACTTCTTA CCAGTTTCAG	1380
AGTTGATAAT CAAGTGTAT GTGACCGAAC TCTGGAGCTT CCTCAACCTA AGAGCGGTA	1440
T	1441

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CGGCTTATGT AGTGGCAATC TTTCTACGTA AGCGAAACGA GGGGAGATTA GAGGCGCTAG	60
AAGAAAAAAA AGAAGAACTA TACAATCTTC CAGTAAATGA TGAAGTAGAA GCTGTAAAAA	120

1323

ATATGCACTT GATTGGACAA AGTCAAGTGG CTTTCCGTGA ATGGAATCAA AAATGGGTCG	180
ATTTATCTCT CAACTCTTTT GCCGATATTG AAAATAATCT CTTTGAAGCA GAAGGCTATA	240
ACCATTCAAT TCGTTTCTC AAGGCCAGTC ATCAAATTGA CCAAATTGAG AGTCAAATTA	300
CTTTGATTGA AGAAGATATT GCGCAATTC GCAATGCTTT GGCAGACTTA GAGAAGCAAG	360
AATCTAAAA TAGTGGTCGT GTTCTTCATG CTTTGGATTT ATTTGAGGAA CTTCAGCATA	420
GAGTTGCTGA AAATTCAGAA CAGTATGGTC AAGCCTTGA TGAAATTGAA AAACAATTAG	480
AAAATATCCA ATCTGAATTT TCACAATTG TAACCTTGAA TTCATCGGGT GACCTGTGG	540
AAGCCGCACT GATTTTGGAT AATACAGAAA ATCACATTTT GGCCTTAAGT CATATTGTGG	600
ATCGTGTCC AGCCTTGGTT ACGACGCTTT CTACAGAATT GCCAGATCAA TTACAGGATT	660
TGGAAGCCGG TTATCGTAAA CTAATTGATG CTAATTATCA TTTTGTGAA ACGGATATTG	720
AAGCGCGTTT CCACCTGCTT TATGAAGCAT TCAAGAAAA CCAAGAGAAT ATTCGTCACT	780
TGGAATTGGA TAATGCCGAA TATGAGAATG GACAGGCACA AGAGGAAATC AATGCCTTGT	840
ATGATATTTT TACTCGAGAA ATTGCTGCTC AGAAAGTAGT GGAAATCTA CTTGCAACTC	900
TTCCAACCTA TCTTCAACAT ATGAAAGAGA ATAATACTTT ATTGGGAGAA GATATTGCAC	960
GTTTGAACAA GACCTATTTA CTTCTGAGA CAGCTGCAAG CCATGTTCGT CGTATTCAGA	1020
CAGAAATAGA GAGTTTGTAG GCAGCTATTG TTGAGGTAAC TTCAAATCAA GAAGAACCAA	1080
CCCAAGCTTA TTCAGTTCTT GAAGAAAATC TTGAGGATTT ACAAACCTCAA CTAAAAGATA	1140
TTGAAGATGA GCAAATTTCA GTTAGTGAGC GCCTGACACA AATTGAGAAA GATGATATTA	1200
ATGCACCTCA AAAGGCCAAT GTTTATGTCA ATCGTCTCCA TACTATCAAG CGATACATGG	1260
AAAAACGCAA TCTGCCAGGT ATTCCACAAA CTTTCTTGAA GTTATCTTTT ACGGCAAGCA	1320
ATAATACCGA GGATTTAATG GTTGAGTTAG AACAAAAAT GATTAACATT GAATCTGTTA	1380
CCCAGTTCT TGAAATTGCA ACGAATGATA TGGAAGCTTT AGAAACGGAA ACTTATAATA	1440
TTGTACAATA TGCAACTTTG ACAGAGCAAC TCTTGCAATA TTCTAACCGC TATCGCTCAT	1500
TTGATGAACG CATTCAAGAA GCATTTAACG AAGCTTTAGA TATTTTGTAA AAAGAATTTG	1560
ATTATCACGC TTCATTTGAC AAGATTTCTC AAGCATTGGA AGTGGCAGAG CCTGGTGTA	1620
CCAATCGCTT TGTACCTCA TATGAGAAAA CACGTGAAAC GATTCGTTTT TAATAAAGA	1680
AAAAGATTTT ATTGTGTGAG GAGCAGAATC AAATCTTTTT CTATAGTTGT GGGGAGATTT	1740
ACTTCATTTT CTCCTGAGAT TGAGTTTTTG CCCAGCCGAT TTATCCACTA CCTCAAACA	1800
GTGTTTTATA CTCTCGAAA ATCTTTTCAA ATCACGTCAG CGTCGCCTTA CCGTACTCAA	1860

1324

GTACAGCCTG AGGCTAGCTT CTTAGTTTGC TTTTGTGATT TCATTTAGTA TTAAAGTGAT	1920
TTGCCCAGTC TTATCTGCAG CTTCAAATCT GTACTTTGAG TAACTTGGTA ACCGTCCAAT	1980
AACGAAGTCT ATTGAAAAAT CTCCAGACTA GAGAACTCAC GGATAGTTCC TAATCTGGAG	2040
ATTTCTTATT TGCACCTTTC TTGTACAAC TTAGTCCACG GTAAATAGAC CTCTAAAACC	2100
TCTTTGTTTA CGAGAGTTTC CTCGTTTGA AGACATTCTA GAAGATAGGA TAGATATTTT	2160
TCGCTATTTA TACTAGACTA AAATCAAAAA GCATTATATA ATAGTGATAT GAAATCAACT	2220
AAAGAAGAAA TCCAAACCAT CAAACACTT TTTAAAGACT CTCGTACAGC TAAATATCAT	2280
AAACGCCTTC AAATCGTTCT ATAGTAAAAT GAAATAAGAA CAGTACAAAT CGATCAGGAC	2340
AGTCAAATTG ATTTCTAACA ATGTTTGA AGTAGAGGTG TACTATTCTA GTTTCATCT	2400
ATTATATTTT GTCTGATGGG CAAATCTTAT AAAGAGATTA TAGAACTTTT ATAGTAGATT	2460
GAAATAAGAT GTGAACAACT CTATCAGGAA AGTCAAATTA ATTTATAGAA ATATTTTAGC	2520
AGCCAAGGTG TACTGTTATA GATTCAATAC ACTATAGACT GTAATCAAAC AACGATTTGG	2580
CGAAATGTAA AAAAATATGA GGAGTTCGGA CTCGACTCTC TCCTTCAAGA AACACGTGGT	2640
GGTCGTAACC ATGCATATAT GACAGTTGAG GAAAAGAAAG TCTTCTTGC CCGCCATTTG	2700
AAGGCTGCAG AGGCAGGAGA ATTTGTTACA ATTGATGCCT TATTTCAGGC TTATAAAAAG	2760
GAGTTAGGTC GTTCCTACAC ACGTGATGCC TTCTATCAAC TGTGAAGTG CCATGGTTGG	2820
CGAAATATTA TGCCACGTCC AGAATCATCT AAGAAAGCAG ACGCTCAAAC CATTTGTCGCG	2880
TCTAAAAATA AAATCTCAAT TCAAGAAGAA AAGAAAGCGC TTTAAAACCA GTAGACGTTT	2940
TCGTAAGGTT CGCTTGATGT ACCAAGATGA GGCTGGTTTC GGTAGAATCA GTAACTGGG	3000
ATCTTGTGG GCTCCAATAG GAGTAGGTCC ACATATCCAT AGTCACTATA TACGAGAATT	3060
TCGCTATTGT TATGGAGCTG TTGATGCCCA TACAGGCGAA TCATTTTCT TAATAGCTGG	3120
TAGATGTAAT ACTGAGTGA TGAACGCCTT TTTAGAAGAG CTTTCACAAG CTTATCCAGA	3180
TGATTATCTT TTAATCGTTA TGGACAATGC TATATGGCAT AAATCAAGTA CCTTAAAGAT	3240
TCCGACTAAT ATTGGTTTTC CCTTTATTC TCCATACACA CCAGAGATGA ACCCCATTGA	3300
ACAAGTGTGG AAAGAGATTC GTAAACGTGG ATTTAAGAAT AAAGCCTTTC AAACTTTGA	3360
AGATGTCATG AATCAACTCC AAGATGTTAT ACAAGGATTG GAGAAGGAGG TGATAAAGTC	3420
CATCGTTAAT CGGAGATGGA CTAGAATGCT TTTTGAAAAC AGATGAGTAT AAAAAGAAAG	3480
TCCTCATTTT AATAGAAATC ACGACTTTCT GATGGATTTA TAGTAAATG AAATAAGAAC	3540
AGGACAAATC GATCAGGACA GTCAAATCGA TTTCTAACAA TGTTTGTAGAA GCAGAGGTGT	3600
ACTATTCTAG TTTCAATCTA CTATATTTT GGAGTGATAG AAAAGCCCTT CATAAGCTAG	3660

1325

TCTACTTGTT CAGGTGCGAG AGCTTTGACA TCTTTTCTG TACTTAGCCA AGTCAGTTT	3720
CCGTTCCTCAA AGCGTTTATA TAGTAGCCAA AATCCTTGAC CATCCAGTA AAGGGCTTTA	3780
AAGCGGTCTT TACGTCCACC ACAAAGAGA AAGACTTGAC CGGAGAAAGA ATCCAATTCA	3840
AAGTGGGTTT TAACTACATA GGCTAATGAG TCTATTCCT GCCTCATATC TGTCTTGCCA	3900
CAACAAGGT GAACTTGACC TAAATCACTT AGTTGAATTA TCATAGTACA ATACCTTTCC	3960
TCCGATAATT ATTTTATC TAGTATACTG GAAGTTGGG AATTAGGATA GATACCTTGT	4020
TATGACGCGC TTACGTAAC TGTAAC TAGC TGCCTAGTTT GATCTTGCT TCTTCATTGA	4080
TTAGCAGTAG ATTTCAAAT GATAAAACG CATAGTATCA GGTATTGAAA TGTACTGCC	4140
CAAAAGTTAG ACAGAAAAA TCTAACTTTT GGGGTGTTTT TGTATGAAA TTAAGTTATG	4200
ATGATAAAGT TCAGATCTAT GAACTTAGAA AACAAGGATA TAGCTTAGAG AAGCTTTCAA	4260
ATAAATTGG GATAAATA TCTAATCTTA GGTATATGAT TAAATTGATT GATCGTTACG	4320
GAATAGAGTT CGTCAAAAA GAAAAAATC GTTACTATTT TCCTGATTTA AAACAAGAAA	4380
TGATTAATAA AGTCTTAC	4398

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AGATTTT TAG ACTTGTCTT TAATCGTTTC TTTTAGGGA TGATTGCGAC ACCTTCTTT	60
GGCTATTAAC TTTAGCAGGA GGGATTATCC TTGGTCTAGC GCCGGCTAGT GCCACCTTGA	120
TGAGCTTATA TGCAGAACAT GGTATAGCT TTCGGGAATA CAGTTTGAAG GAGGCTTGGT	180
CTCTTTACAA GCAAATTTT GTCTCAAGCA ACCTGATTTT CTATAGCTTT TTAGGTGTGG	240
GTCTAGTTTT GACCTATGGT TTGTATCTCT TGGTGCAATT GCCTCATCAG ACCATTGTC	300
ATTTGATTGC GACCCTTTG AATGTCCTAG TAGTTGCCCT GATCTTTTG GCTTATACAG	360
TATCTTTAAA ATTACAAGTT TATTTTGCTT TGTCTATCG AAATAGTCTC AAATTATCCT	420
TGATTGGCAT CTTTATGAGT CTAGCAGCTG TGGCTAAGGT TCTCCTTGGG ACTGTGCTAC	480
TTGTAGCAAT TGGTTATTAT ATGCCTGCCC TGCTATTTT TGTAGGAATT GGGATGTGGC	540
ATTCTTTTAT CAGTGATATG TTGGAACCTG TCTATGAAAT CATCCATGAA AAATTGGCGT	600

1326

CAAAATAGAA TGAAGCAGTT TTGGCTACAT ACGCTTCTAA GAACCTATAG TTCAGTGATG	660
ATCATTATCA TTGCGAGTTT TGCAATCTTA CTCTCTTACG CTGTCTGGGA TTCACGTG	718

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TCGGTACCAA AATTCTGGAT TTATACTAGC AAAGATCCAA GAGCAAATTA TTAAACAGAT	60
TTAGTCTAG TTTTCCCTGA ATCATTAAAA GAATTTGAGA GTGAAGATAG TTTTGCAAAG	120
GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT	180
GATGATAAAA CTCTTGAAGC TTTACAAAAA GATCCTCTTT TAGGTAAAT AAATGCAATT	240
AAAAATGGTG CCGTTGCTGT AATTCCAGAT AATACACCGT TAGCAGCCTC ATGCACTCCA	300
ACACCACTTT CAATAAACTA TACTATTGAA GAATACCTAA ATCTTTTAGG AAATGCATGC	360
AAAAATGCGA AATAAAAAAC AAATAAACCT AGGCATAATT TTTATAATCT GCCTAGGTCT	420
TCTTATTACA ATATTTTGT CATTAAGCT TGAACAAAA GAAATTAATA TCAGAGATTT	480
TTTAGCAGCT TTTGGAATGG GTAATACAAA TGATGATTTT ATTAAATCAA TTATATATAA	540
TAGAATACCT AGAACTATTT TTGCAATTT AGCAGGTTCT AGTCTTGCCA TAAGCGGTGT	600
ATTGATGCAA TCAGTTACTA GAAACCCAAT AGCTGATCCA GGTATACTCG GTATAAACAC	660
AGGAGCAAGT CTTAGTGTAG TAATTGGTCC TTCTTTTAG GGAATTCATC AAGCATAA	718

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GAACATCA TTTTACAGG ATGAGATTTA CAGCAGAGAG TTTGAAGGCT TTATCAAAGG	60
TTTTTCTTGG CATAATGACT TTCTCTCGTT TCCACTTAAT TTTGTGTCTA CTTTATTATA	120
CCAAGTCCAC SCTTAAGTTA GATAATAAAT CTAACCTAAG GAAGCTAGAA GGATGAGAAT	180
CCAGTGCGTC AAGAGTCCCA AACTTAAGCT GATGGGGACA CCCAGAATAA TTTGCTTTTT	240

1327

GAAGGCAAGG CCACGTTCCCT CTATATTGGG AAGTGAGAGT TGAATGAGAG AACCAGCTGA	300
TGAAAAGGGT GAGATATTAG TAGATAGAGC GCCAATAACG GTGGCTGTTG TGAGTAAGTG	360
AATATCAATC TGAGGATTTT GAGCACTGAT GATAGCAATG ATGGGAAAGA GGGCTGGAGC	420
TACAACGGAT AGGGTGGAAC TAAAGAGTGA CATCACTCCG GCTATCACAC AAAAGAACAG	480
AGGTAACCAG AAATGAGGAA TGGTTGTTGT CATGAGGTGC CCTATCAGTG TGAATAAACC	540
TGACTTGACC GCTAGAGACA TTAGTAAGCT CATGCCGCGAG AGCATGATAA TTGTAGCCCA	600
GGGAACCTTA GCTAAAATGG CTTCTTGCTT CCCTAATTG AGCCTTAAGG CGAGGCAGAC	660
CATGAGTATT GAGACAAAGC CAATATCAAA TGTTTTTTGA TAAGTAGCTA TCCAGGCGAT	720
GTTTGGGAAA ATGAGATGCA ACAAGGGAAA AAGCCAAACC AAAACCATGC TGCTGATCAT	780
GAGCAAGGTG GTTTGTCTTT GAACCTTGCT GAGGAGTGGT GGTGTTGTCAG TAGTCAAGGA	840
TGAGTTTGTT CTTCCCTTAC TATAGTGACT GTAACAGGAT AATAAAAGCA AGACGATGAG	900
TGGGTAGATA ATGCTGACGA TAAAGATATG ATTGCCAAGT GAAAAAGCTT GCTCTTCCCA	960
TCCCATTGTC TTAAACAGGC CTTGAAAGAC AATGCCTGAG CTAAGGTTA TCAAATTAGC	1020
CCCTCCTGAA GCTCCCAAT TGACGGCTTG AGCTCCAATC AAAGGGTGTT TGTCCGCTTT	1080
TTGACAGAGG GTAATCGCTA GAGGACAGCA AACGGCCATA GTAGTAAAA ATCCAGCACC	1140
TAAAGCAGAC AAAAGGGTTG CCATCAGGTA TAAATCATG TAGAGGCGT TAGGGTGGGT	1200
GCGTGTGCGG TAGAGAATGT GTTGAGCCAA AACATCAAGA GTACCGTTAG TTGTTGCAAC	1260
GTTATAAAG AGAGAGACGC TAAAAATGGT AAAAAAGAGT GAGGTTGGCC AAAAAATGAAG	1320
AAGTTCTTTG GGGCTTAATC CCATGAGAGT GGTGCGATG AGGTAAGAAA AAGCAATAGC	1380
CAGCAGGCCA ATATTGATTT TGGTGCGGTA ACCAATTCCA ATGGCTAGAG CAATGG	1436

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1696 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

CCATTTGGGA AAGAACGTAA GAGTTTGAG GGTGAGATTC CAGAAGAATT TTCAATGTCA	60
GCCGTTGACA TGTCTATGAT TGACCACATT CCAGATATGA TTGAAAATGG TGTGGACAGT	120
CTAAAAATCG AAGGACGTAT GAAGTCTATT CACTACGTAT CAACAGTAAC CAACTGCTAC	180

1328

AAGGCGGCTG TGGATGCCTA TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC	240
TTGGTGGACG AGATGTGGAA GGTGCCCCAA CGTGAAGTGG CTACAGGATT TTACTATGGT	300
ACACCATCTG AAAATGAGCA GTTGTMTGGT GCTCGCCGTA AAATTCCTGA GTACAAGTTT	360
GTCGCTGAAG TGGTTTCTTA TGATGATGCG GCACAAACAG CAACAATTCG TCAACGAAAT	420
GTCATTAAACG AAGGGGACCA AGTTGAGTTT TATGGTCCAG GTTTCCTGCA TTTTGAAACC	480
TATATTGAAG ATTTGCATGA TGCCAAAGGC AATAAAATCG ACCGCGCTCC AAATCCAATG	540
GAACTATTGA CTATTAAGGT GCCTCAACCC GTTCAATCAG GAGATATGGT TCGTGCATTA	600
AAAGAAGGAC TCATCAATCT TTATAAGGAA GATGGAACCA GCGTCACAGT TCGAGCTTAA	660
GAAAGGAAAA GGAAATGATA GAGGCACAGG GTTCTTAGT GGATAAGCAA ACAAGATGCA	720
TTCATTACCA TAGCAAGCTG GATATTATTG CTTTACAATG CTATGATTGT AAAAAGTATT	780
ATGCTTGTTA TCGGTGTCAT GATTCAATAG AACATCACCC TTTTGAGCCG TATCCCTTAT	840
CTTTGATACA GGATAAGCCT ATTTTATGTG GTGTTTGTCT AAAACTACTA ACATATAAGC	900
AATATAAAGA AAGCTTAAGT TGCCCTTTT GTTTTCTCG CTTTAATCCA GGTGCCAAA	960
ATCATAAGGA ACGCTATTTT AAATAGCAA TCATCTAGTT TTGAAGTAGG AGAAAACCTCA	1020
ATTTCAAGAG AAAATGAAGT AAATCTTCCC ACAATAAAC GCATAATATC AAGATTGTTC	1080
AATACCTGAT ACTATGCGTT TTTAAGATTT TAAAGACTTT TTTCTTTAT CTGGTATTTT	1140
GACTACTTGT TAAACTGGG TTAATTTTCG ACTGTTAAT AGTTATTATG CAAAGTCTAA	1200
AAGGTTAGAA TTGTCAAAAC AATCCGTCTA GAGTATGCGT GATGCCAACC GTGGTGGATG	1260
TTCTCAGTCA TGCCGTTGGA AGTACGACCT TTACGATATG CCATTTGGGA AAGAACGTAA	1320
GAGTTTGACG GGTGAGATTC CAGAAGAATT TTCAATGTCA GCCGTTGATA TGTCTATGAT	1380
TGACCATATC TCAGATATGA TTGAAAATGG TGTGGACAGT CTAAAAATCG AAGGACGTAT	1440
GGAGTCTATT CACTATGTAT CAACAGTAAC CAACTGCTAC AAGGCGGCTG TGGATGCCTA	1500
TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAAGAC TTGGTGGACG AGATGTGGAA	1560
GGTTGCCCAA CGTGAAGTGG CTACAGGATT TTACTATGGT ACACCATCTG AAAATGAGCA	1620
GTGTTTGGT GCTCGTCGTA AAATCCCTGA GTACAAGTTT GTCGCTGAAG TGGTTTCTTA	1680
TGATGATGCG GCGGTA	1696

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1022 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

CCGAGTTTAT TATGGTTTCT TCGGAATTTA TCTCAAAGAT TGAATTTGCT TGCAATAAGA	60
AAGAAAGTCT TTATAGTCAA AGCAAATTTA AGTATGCGAT TCGTTCCGATG TTCGCAGGTG	120
CATTTTTTAAC CTTCACTACT GCTGCAGGTG CAGTTGGGGC TGAATTGATT AATAAAATTG	180
.CACCAGGTAG TGGACGCTTC CTCTTTCCAT TCGTTTTTGC TTGGGGCTTG GCCTACATTG	240
TTTTTTTGAA TGCCGAGTTG GTCACCTCAA ACATGATGTT CTTGACTGCT GGTAGTTTCT	300
TAAAAAAAAT CTCTGGAGA AAAACAGCTG AGATTTTACT ATACTGTACC TTGTTCAACC	360
TTATCGGAGC CTTGATAGCA GGGTGGGGCT TTGCTCATTC GGCAGCCTAT GCGAATCTGA	420
CACACGATAG TTTCACTCTCA GGTGTTGTTG AGATGAAGTT AGGCCGCTCA AATGAATTGG	480
TCTTGCTTGA GCGGATTTTG GCAAAATTTT TTGTAAATAT TCGGATTCTG TCATTTATTT	540
TGGTCAAAGA TGGTGGTGCC AAACPTTGGC TTGTGTTGTC AGCTATTTAC ATGTTTGTAT	600
TCTTAACAAA CGAGCACATT GCGGCGAACT TTGCTTCTTT CGCGATTGTG AAATTCAGTG	660
TTGCTGCGGA TTCAATTGCC AACTTCGGTG TTGAAATAT GCTTCGCCAC TGGGGTGTGA	720
CTTTCATCGG AAACTTTATC GGAGGAGGCC TCTTGATGGG TCTTCCATAT GCCTTCCTCA	780
ATAAAACGA AGATACTTAT GTAGATTAAG AAAATGAGCA CGATTGAGTC GTGCTTTTTT	840
CATTTTCAA ATAAGGTAAT AGCTATTTCT TATATCAAAA TATAGAAAAC TGATATTTGT	900
AxACTATAAC TCAAGGTGCT ACAATATCCT TAATAAATA ATATGGAGGT CACCTTATGA	960
CTTGTGATTT TAAATnTGAA ACTCTACAAC TACATGCTGG TCAAGTTGTG GCTCCAGCTA	1020
CT	1022

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

CCTTAAGTAA TCTCTGATAA TATTTTCTTT ATTAGCATAG GCGAATATCG ATATAATGGC	60
TTCAATTATGA GTGGCAGGAA TATCCAATAT GGCAACTTTT CCAATAGATA ATTTAAAACT	120
CATTAATAAA GTTCCTTTAG GTGAAATGTC TATTTTCTTT GATTTTAATG CTAATTTAGA	180

1330

AATAGATTCT CTCGCATTAG TTACATAACC AGATATAGGC ATATCTGATA TAGATACCCA	240
AGGTATTTCA GTTCCCCAAA AAGTAGCTTC ACTGCGTGGA GGAGTTTTTC CTATTCTGAA	300
GTTAACTAGG CTAGCAAATT TAATATATCT CCATGCTTCT GGGATTTCAT ATATAGGATA	360
AGAGGTTGTT TCGTCTTTGT TCCATAATA AGAGTTATCA TCTCCTTGGG AAACAATAGA	420
AATGTCCAAA TCTTTCTTTT TAATCTTGCC TTCTTCAAAG AGTTTTTGTT TTTCTGCTCG	480
TATTTTTTCA AGTAAACTT CGACTGATTC ATCATTGGG TCTGTTCAA CTAATTTTCC	540
TTGCATAGCA TATTGAAGAA TAGATTTTTT TAGTTTATCT GGAAATCTT TATCTAGCTG	600
TTCTAGTCTA TTATAACTTT CAGCATATTC ATCTACTTTT TCTAAAGCTG ATTCGATTGC	660
TTC	663

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 881 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

CGTCGCTGAA CATGTCAACA GCAAATTAAA CTAAACAAAC TAAAATTATG TGATACTTCA	60
CATAATTTTC TTTAGAAAAT ATTATCAGAA GAAAGTTGAG AAAAATGGCA GAAAAACAT	120
ATCCTATGAC CCTTGAGGAA AAGGAAAAAC TTGAAAAAGA ATTAGAAGAA TTGAAATTGG	180
TTCGTCGACC AGAAGTG GTA GAACGCATTA AGATTGCCCG TTCATACGGT GACCTTTCAG	240
AAAACAGTGA GTACGAAGCA GCTAAGGATG AACAAGCCTT TGTCGAAGGA CAAATCTCTA	300
GCTTAGAAAC AAAAATCCGC TATGCTGAAA TCGTCAATAG CGACGCAGTT GCCCAGGACG	360
AAGTAGCGAT TGGTAAAACA GTCACCATCC AAGAAATTGG TGAGGACGAA GAAGAAGTTT	420
ATATTATCGT AGGTTCAGCT GGTGCAGATG CCTTTGTAGG TAAGGTTTCA AATGAAAGCC	480
CAATTGGGCA GGCCTTGATT GGCAAGAAAA CAGGTGATAC AGCAACCATT GAAACGCCTG	540
TTGGTAGCTA TGATGTAAAA ATCTTGAAGG TTGAAAAAAC AGCCTAAAAA CAGAAAAAGG	600
AGTGGGGAGG CGATGTGCTT CACTCACTCC TTTTCCATT TTGCTACTCT TCGAAATCT	660
CTTCAAACCA CGTCAGCGTC GCCTTGCCGT ATGTATGGTT ACTGACTTTG TCAGTTTCAT	720
CTACAACCTC AAAACAGTGT TTTGAGCTAA CTTCGTCAGT TTCATCTACA ACCTCAAAAC	780
TATGTTTGA GCTGACTTCG TCAGTTTCAT CTACAACCTC AAAACCATGT TTTGAGCCGA	840
CTTCGTCAGT TTCATCTACA ACCTCAAAAC TATGTTTGA G	881

1331

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 949 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```
CCTTTTTTAA TACAAGTTAT TTTGATTTAA CCGGCTTGTC TTGAGCTGTC TGCAAAGCTG      60
TGGCAATCGT ATCTGCATAC AATTTTGCTC CTGCTTCGAT AGTGCTACTC TCACTCCCGA      120
AATGAACCTG GTCTGTTCCTA GCCCAAATTT CTGGATGCTC TTTCGCAACT TGATTCCAAT      180
CTGCTATCGT AATGTAAGGT GTCTTCTCTG CCAATTCTCT CATATAGGCA GCAGCCTTCT      240
CAACGATGGC ATAGGTCTCT TTTGTCTTAT CTCCTTCATA AGGAGTCACC AAAATCATAT      300
GGTGTCCCTT AGGAAGATTT TTCACGATAC TGTCCAGTC ATCCTTGTA TTTCTCAGGAT      360
TATTTACCCC AGTCGCAATG ACCACCGTCT TAGGTAAAAA TTTATTCTGG CTATTATTTA      420
GCATGATTTT ATTTGCGGTC TTGGTTGTTA CGCTGACCTG CGCGTTAATC TGTGCTCCAG      480
GAAGAGCTGT CTGTAGTGCT GTATTTGCCC TTAAAGCCAC TGAGTCACCA ATTAACATAG      540
TGCCATCAGC AATTCCCAA CTGTTTGCAT CTGCCCGTTC TGCCATCACC TTGGTCTGGC      600
CAATATTTGT TGCAGCTTGC TTCAAGCCAT TGACAGTCAA GTCTGTCTCA AACGCTCCCA      660
CTTGTTGGTG CAACAAGGTC ACCGTGCAGA CAATGATGGT CAAGATTCCT GTACCTGCTG      720
CAAGAATTGC GTGAATATAA GGCAGGGGAC GAAsGGTTTG GACAATAGGT GTGTTCTTGC      780
CTGCAATCCA AGGTTCCAAT ACATAAAATG ACAGACTGGC AAAGCCATAA GAACAAATCA      840
GAGTCAGTAA TACAGCAAGA AGATTTGATG TCAACTGTGA GAAAATGATA TAGAAAGGCC      900
AATGGAAAAG ATAAACCGCA TAGCTAGTAT CCGCTAAAAA GCTGATAAT      949
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(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 622 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

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AAGATATATT TTTTACACAG AAGTATGCAA AAGTAAAGAG TGCAAAAAAT GGAATTAAAG      60
```

1332

CGAAAATAAA AGCCGTGTAC AGGCGACCAA ACCAACGTAC ACGGCTAAGG AAAAATAACA	120
AAACTCAAGC AAAGGCAAGG CGCGTGGTTT TGTTAGGTAT TTAGCAAGGG GACAAACCCC	180
TTTGTAATA ATCTCCTCTT ATTTTATCAA AATTAGAGGA AAATGACAAC TTAATTTATA	240
AAAAGGAAAA ATGGAGGATA TAAATGGAAA TTCTGTCTAA AGAAATACAG TTACAGGGCT	300
TACAACCTCT TAAACAGACT CTTGAACTT TAGTTGAGCT AGAAAAACAA CGATCTAGTA	360
AGTTAGATTT AATTCTCGT AAAGAATTAA TGGATCTGCT AGGTATAAGT GCTACAACCC	420
TTGATAACTG GGAGGATCTT GGTCTTAAAC GATATCAGAC TCCGATGGAT GGAGCTAAGA	480
AAGTATTCTA TCGTCCGTCA GATGTGTATT TATTTTTCAGC AATAAAATAG GAGTTATGAA	540
ATGAAAATTG TTAATTTCAA ACCAACTAAA CAAATAGACG ATGGGTTTTC ACTGCCAGGT	600
ATTGACATTC TATTTGTCTC AG	622

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1929 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CGCTAACTTG CAAACAAAAG AAGAACGCAA ACTCCACAAA TCCTTTACGC AGAACTCAA	60
TCTCATCTAC TTACCTTGCT GACTTGGTAG AGTATGTTGC AGACAAAGAC TTCTCAGTAA	120
ACGTAATTTC TAAATCAGGT ACAACAACTG AACCAGCGAT TGCTTTCCGT GTCTTTAAAG	180
AACTCTTGGT TAAGAAATAC GGTCAAGAAG AAGCTAACAA ACGTATCTAT GCAACAACTG	240
ACCGCCAAAA GGGTGCTGTT AAGGTTGAAG CAGACGCTAA CGGTTGGGGA ACATTGTTG	300
TTCCAGATGA TATCGGTGGA CGCTTCTCAG TATTGACAGC CGTTGGTTTG CTTTCAATCG	360
CAGCATCAGG AGCTGACATA AAAGCTCTTA TGGAAGGTGC GAATGCAGCT CGCAAAGACT	420
ACACTTCAGA CAAAATCTCT GAAAACGAAG CTTACCAATA CGCAGCTGTT CGTAACATCC	480
TTTATCGTAA AGGCTATGCA ACTGAGATCT TGGTAACTA TGAGCCATCA CTTCAATACT	540
TCTCAGATG GTGGAACAA TTGGCTGGTG AATCAGAAGG AAAAGACCAA AAAGGTATCT	600
ACCCAACCTC AGCCAACCTC TCAACTGACT TGCACACT TGGTCAATTT ATCCAAGAAG	660
GAACCTCGTAT CATGTTTGAA ACAGTTGTCC GTGTTGACAA ACCTCGTAAA AACGTGCTTA	720
TTCTACTTTT GGAAGAAGAC CTTGACGGAC TTGGTTACCT TCAAGGAAAA GACGTTGACT	780
TTGTAAACAA AAAAGCAACT GACGGTGTTT TTCTTGCCCA CACAGATGGT GATGTACCAA	840

1333

ACATGTATGT GACTCTTCCA GAGCAAGACG CTTTCACTCT TGGTTACACT ATCTACTTCT	900
TCGAATTGGC AATTGCCCTT TCAGGTACT TGAATGCTAT CAACCCATTT GACCAACCAG	960
GTGTTGAAGC TTATAAACGT AACATGTTTG CCCTTCTTGG AAAACCAGGA TTTGAAGAAT	1020
TGAGCAAAGA ACTTAACGCA CGTCTATAAT AGAAGAAAAG AGTGGTTTGC CCACTCTTTT	1080
TACTCTCTTT ATCCATAGAA ATTGGACTCA GCCAAGACTT GTGATATAAT ATAGAAAGCA	1140
AAAAGGCAGA CGCCTAGATA ATAGGAGAAA CTATGTCAA AGATATCCGC GTACGTTACG	1200
CACCAAGTCC AACAGGACTA CTACACATCG GAAATGCTCG TACAGCATTG TTTAATTACT	1260
TGTATGCGCG CCATCATGGT GGAACATTTT TCATCCGTAT CGAAGATACT GACCGTAAAC	1320
GCCATGTCGA GGATGGTGAA CGTTCACAAC TTGAAAACCT TCGCTGGTTA GGCATGGATT	1380
GGGATGAAAG TCCAGAATCA CATGAGAATT ATCGCCAGTC TGAGCGTTTG GACTTGTATC	1440
AAAAATATAT TGACCAACTA TTAGCTGAAG GAAAAGCCTA TAAATCTTAC GTTACAGAAG	1500
AAGAGTTGGC AGCTGAACGC GAACGCCAAG AAGTAGCTGG CGAAACACCA CGCTACATCA	1560
ATGAATACCT TGGTATGAGT GAAGAAGAAA AAGCAGCTTA CATCGCAGAA CGTGAAGCAG	1620
CAGGGATCAT CCCAACTGTT CGTTTGGCTG TCAATGAGTC AGGTATCTAC AAGTGGCATG	1680
ATATGGTCAA AGGCGATATC GAATTTGAAG GTGGCAATAT CGGTGGTGAC TGGGTTATCC	1740
AAAAGAAAGA CGGTACCCA ACTTACAACT TTGCCGTTGT TATCGATGAC CACGATATGC	1800
AAATCTCTCA TGTATCCGT GGAGATGACC ATATTGCTAA TACACCAAAA CAGCTTATGG	1860
TCTATGAAGC TCTTGGTTGG GAAGCTCCAG AGTTCGGTCA CATGACCTTG ATTATCCACT	1920
CTGAAACTG	1929

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AAATTTAAGA AAAAGGAGAC ACATCATGTC TAAAAAGTA TTATTTATCG TCGGATCACT	60
ACGTCAAGGT TCTTCAACC ACCAAATGGC GTCGAAGCT GAGAAAGCAC TTGCTGGTAA	120
AGCGGAAGTT AGCTACCTTG ATTATTCAGC CTTCTCTCTC TTCAGCCAAG ATTTGGAAGT	180
TCCAACACAT CCAGCTGTAG CTGCTGCTCG TGAAGCAGTT CTCGTTGCGG ATGCTATCTG	240

1334

GATTTTCTCT	CCAGTCTACA	ACTTCTCTAT	CCCTGGTACA	GTGAAAAACT	TGCTTGACTG	300
GCTATCTCGT	CCCCTTGACT	TGTCTGATAC	ACGTGGCGTT	TCTGCCCTTC	AAGACAAGTT	360
TGTCACAGTA	TCATCTGTAG	CCAATGCAGG	GCACGATCAA	CTTTTCGCTA	TCTACAAAGA	420
CCTCTTGCCA	TTTATCCGTA	CACAAGGCGT	TGGTGATTTC	ACTGCTGCAC	GTGTTAATGA	480
CTCTGCCTGG	GCASACGGAA	AATTGGTTCT	TGAAGAAACA	GTCCCTAACT	CACTTGAAAA	540
ACAAGCTCAA	GACTTGGTCG	AAGCTATCAA	GTAACATAACA	CTCAATAAAA	ATCAAAAAGC	600
AAACTAkGAA	GCTArCCGCA	AGCTACTCaA	gCACTGCTTT	GAGGTGTAG	ATAGAACTGA	660
CGAGTGThnA	ACATATATAC	GGTAAGCGCA	CACTGACGTG	GCTTGAAa		708

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CTTCTTTTCT	TGGAAATAGG	TGTATAATAC	GTTTATTAAA	TTTTTGAGGA	GTTGTCTATG	60
AAGAAAAGTT	TTATCCATCA	ACAAGAAGAA	ATTCCTTTG	TCAAAAACAC	TTTACCCAG	120
TATTTGAAAG	ATAAGCTAGA	AGTTGTCGAA	GTCAAGGTC	CTATCTTGAG	TAAGGTCGGT	180
GACGGAATGC	AGGACAACCT	GTCTGGTGTG	GAAATCCAG	TATCGGTCAA	GGTCTCCAA	240
ATCCCTGATG	CTACTTATGA	AGTGGTGCAC	TCACTTGCTA	AATGGAAACG	CCACACCTTG	300
GCTCGTTTGT	GCTTTGGTGA	AGGAGAGGGT	CTCTTTGTCC	ACATGAAAGC	CCTTCGTCCA	360
GATGAGGATT	CCTTGGATGC	AACCCACTCT	GTTTATGTTG	ACCACTGGGA	CTGGGAGAAG	420
GTTATCCCAA	ATGTAAGCG	TAACATCGTT	TATCTAAAAG	AAACAGTTGA	GAAGATTAT	480
AAGGCTATTC	GCCTGACTGA	GCTAGCTGTT	GAAGCCCGCT	ATGACATCGA	GTCTATCTTG	540
CCAAAACAAA	TTACCTTTAT	CCATACAGAA	GAATTGGTAG	AACGCTACCC	AGACTTGACA	600
CCGAAAGAAC	GTGAAAATGC	GATTTGTAAA	GAATTTGGAG	CCGTCTTTTT	GATTGGTATC	660
GGTGGCGAGT	TGCCAGATGG	TAAACCGCAC	GATGGACGTG	CACCAGACTA	TGATGACTGG	720
ACAAGCGAGT	CTGAGAATGG	CTACAAGGGT	CTAAATGGTG	ATATTCTTGT	CTGGAATGAG	780
T						781

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:

1335

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```
CCCGCATCTT GTAGGGTTTT AACGGGCACG ATTTTCATAT CCGTCTTGAT TGTTTTAGCC      60
GCTTCTAGGG CTGTTTGGA GTTGTTTTTC GCGCCGGAT GCGCCTTTTG TTCTTCTTCG      120
CTAACAGGGT TATCAGGAGC AAAGAAAATA GCAGCACCTG CCCTAGCCGA AGCTACAACC      180
TTCTTATCAA TACCTCCAAT GTCTCCCACA TTACCATCGC GGTCAATGGT ACCTGTACCG      240
GCAACAATAC GACCATTACG AAGATCTGGG TGAGCTATTT GAGTATAGAT AGCTAGACTA      300
AACATGAGAC CAGCACTTGG ACCGCCAATA CCAGCTGTTG AAAAGCTAAT TGGGACATTG      360
CTGATTACCT CTGTACGGTC AATCAAGCCG ATTCCAATTC CATTTTGGCC ATTTTCCAAG      420
GTGATGATTT TTCCTTCTGC AGACTTGGTT TGCCCATCCT CTTCATAGGT GACCTTGACG      480
GAATCCCCTA ATTTTGTAGA ACTGACGTAA TCAATCAAGT CTTTGGAAC TCAAAAGGTC      540
TGATCATTGA CTGCTGTGAC TGTATCAGAG ATATTGAGAA TCCCTTTAAA GGTGAATTA      600
TCCGTACAT TCAAAACATA AACTCCAAAG TACTTGAGTT CGATATCCTT ACCAGCTGTT      660
TTTAGTCCTT GATACTTGGC CATATTTTGC GATGTTTGCA TGTAAGATTG ATGATTCGC      720
ATAAATTCAA CATCGGAAGA ACCACCTGTA GTCTCCTGAG CACTACGAAT ATCTGTAAAA      780
GGTGTCAACC AAGCATAAAT CATATGAGCT AAAGTGGCAT GTTGAACACC AACCGTAACG      840
AATTGT
```

(2) INFORMATION FOR SEQ ID NO: 307:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 829 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```
GCGATCTGCT TGGGCTTTTC CTATTACCTT ATCTAATAAA TAGGTACGCA GACTCATAAC      60
CATATAAAGT CCACCCCCCA TGGCACCGAC AAGAGCTACA TAAAAGAAGC TCCACAAACG      120
TCCACTTGGT TGGAAGAAAA ATCCTAACAG CCACTGGATG GTTCCTATTA ACAGAAACAT      180
GACTAGGGTC AGCAAACCTGA TTAATATGGT TCGCTTCAAA ATCACCTTGC GCTTGACACC      240
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1336

AGTTACTTTA CAAATATCCC GATACATCAA GACGTTAGGA ATGATGAGAG CAATGGTTGT	300
TGAAATCAAA GGACCATAAC TGTGGAAGAG GGCATGGTA GGTAGTTGCA AGACTAGCTT	360
GGCAATAGAA CCATAGATAA AATAGAGAAC GGCCTTGCGG TTGCGGAACA TGGCCTGAAG	420
CATTGGAGAC AAGACCATGT ACAAGCCTAA AATAATAGAC TGCAAACTG CAAAGACAAA	480
TAAGCCCAGA GCCAACTAT CTGGCTTACC ATAGAAGACC GTATAAAGAG GTTCTCCTAC	540
CATAACCACT CCAACCGTTG CTGGTAGCAA GAACATAAAG AGTAGGGTGA GACTGTCCTG	600
AACGAGACGA GAAGCTGCTT TCAAGTCCCC CTTGACATAG TTTCCGTCA AAAGTGGCAA	660
ACCAACACTC CCAATCGAAA CCCCTACAGA AATCAAAATC ATCGTGATTT TATTAGGATT	720
GGCTGAGAAA TAAGAAAACA TGACAACCAA GTCCTCATTT CTGTAGTTGG TAAACCAGCT	780
CATACTATTG ATAAAGGTCA GCTGAGTCCA AATCTGGAAG AGCTGGATG	829

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CGAACATCTT GCTGGCTGAT TCGTCTGCCG CCATCGCAGC CCCGAACACA TTGCGACCCA	60
TGGCAAGCGG GCTCAATCCG CACATGGGAT CCGTGCCAAA GCGCCGCGTG TGCATCATTT	120
GCTCATCTAG TAACGTATGA GGTTCGCTT CGTGTCGAT AAACCGATAT TCAATCGCAC	180
CACTGCTCGT TCTCCGCGGA GGGGAAACCG ACTGCGGTAG GATGAACTCC AGAGAAGAGA	240
GATCACGACC TACCAGGTGC GGCTCGTTGA AGCTGTTGCC GCTTAGCAGC AGGCTCGCCA	300
CCACGCATTC CCAGAACTCA ACGGGGGTTT GATCGGCGTT CGGTTGCTGA CTAATAACTC	360
GGTGACGGG ATGCGAAGTG GCCACTTCTG GCACACCGTT CTTGTCTTCG TAGAGAGCAA	420
TTGGGAGGGT GGCCAGCGTT TCGGCGATGA GCGCACGCA GGCC	464

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

1337

CCGTCCTATAA TGGAATAGA TTTTATTGG AGGTTTTTAT GTCATTCTA TCAAAAAATG	60
GAGCAGGTAT CTTGGCCTGC CTTCTCATTT CCATCCTATC TTGGTACTTA GGAGGATTCT	120
TCCCTGTGGT TGGCGCGCCC GTTTTGGCCA TTTTCATAGG CATGCTCCTA CATCCCTTTC	180
TCTCGTCCTA TAAACAACTG GATGCTGGTT TGACCTTTAG TTCCAAGAAG TTGCTCCAAT	240
ATGCCGTGTG CTTGCTTGGT TTTGGTCTCA ATATCTCGCA GGTCTTCGCA GTTGGCCAAT	300
CTTCACTCCC TGTCATCCTG TCCACTATCT CAATAGCTCT GATTATTGCC TACCTCTTCC	360
AGCGTTTCTT TGCCCTGGAT ACAAACCTGG CTACCTTGGT TGGAGTAGGT TCTTCTATCT	420
GTGGGGGTTT TGCCATTGCA GCGACAGGCC CGTTATTGAT GCTAAGGAAA AGGAAGTAGC	480
CCAAGCCATT TCCGTTATCT TTTTCTTCAA TGTCTTGGCT GCGCTCATCT TTCCAACCCT	540
CGGCACCTGG CTTTCATCTAT CCAATGAAGG CTTGCGCCCTC TTTGCAGGGA CTGCGGTCAA	600
CGACACTTCC TCTGTAACGG CTGCCGCCAG CGCTTGGGAC AGTCTTTACC AAAGCAATAC	660
CCTCGAGTCT GCAACCATTG TTAACTCAC ACGTACTTTG GCCATTATCC CTATCACGCT	720
CTTCTATACC TACTGGCAAA GTCGCCAACA AGAAAACAAG CAAAGCCTGC AACTGAAAAA	780
AGTCTTCCCA CTTTATATCC TTTACTTTAT CCTTGCCTCT CTCCTCACTA CACTACTCAC	840
CTCTCTAGGT GTGTCCAGTA GTTCTTTTAC TCCTCTCAA GAACTCTCTA AATTCCTTAT	900
TGTCATGGAC ATGAGTGCTA TCGGTCTCAA AACCAATCTG GTCGCTATGG TCAAATCCAG	960
TGGAATATCC ATTCATCATG GA	982

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CTAGCTGCCA ATATGATTGG GGTGCAGAAG CGCGTGATTA TCTTTAATCT TGGCTTGGTT	60
CCTGTGGTCA TGTTTAACCC AGTGCTTCTG TCCTTTGAAG GATCCTATGA GGCAGAAGAA	120
GGCTGTTTGT CCTTGGTAGG TGTGAGATCA ACTAAGCGTT ATGAAACCAT AAGGCTTGCC	180
TATCGTGACA GCAAGTGGCA GGAACAGACC ATTACCTTGA CAGGCTTCCC AGCTCAGATT	240
TGCCAGCATG AGCTGGATCA CTTGGAAGGA CGAATCATTT AGGAGGAAAG CAAATGAAAC	300
GAATAGTCTT TGAACCTATT TTTATCGCAA CGACCTGGTA TATCTTTTTC CCGCCCCTTA	360

1338

ACCTGACCAG CTGGGAATTT CTCTTCTTCC TCTGTGGGCA TTTGTTAGTT GTGGCAATAT	420
TATTTGGCTT TGGCAAGGGG ATAAACCTTG TCAAAACGGT TCATGTGCGC CACGGTAAGG	480
CGGAAGCTGC CTTAAATCTT GAGGGTTTCA AAATCAATCG GTTAGGGAAA ATTCTGTTAG	540
CTTCGATTGG AGGAATTCCT CTCTTGGCAG CTTTGGTTTc CTTGGTAACT TCCAGCATGT	600
TTCAGGCTAA AAATTATGCC AATGTAGTCA CGGTTACGGA AAAAGACTTT ACTGAATTTT	660
CTAAGAGTGA CACCAGTAAG GTTCCTATCC TAGATAGAAG TACTGCTGAA AAAATTGGAG	720
ACCGCTACTT GGGTTCCTA ACCGATAAGG TGTGCAATA CGTAGCGGCA GATACCTATA	780
CCCAATTGAC AATTGATGGG AAACCTTATC GGGTCACACC ACTAGAATAT GCAGACCCTA	840
TCAAAATGGT TAACAATCAA GCCAAGGGAA TCGGTGAGTA TATTAAGGTG GACATGGTAA	900
CTGGAAATGC GGATTTGGTG GACTTGAAGA CACCAATCAA GTATTCAGAC TCGGAGTATT	960
TTAACCGTGA TGTCAAACGT CACCTGCGCT TGAAGTACCC GACCAAAATC TTTAAAACTC	1020
CATCTTTTGA GGTGGACGAT GAGGGCAATC CTTTCTATGT AGCAACGGTT TACCAAAAGC	1080
AATTGGACT TGCTGTTCCT CGTCCTGCTT CAGTCATTAT CTTGGATGCT ACAAATGGAG	1140
AAACCAAGGA ATACAGCTTA TCAGATGTTT CAGAATGGGT GGACAGGATC TATCCAGCAG	1200
AGGAAACCAT TGAGCAAATC AACTACAACG GCAAGTACAA GGACGGTTTC TTGAATGCCA	1260
TGATTTCCAA GAAAAACGTG ACCCAGACTA CCAATGGCTA TAATTACTTG TCTATCGGTA	1320
ATGACATCTA TCTCTACACA GGTGTGACGT CGGCTAATGC GGATGAGAGT AATCTTGGTT	1380
TCATCCTTGA AAATATGCGA ACAGGAGAAA TCACTAAGTA TAGCTTGGCT TCTGCGACAG	1440
AAGAATCAGC CCGTGAATCA GCAGAAGGTG CTGTTTCAAG GAAATCCTAC AAAGCAACCT	1500
TCCCAATCCT CATCAACCTC AATGACAAGC CTCTCTACAT CATGGGCTTG AAGGACAATG	1560
CTGGCTTGGT CAAAGAGTAC GCCCTGGTAG ACGCAGTCGA GTACCAAAAT GTTATCGTTG	1620
CTACTACAGT GGAAGAGATG CTCAGCAAGT ATGCCAATAA AAACGACCTT GAAATGACA	1680
ATGCAACGAC AGAAAGCATC AATGGAGTAG TAGCAGACCT CAAATCAGCT GTTATCAAGG	1740
GAGACACTGT CTACTTCTTT AAAGTTGATG GCAACATCTA CAAGGTCAAG GCTTCAGTAT	1800
CCGATGACCT TCCTTACCTT GAAAATGGTA AAACCTTCGA AGGTCAAGTA GGAAAAGACA	1860
ATTATCTCAA GACCTTTAAG CTACGGTAAA AATAGGTTTT TTTCAGAAAG TATATGTTAT	1920
AATAAGGTAA ATTAAGCCG	1939

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid

1339

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CCTGCTAATA GAGAGAAAGA CTAGGACTAG AAGTAAGCCA ATTAAATAAT GAGAAAGTTT	60
CATACCCCGT CCTTTCATGT AGATTGGTA TCGAAAGATA TCTGCGGATA TAAATGTAAC	120
ATTATTTTTC TAATCTGTCA ATAAAATTTC TGACAAATTA ATAAATACAA CAAGGAGAGA	180
GCAACAAGAC TTTCTCCTTT GTTATCCTAT TCTAAAATGT TTTTACCTTA ATCTGATAAA	240
ATAATATCTT CGAGGGAGTA GCTAGCCGTC CAATCAAGAT ATTGTTTAGC TTTTGAAGCA	300
TCTGCTAGGA CACTGGCTGG GTCAC TAGCA CGTCGAGCAA CAATCTCGTG TGGGATTTT	360
TAATTTAGTA ATTCTTCAGC AGTTTAAAG ATTTCTTTGA TAGTATAGCC TTTT TAGTT	420
CCTAAGTTAA AGATTGAGA AGAACTGTCT TCTGAAATA GGTAGTTCAT TCCTTTAACA	480
TGAGCCTATG CAAGGTCCAA GACATAAATG TAATCTCGAA TACATGAACC GTCACGTGTA	540
TCGTAGTCAT CTCCAAATAT TTTTAAGCTA TCATTTTGTC CCAATGCGGT CTGTGTTGATA	600
TTTGGAATGA TGTGAGTTGG ATTTTTCACA CGCAGACCGT TTGAAGCATC CATTTCAGCC	660
CCAGCAACAT TAAAGTAACG GAAAATAACA TATTTCCAGT CGTAGCGATT GGCCATCCAG	720
TAAATCATTC GTTCGCCCAT CAGTTTGTG TCTGCATAAG GGTGACAGG GTCGAGCAGG	780
GTATCTTCAG TCACCGGCTT GTCAATACAG TTATTTCCAT AGAGAGAAGC AGTCGAAGAG	840
AACATGATTT TTTGAATGCC AACTTCAGAT AAGACTTTGA GAACTGGTT CATACCAGCA	900
ACGTGG	907

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CCACATAAAG GTAAATATCT TTTGTACTAT CTTGGGCATC CAAGAAAAGC AATTGGGCAA	60
TAACAGAGTT AGCCATATTG TCTTCAACCG GACCTGTCAG CATAATGATG CGGTCTTTGA	120
GAAGACGTGA GTAAATATCG TAAGAACGTT CTCCACGGCT TGTTTGTTCA ATAACTACAG	180
GAATCATTC TTTCTCCTTT TGAGTTTAA TTTTGTGGT CAAATGACTG AAGATAAGAC	240

1340

TATTATAATA TCTTGGTCAA AAAAGGTCAA ATTTTGTGCTC TGCTTTCATT AGACAGAAAC	300
AAAAACCCAA CCTCCTTTCG TGA CTGGAAA TACTTTTCCA AGTCATTCTT CTTTTCGATC	360
TTATTTTGTA CCGAACAAGC GGTCTCCAGC ATCTCCAAGA CCTGGAACGA TATAACCGTG	420
TTCGTTCAAA CGTTCATCCA AGGCTGCTGT AAAGATTTCT ACATCTGGAT GAGCTTCTTG	480
AAGGGCTTTT ACACCCTCTG GAGCAGATAC AAGGCAGACA AATTTGATAT TTGATGCGCC	540
ACGTTTTTTA AGAGAATCAA CAGCCAAGAT TGCTGAGCCA CCTGTTGCCA ACATGGGTC	600
TACTACAAA ATTTGACGTT GGTCAATGTC CTCAGGCAAT TTCACCAAGT ATTCAACTGG	660
TTGAAGTGT TCTTCATCAC GGTACATACC GATGTGGCCA ACTTTAGCAG CTGGAACCAA	720
GTTCAGAGA CCATCAACCA TCCCAGATACC TGCACGCAAG ATTGGGACGA TGGCCAATTT	780
CTTACCTGCC AATTGTTTTT GAACTGTTTT TGTAATTGGT GTTTCGATTT CCACATCTTC	840
TAGTGGAAGA TCACGAAGTA CTTCATACCC CATCAACATT GCAATCTCAT CTACTAGCTC	900
ACGAAAAGCT TTTGTAGAAG TATCTGTACG ACGCAAGATT GACAATTTGT GTTGAATCAG	960
TGGGTGATTA ATAACCTCAA TTTTCCCAT TTTTGGAAAT CCTTCTTTCA ATTTATTCTT	1020
CTTATTATAC CAAAAACGG TTTAAAAATC TTTCTAAACC ATTTATTTTT GATAATTTTT	1080
ACATTAGATC AGCCTCTTTA AGAGCTGTCT GTACTGTCTC AAGTGGTAAA TGGGTCAATT	1140
CTGTCCCTTT TTCTTGATAA AGGTATTGGG CGTAGTCGTC CATTCGGTAC TGTTTGATAT	1200
AAACCACGCG CTTGCAGCCG ACCTGAAGCA ATTGTTTTGT ACAGTTGAGA CAAGGAAAAT	1260
GGGTACATA GGCTGTAAAG CCTTTGGGAA CACCACGCTC AGCACCTTGA AGGATAGCAT	1320
TGACCTCAGC GTGAAGGGTG CGAACGCAGT GGCCTTCAAT GACCAAACAT TCGTGATCAA	1380
TACAATGCTC AGTCCCTGAC ACCGAACCAT TGTAACCAGT GGAAATAACC TTATTATCTT	1440
TTACCAGAAT CGCGCCCACT TTAGCACGTT TACAAGTGA ACGATTGCGA ATTAGTAGAG	1500
CTTGGGCTGC AAAATACTCA TCCCAGGCCA GTCTTTTTTC AGTCATCTCT TTTCTCCTTT	1560
TTCTCTATTT TTTAAAAAT GGTAAACCTA AATCTGCAAT CTTTTCAGCT GGTACCTTCA	1620
TGCCATCCTT GATCCATTTT AGAAGGACAG AGACGATGGC TGAGCTCCAG AAGGAATGAA	1680
GATAAGAGCT GACACCTTTT GATTTCCCAT GGTATTTTTC TAGAAATTCC TGATGGCTT	1740
GGACAAAGAT TTTTCCAGA TGGTAATCCA AGGCCAATTG AATTACTCTA GCTTCCTTTC	1800
TGGCCTCCCG GAAAAGGTGA ACCCAAACCA AATAAAGGTC TGTCTTTAAA TCGTAATGAT	1860
GCAGCTGTT CATAATATTG TGGACAGTTC GTTTAAAGAC GCTCTCTAAA ATTTCTCTT	1920
TGGAGTCATA ATTGCGATAA AAGGCCGCAC GCGAAACACC TGCACGTTG ACCAATTCAG	1980
AAATACTAAT CTTGGTCAGT TCCTTTTTTT CCAAGAGTTG CAAGAGGGCT GTTCAATGG	2040

1341

CTTCTCTGGT TAATAAATTG GATTCTTGGT TTGATTTTCT GAGATTTTCA AGAGACTTTT 2100
 CAGAGATTCT ACGTTCAGAC ATAACATTTT CTTTCTACTT GTCACAACAG ACGGATGATG 2160
 CTTTTGTTC 2170

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATCTGCACGA ATCAGGGCTT TCTAAGTGAC TATTTCCACC GAAATATTAT TTATATCAGG 60
 AGGACATTCA TATGTCACGT TATACAGGAC CATCTTGGA ACAAGCTCGT CGTCTTGGCC 120
 TTTCATTAC AGGTACAGGT AAAGAATTGG CACGTCGTAA CTACGTACCA GGACAACACG 180
 GACCAAAACA CCGTTCTAAA TTGTCAGAAT ACGGTTTGCA ATTGGCTGAA AAACAAAAC 240
 TTCGTTTCAC TTACGGTGTA GGTGAAAAAC AATTCGTAA CTGTTCGTA CAAGTACAA 300
 AAATCAAAGG CGGAATCCTA GGTTCAACT TTATGCTTCT TTTGGAACGT CGTTTGATA 360
 ACGTTGTTA CCGTCTTGGT CTCGCGACTA CTCGTCGTCA AGCTCGTCAA TTCGTAAACC 420
 ACGGTCACAT CCTTGTGAC GGGAAACGCG TTGATATCCC ATCATrCCGC GTAACCCAG 480
 GTCAAGTGAT CTCAGTTCGT GAAATCAT TGAAAGTCC AGCAATCCTT GAAGCAGTA 539

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 667 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCGGTTTTGC TCCTTCTCTA CGGCTACGAC GTGATGTATC TCTGATGATA TCCACTGTTT 60
 CTGTAGCAGG CGTAGGTGTT TCTGGACCTG CTTGTTCTGC TTTTCTCTT GCCGTCGTAT 120
 AGGAAACAGC TACCCTTGTT GGGGTTTCAT TGTATTCTCT TTCAAGTTT TTAGGTCTAA 180
 CAGGACCTGG ACCTGGTCTT GATCCACTTT CTTCCGCTGG AGAAGAAGGT ACATCTTGAC 240
 TTGGATGACT TGGAACACCA GGAGTTTCTC TTTGAATCTC ATCTGCTGGA GAAGCTGGTA 300

1342

CACCTTGACT TGGGTGAGTA GGCACGGTAG GAGCTTTTCT CATAATCTCC TCTACCGTTG	360
ACAAGGAATC AGCCATGAGT TCTTCAGTTG AAGGTTTCATT TGCAGGAGTG CGAACTACTG	420
CCTCATCTTC TTTCAGAACT TCATCATAGC CTTTTACTTT TTCTAAATCT CTCAGAACTCT	480
GCTCTTTAAA GCGTAATTC TCTTCTGCTC TTGACTTTTC ACTCAAAAGT TTTTCCTCCT	540
TGTTGAGAAT CCATAATATT AGAGCTGAGA AGTCCAAAAA AAGCAATCTA TGATACTTTT	600
CCTAACGGAT TTTGTCATTT CCCAGACCAT ATCATACCAT GTTCCCCCTG CAAAGGTTGA	660
CTGGGAA	667

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GGGAAGCCAA GGTATTTTAT CGGATGAAGT TGTTACTAGT TCTTCACCGA TGGCTACAAA	60
AGAGTCTTCT AATGCAATTA CTAATGATT AGATAATTCA CCAACTGTTA ATCAGAATCG	120
TTCTGCTGAA ATGATTGCCT CTAATTCAAC CACTAATGGT TTAGATAATT CGTTAAGTGT	180
TAATAGTATC AGCTCTAATG GTACTATTCTG TTCCAATTCA CAATTAGACA ACAGAACAGT	240
TGAATCTACA GTAACATCTA CTAATGAAAA TAAGAGTTAT AAGGAAGATG TTATAAGTGA	300
CAGAATTATC AAAAAAGAAT TTGAAGATAC TGCTTTAAGT GTAAAAGATT ATGGTGCGGT	360
AGGTGATGGG ATTCATGATG ATCGACAAGC AATTCAAGAT GCAATAGATG CTGCAGCTCA	420
AGGGCTAGGT GGAGGAAATG TATATTTTCC TGAAGGAACT TATTTAGTAA AAGAAATTGT	480
TTTTTTAAAA AGTCATACAC ACTTAGAATT GAATGAGAAA GCTACAATTC TAAATGGTAT	540
AAATATTAAG AATCACCCTT CCATTGTTTT TATGACAGGT TTATTTACGG ATGATGGTGC	600
GCAAGTAGAA TGGGGCCCAA CAGAAGATAT TAGTTATTCT GGTGGTACGA TTGATATGAA	660
CGGTGCTTTG AATGAAGAAG GAACTAAAGC AAAAAATCTA CCACTTATAA ATTCTTCAGG	720
TGCATTTGCT ATTGGGAATT CAAATAACGT AACTATAAAA AATGTAACAT TCAAGGATAG	780
TTATCAAGGG CATGCTATTC AAATTGCAGG TTCGAAAAAT GTATTAGTTG ATAATTCTCG	840
TTTTCTTGGG CAAGCCTTAC CCAAACGAT GAAGGATGGG CAAATCATAA GTAAGGAGAG	900
CATTCAGATT GAACCATTAA CTAGAAAAGG TTTTCCTTAT GCCTTGAATG ATGATGGGAA	960
AAAATCTGAA AATGTGACTA TTCAAAATTC CTATTTTGGC AAAAGTGATA AATCTGGGGA	1020

1343

ATTAGTAACA GCAATGGCA CACACTATCA AACATTGTCG ACACAGAACC CCTCTAATAT	1080
TAAAAATCAA AATAATCATT TTGATAACAT GATGTATGCA GGTGTACGTT TTACAGGATT	1140
CACTGATGTA TTAATCAAAG GAAATCGCTT TGATAAGAAA GTTAAAGGAG AGAGTGTACA	1200
TTATCGAGAA AGCGGAGCAG CTTTAGTAAA TGCTTATAGC TATAAAAACA CTAAAGACCT	1260
ATTAGATTTA AATAACAGG TGGTTATCGC CGAAAATATA TTAAATATTG CCGATCCTAA	1320
AACAAAAGCG ATACGAGTTG CAAAAGATAG TGCAGAAaTwT TTAGGAAAAG TATCAGATAT	1380
TACTGTAACA AAAAATGTAA TTAATAATAA TTCTAAGGAA ACAGAACAAC CAAATATTGA	1440
ATTATTACGA GTTAGTGATA ATTTAGTAGT CTCAGAGAAT AGT	1483

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CCTGAACGCT TTTTATATAA TATCATAAAG CCAATCTGAT TTATCAAGTG TGTCTAAGCG	60
ACGCGAATTA AAATTCATTG CATACTCCAT CGCTTCTAAA AAATCATT TTGAAAAGAC	120
GTAAATCA TCTAAATCT GACTCCAATA TAATAACAAA ACCAATCCCA TAATATCCTC	180
TGGTTGATTA TTCAATAAAT TTAAGTTGGT TTCATAAAAC CCTGGAGTTC CAAATAGAGG	240
CAACTTTTT TCTCAATTT GAGTTTCTT CCTTAGGGCA TGCTCAAAGT CTATAATATA	300
AATATTATTT CTATTATCAA TAAGTATATT ATTAAATGAT AAATCTCTAT AGGAAAGATT	360
ATATTTGGAG TTTATTATCT CCATATAATC AATTAATGTT AAAAACCAAT CATACGAGCC	420
ACTAACCATA TTATACTCGC TTAATTTATC TGCAATAATA AACTCAAATT CCACAAAATA	480
CGAATCTTT ATGTAAAAAT CGTTAAAAAC TTTTGGAGTA AATTCCTCCT TTTCCAATTC	540
TACTAATAT TCTCTTCAT TTATTAAACG ATTCACAGAA TCTCTATTG TAAAATCAAC	600
CAACGATAAA TCACTAGCTT CTTTAAATAA AGAATAAACT CGCTTTTGAG TATTAAATAC	660
TTTATAAACT CCACCTTTGG CATTTTGA AATCACTTCC AAAATAATAT ATTGATCAGG	720
AATAGTGTTA TATCTTGGA TATAGTAATC CCTTATTGGA ACATTCACAT TTGAAGGGAT	780
TTTCTTATCT CTTTATCCT TGAAAGTGCT ATCTTTTACG AACTCCCAT ATCTGTAATA	840
TACAACCTCG CTAAGTTGAA ATCTGAAATC TGATGGTATG TTTACACCCT TTACACCTTT	900

1344

ATACAATATT TCTAATTTGT GTAACAAACG TTGAAACTCT TTATTATCTT TTGGATAAAT	960
TGTAATGAAT TTCCCGACTT GTGAATAACC ATTAAGCCCT GTATTTTGCA AAGAAAGTTC	1020
TTTAATGCTA ACCAAAATTT TGAAATTTAT CTCTCTCTCT CTAGAAAATA TAAATCAAA	1080
GAATTTTTTA GCAACCAAAT TAGCATTAA TATTGAAGCG CTCAGGTGTA TTTTAAATCC	1140
CTTAGATTGG GTGATATTAG ACGGCAAAT ATATAACCAA TGTTCATCAC TAAATTTATC	1200
ACTAATTTTA TATTCTAATA ATAAATTATG GTATGCGTCT TCTATTTTCTAG TTTTCATAGTC	1260
CAAATAGTTT AAATACTTTT CGTAATTCAT ATTAAGAAAT CTCTCCATA AATTTTTAGA	1320
CCATCATTTA AAGCCAAACA ATTTAAAGCG TGATAATAAA TGTTGATAAT CAATGTAAC	1380
TTCACTCCTC TATTTTGTA TCCCTTCACC AATAATTTTA TGCTATATCT ATTTTCTCGA	1440
GGCAATTTAT AGGACTTCAA GATAAAACCA TAAAAGAGAT AAGTATTATA ATCTGACAAT	1500
CCAGTTTCAG AATAATTTTT TAGAAAAATA TCTAGTGATT CTGATAATTC ATCCGGAATA	1560
ATTCTTTTAA CATCGTATTT ATTTTTCATA TCGGCCACTC TTCCTTAAAA AGCTCACAA	1620
AAAATTTTAA ATTTCTATAC AACATCCGA GAGTAGTCTC ACAATTTGAA CATTTACAT	1680
CACCTCTAAT ATATAAAAA TGAATTAATC AGAAACCTCT GACTAAGATT TCCTAATTAA	1740
TTCACTTTCT ATATCATAGT AAGGAATTCT ATTATCCCTA ATTGAAAATT GAAATTTTAT	1800
GTTTTATATA TTAACAATTA TCGGATTTGT AAATCTTGTC TAACAAAATG GCAAGTGCTA	1860
CTATGTGCCC CAGAAGCGA TGCAACGCTA TTTTGAATG AAAGAGCATA ATCATCCATA	1920
TCATTTAAGT CACGGATTAG CAATGCTTCC TTCTCTCTC CGACAATTCC AAATTTTCTA	1980
ATTACCTTTT CAGGATTATC AAAAAATTCT CCAACAACCT CCATATTTCC TTGAAGTTCA	2040
TTCAAGAAAG CTTTCATTG ACTACTCATT ATATAGCTCC TTTTCTATTA CTTTATTTGG	2100
AATCAAACT TACTTGACATA TTGAAACAC CTCTATTCTA CGCTTTCATA TTGCTGCATG	2160
ACACTTTCAA AATCAAATG CTAATAATAA TTTTTTAAAG CTTAATTTAG ATTTAATTAC	2220
ATATATCTCA AAAAATTGTT TTGAAATTAG TAAATTAAAA TAGGTTTCTG TACTTATAGG	2280
AACTAGTTAT AAAAATTCTG CCCATCATAA AATATCTATT TAAGTAAAC AAAAATTTTA	2340
TAATTTTTTG ATTTTAAAGT GACTATAATC TCCTATCTAT AAATACCATT CGCAGGACCT	2400
GGATCAATCC CTCTAGCCAT CTTATGAACT TGAGTTCCTC CAGACAGTCC CGG	2453

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1049 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCAATTTGAA GGCTCTAAAA CAATGGAAAA GTGCTACACA GATGTGACAG AATTTGCCAT	60
TCCAGCAGTA CTCAAAACT TTA CTTATCA CCAGTTT TAG ATGGCTTTAA CAGCGAAATT	120
ATTGCTTTTA ATCTTCTTG TTCGCCTAAT TTAGAATAAG TACAAACAAT GTTGAACAG	180
GCATTCAAAG AGAAGCACTA TGAGAATACG ATTCTCCATA GTGACCAAGG CTGGCAATAC	240
CAACACGATT CTTATCATCG GTTCCTAGAG AGTAAGGGAA TTCAAGCATC CATGTCACGC	300
AAGGGCAACA GCCCAGACAA CGGCATGATG GAATCTTCT TTGGCATT TT GAAATCGGAG	360
ATGTTTATG GTTATGAGAA GAAC TT TAGA TCTTTAGAAA ACCTTGAACA AGCTATTGTG	420
GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTAA AGCTAAAAGG ACTTAGCCCT	480
GTGCAATACA GAACTAAATC CTTCCGATAA ATTAATTGTC TAACTTTTGG GGTGCAGTAC	540
ATTTTGGTA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT	600
GGATGTA ACT TACTATATTC ACAATGTTAT CCAGTGTTT TTCTCTAATA TTAAAGGAGT	660
GTTCTGTTTC TCGAATAAAT TCTTCAAAGT TTAACCCGTC AACTTGTTCC TGAACAAGAA	720
AATAATCATC CACGATATAA AATTCATCAG TTA AATTAGT AGTATAACTT TTATCGGCTA	780
ATTTTTTAG CATGTGAGCT TCATTTTTTA TATCATCAAG AGCTGTCCAT TCTCCTCAG	840
CATCATAATT CACAAAAGGT CTTGACTGCT TGATGATTAC TTTTGGCCG TCCGATTTTC	900
TAATTGCCCG ATAAACATTT CCTTTATTG ATCTCTTAAT AATTTTTC ATTTGTATT	960
TATTTATGTC AGAGTCCTTA CTTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTTT	1020
CTTCTTCTGA AAATAAATCC ATTTCCGG	1049

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 776 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

TTAGTTGGTT AGAATCAGAA AATCGCCGAA GTGGTTATTT ATTTTGAAT AAATTTAACG	60
AACCAATTAC AGCAAGAGGA GTTGCTCAAC AGTTAAAAA TTATGCTGAT AAATACAAAA	120
TGAATCCTAA AGTAATTAC CCTCATCTT TTAGGCATTT ATTTGCTAAG AATTTTTTAG	180

1346

CGAAGTATAA TGATATTGCC TTGCTTGCAG ATTTGATGGG ACACGAAAGT ATAGAAACTA	240
CTCGAATTTA TCTAAGGAAA ACAGCTACTG AACAAACAAA TATTGTAGAT AAAATTGTTA	300
ATTGGTAAAA AATAACAGGT GGTCAAACCTG ACTACCTGCT ATTTTGTGA TTATGGCTCT	360
TATTATGGGA ATATACCTAT GAATTGGGTT GTTATAAAAA TAAAAGATAT TTTTCAATA	420
AATACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATTA ATAATAAAGG TGTAGAATT	480
ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTTCTCTGT TGGATAATGA TTACTACATT	540
GATACACAAT TCATCTCCTC TGAGCAAGTT TATTTAAAC ATAATCAGCT AATAACACCT	600
GTATCAACCT CTTTAGAACA TATTGAAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT	660
GTGTGGCTG GTGGATGTAT TTTCCAATTA ACACCATTCG AAAGTGCAGA GATGATGTCA	720
AAATGTCTAT TATGTAACCT GTCCTCTCCG TTATTTTATA AACAAATGAA AGCAAT	776

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA	60
ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTCGATC AGGATGATCT	120
GGACGAAGAG CATCAGGGGC TCGCGCCACC GAACTGTTCG CCAGGCTCAA GGCGCGCATG	180
CCCGACGGCG AGGATCTCGT CGTGACCCAT GGCATGCCT GCTTGCCGAA TATCATGGTG	240
GAAATGGCC GCTTTTCTGG ATTCATCGAC TGTGGCCGGC TGGGTGTGGC GGACCGCTAT	300
CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA ATGGGCTGAC	360
CGCTTCCTCG TGCTTTACGG TATCGCCGCT CCCGATTTCG AGCGCATCGC CTTCTATCGC	420
CTTCTTGACG AGTTCTTCTG AGCGGGACTC TGGGTTTCGA TGTCGACAGC CCGCCTAATG	480
AGCGGGCTTT TTTTTCCTGA GGCTGGACGA CCTCGCGGAG TTCTACCGGC AGTGCAAATC	540
CGTCGGCATC CAGGAAACCA GCAGCGGCTA TCCGCGCATC CATGCCCCCG AACTGCAGGA	600
GTGGGGAGGC ACGATGGCCG CTTTGGTCCC GGATCAATTC GCGCGACCGG ATCGATCC	658

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1475 base pairs
 - (B) TYPE: nucleic acid

1347

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

CCGGCTTAAT TTTTAGAAAA CGTGGGCAGG GAACCTTTGT TCTCTCTCGT GGCAGCTCAA	60
AAAGAAAATT AATCGTTCCA GAAAGAGATA TCCGGGGACT GACAAAAATA TCTGAAGATG	120
CTCATTTCTAC AATTGACTCG AGGATTATTC ACTTCAAATT AGAATTTGCA AATGAATTTT	180
TAGCAGAAAA ACTACAGGTC GCTTTGCAGA GTCCAGTTTA TAATATTTAC CGCCTGCGTA	240
TTATTGACGG TAAACCTTAT GTTCTGGAAC AAACCTATAT GAGTACCGAT GTTATTCAG	300
GTATTACTGA AGATATTTTA CAAAAATCGA TTTACAATTA CATTGAAGGA AAGTTAGGAT	360
TGCATATTGC CAGTGCTACA AAAATCTTAC GAGCTTCTTC TAGTTCAGAA AATGAGCAAC	420
ATTACTTGCA GCTCCTTCCA ACGGAACCGG TATTTGAAGT AGAACAAGTG GCTTATTTGG	480
ATAACGGAAC TCCGTTTGAG TACTCGATTA GTCGTCATCG CTATGATTTA TTTGAATTTA	540
ATTCTTTTGC ATTACGACAT TCCTCCTAGG AGAAAAATGTG AAAATGAAGC CAATCTTTTA	600
CAGACTCTAG TTTAAGAAAA ATTTAAACA GGGCAAGAAG GTCCCATCTA TGCTTAAATG	660
GTTTCTCTTT TCTAAATAAG ATGGCTTTAA AAGAGTGATC GTTGTATCCA TCATGTTGAA	720
AAATATCTTC GTATAGCTTA TAGAGTAGGT ACTGAAATTG TTCACCTGAT CTACTTCTTA	780
TAGTTATTTA GTTTTAAATA GTGTTTCAAA CATTCTTACA CTGACGAGAA GTTTTGTAGT	840
CTTTTCTTGT AACACATATA GTATACTGTG GTTAGAATAG TAGACTGTGA CTTCTAACAA	900
ATTGCTAGAA ATGAATTTCA ATCTCCCAAT TTATTTGTTC ATATCTTCTT TTAATATATT	960
AAATAAATTC TAAATCATAA TCATTTAAAA AAATTTTATT TTTTATTTTT CATTACGAAT	1020
AATATAGATG AAGGGGAAAG AGTATGAAAA CAGAACTGTT TCTTTTGCTA TTAGTTCAAA	1080
AGGAGAAAAA ATGAAAGTAG AAAATATTTT GTATAGGGTG GATCATCGTA AATTGTTTGA	1140
TAATATTTCT TTTGATACCT CGAGTTCAGA CGTGACATTA ATTACTGGTA AAAATGGTAC	1200
AGGAAAGTCA ACTTTACTAT AGTAGATTGA AACTAGAATA GTACACATCT ACTTCTAAAA	1260
TATTTGTTAGA AATCGATTTG ACTATCCTGA TCTATTTGTC CTGTTCTTAT TTCATTTTAC	1320
TATATCTCAA ATTGAGTATG ACGAAGTCCG CTCCCATGTC CTGGGAACGC ACTTCTTCA	1380
TATTTTTCAT ATTCTTGAAT CCATCGATAA AGACTATTGG GATGAATTTT TAAAGTTGAA	1440
CTAATCATTT TTACAGGATG AGATTTACAG CAGAG	1475

(2) INFORMATION FOR SEQ ID NO: 321:

1348

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTTC ATGCCCTCAT	60
ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACTAA	120
TAAGTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATAACA CCACTATGAA CTCGTTGGTC	180
TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTTGTTTTC GGTGCGGGTT	240
TGAATTTAAA AAATTTGTTA TGTAAGTACCT AATCTAAGGA ATTAGAACAA TGCCTCTAAT	300
TTTTCTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTGTAAAC AGCTCTTCTT	360
TGCTCCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTC CTAACGCTAC TTGAGTTTTT	420
TTTCTAAAT ATTCTTTTCC GTTGCCATCT TTAGAAAAAT CATAACCTTC CCTATCTACG	480
CTGTTACACA AATTAGCTAA AAAAaACTCT GGGGTTGGGA AAGGAAGATA AGAAaCGTAT	540
TTAGCCCATATA ATCTATAAAG	560

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CCGCCCCGCC ACCGCTGCCT ATCCTCGGGA GAGGGTCACC TGGAGTGAAC CTAGAACGAT	60
AGACACGGTG CGGTACGACC TCGTACTACT TTCGCCGACG GCCTCGTCCG TTGTCATCCA	120
CGAACTGATC GGACATGGGT GCGAACACTT CAGAGAAAAA ATCGTTGGAC TCGGTGTCCG	180
GCCTGAGGAA CTACGGGTGG TGGCTTTTCC GAAGAACGGC TCCGGGTTTG ATGACGAGGG	240
TACACCCTCC GAAGAGATTG TACTTGTGGA GAACGGCATT GTGAGGCACG CTGTCAGGGA	300
TCGGGCGACT GGAGGAATGG CGCCTTTTTC CGGTTTGACC AAAGTGGCAT CACATGGTGT	360
CAAACCTGGC TCAAGATGTA CGCATCTCAA GCGGAAGGG GAATCGTCAC AGGAAGGAGT	420
TACCGGAGTA CCCGCCGAAC GCACCGTTTG GATAGAGCAT TTTTCTGCAG CGAACTACCA	480
TTCAAGGTCGA GCCTTTTTCG GGTCTGGCCT TGCCTGGGTA GGCAGCCGAG AAGAACTCTT	540

1349

ATATCCCTTA ATGCCTTTCA CCATGTCAAT TGATATCTAC GAACTGGCCA GCTTATTGTG 600

GCATTTAGAC GGTCAAACGG AACGAGCAGC TAGGGTACTG TGC 643

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 780 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTTGAT GAATTGTGAA CAGTTGCCCT TGGGTCGTTT TGCAGTTGA 60

AGTCAAGAAG AGGAAAAA CAAAAGGAG AAATACTCAT GGCAGTAATT TCAATGAAAC 120

AACTTCTTGA GGCTGGTGTA CACTTTGGTC ACCAACTCG TCGCTGGAAT CCTAAGATGG 180

CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTTAT CGACTTGCAA CAACTGTAA 240

AATACGCTGA CCAAGCATAC GACTTCATGC GTGATGCAGC AGCTAACGAT GCAGTTGTAT 300

TGTTTCGTTGG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAGCA GTACGTTTCA 360

GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAACCTT TACAACTGG GGAACAATCC 420

AAAAACGTAT CGCTCGTTTG AAAGAAATTA AACGTATGGA AGAAGATGGA ACTTTCGAAG 480

TTCTTCCTAA GAAAGAAGTT GCACTTCTTA ACAAACAACG TCGCGTCTT GAAAAATTCT 540

TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTAATG ACCCACATAA 600

AGAGCAAATC GCTGTTAAAG AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGGTTGA 660

CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG 720

TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT 780

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 624 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGGAAAAAT CAGATTGTGG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAAC 60

AGGTGTCGAA TTGGAATAT CTCCCATGAG TTTTGATAAT GTACTGGCTA GTGTTCAATC 120

1350

AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT	180
TGACTTTTCC ATTCCCTACT ATACTGCAAA AAATAAACTC ATTGTCAAAA AATCTGACTT	240
GACTIONTAT CAGTCTGTAA ACGACTTGGC GCAGAAAAAG GTTGGAGCGC AGAAAGGTTC	300
GATTCAAGAG ACGATGGCGA AAGATTGCT ACAAAATTCT TCCCTCGTAT CTCTGCCTAA	360
AAATGGGAAT TTAATCACAG ATTTAAAATC AGGACAAGTG GATGCCCTTA TCTTTGAAGA	420
ACCTGTTTCC AAGGGATTG TGGAAAATAA TCCTGATTTA GCAATCGCAG ACCTCAATTT	480
TGAAAAAGAG CAAGATGATT CCTACGCGT AGCCATgAAA AAAGATAGCA AGAAATTGAA	540
AGAGGCAGTT CGATAAAACC ATTCAAAAGT TGAAGGAGTC TGGGGAATTA GACAAACTCA	600
TTGAGGAAGC CTTATAAGCA TCCA	624

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TCTTATGAAG CCGAAGCGTG ATTTATGGCG GATAGGTTTG GTCTGCAGAA AGTGACAAAT	60
CTAGTGCCAT CAGCGTATAT GGAATCTnTG GCTGAGAAAC AGTCCCGGGG TGAAGTACT	120
TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATTGATGC GAGTACAGAG	180
GAGGCAGACT TGGTTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTAGCTTC	240
AGTCCTGCGA TCTTACTTGC TATTCATAAG GAGTTGTTTC AAGATATATT TGAACCTCG	300
ATTCCGGTAG GTCAATTCG TCAGACTAAT ATCACAAAGA ATGAACCTGT TTTGAATGGT	360
GAAAGTGTG TGTACTCTGA TTACTIONATG ATTCAAATGA CCTTGGATTA TGATTTTAAT	420
CAGGAAAAAC AAGTTGCATA TGCGACACTA ACCCAGGCGG ATATGGTTAA AAAAAATCCAG	480
CATTTTATTT CAGGAATCTG GCAGATTCAT CCATTTCCGG AAGGAAACAC TCGGACGGTA	540
ACGGTATTTT TGATTCAGTA TCTTCGTGAG TTTGGTTTTC ATATTGATAA TACACCATT	600
CAGCAACATT CCAAGTATTT TCGTGATGCC TTAGTGTTAG ATAATGCAAA GATTTTACAG	660
CGACGTCCTG AGTTTTTAAC AGCTTTTTTT GAAAATCTCT TGCTCGGTGG TCAAAATGAT	720
TTGTCTTCAG AAAAAATGTA TCTAGATTTA GACCTCGATC TTTCATAATC CTAATACTGA	780
GTAAACATTG AATTTTAGGA AAAAAATGAAG TAAATATTCT CACAAGAAAA CGTATATCAT	840
CAAAGTTTGG CTCTTTGTCA ATTGTAGTGG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC	900

1351

AAATTTTCGGC CTTTCCTTTT TGATGTTTTCAG AGCGATAAAA ATCCGGTMTT TTGAAGTTTT	960
CAAAGTTTCG AAAACCAAAG GCATTGCGCT TGATAAGTTT GATGAGATTA TTGGGCGCTT	1020
CCAGTTTGGC ATTAGAATAG TGATGTTGAA GGGCGTTGAT AACCTTTTCT TTATCTTTGA	1080
GGAAGGGTTT AAAGACAGTC TGAAAAATAG GATGAACCTG CTTAAGATTG TCCTCGATAA	1140
GTTCGAAAAA TTTCTCCGGG TCCTTATTCT GAAAGTAAA CAGCAAGAGT TTGAAGAGCC	1200
GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAAG	1237

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTTT CTGAATTAGA AGAGATTGAA TTGCCTGCAT CTCTAGAATA TATTGGAACA	60
AGTGCATTTT CTTTGTAGTCA AAAATTGAAA AAGCTAACCT TTTCCTCAAG TTCAAAATTA	120
GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAATT TAGAGAACT AACATTACCA	180
AAATCGGTTA AAACATTAGG AAGTAATCTA TTTAGACTCA CTAAGCTT AAAACATGTT	240
GATGTTGAAG AAGGAAATGA ATCGTTTGCC TCAGTTGATG GTGTTTGTGTT TTCAAAAGAT	300
AAAACCCAAT TAATTTATTA TCCAAGTCAA AAAAATGACG AAAGTTATAA AACGCCTAAG	360
GAGACAAAAG AACTTGCATC ATATTCGTTT AATAAAAAAT CTTACTTGAA AAAACTCGAA	420
TTGAATGAAG GTTTAGAAAA AATCGGTAAT TTTGCATTTG C	461

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTAAACAAT	60
ATATCAAACA TCAATGACTA GAATACTTGC ATCATCCTTC TTTCCATAGA TTGGATCAAT	120
AGCAGAAGAA TTAAATCTCA TCTTAATTAA CTCTTCAAAA GTTTTATTTT GATTATTTTG	180

1352

ATAGAATTCA TAAAAGCCAT CGCTCATTAA AACAAATTGT TCACTAGTAA CATCTATTTG	240
ATTAATAATA GCATGGTCTA AAAATCTCTC ATCCAACGAA CCTATCCAGT ACCCACTCGG	300
TTGATTAGAT AATTTTCTGA TTTTTTGTA AATAATTTT TTATTTAAAA CACTATTTGT	360
ACCAATTGAA TCTTTTATCT CATTTTCCCC TTTTCAAAT AAGTTATCTA CTCTATGATC	420
AGTTATTTCC ATTCGTTTA CTAACATGAC GCAGTCACCT AGCATCATAT ACTCCAACCT	480
TTTTTCTGAA AGTTTAGCAA ATATTGGTAA GCGATAATAT AGTATATTGA AACTAGAATA	540
GTACACCTCT ACTTCTAAAA CATTTGTTAGA AATCGATTG ACTGTCCTGA TTGATTTGTC	600
CTATTATTAT TTCATTTTAC TATACTCTGT TAATTTATAT GAGTTTAAAC CGATTTTCATC	660
TTTAACCTCG AGTAAAGCAG TTTCAAATAT TTGTTTAAAG GTTTTGTATT CTTTACAATT	720
AACCGACAAA CTTTCTGATA AAATATGTAC AACTTCTGAG ACTGAATAAC CTATCTCCTC	780
TTTAGAATTA TATAAATCTG TAGCTCCACC AATAATCCAA AAATACTGAT TTTGTGAACC	840
TACAATATCC TCATTTTCTA CGGAACCTCC TTGTATCGAA CAAATTTTAT TTATCTTTAC	900
CATAATACTT CAACCCTTT AGTGTCAAAA GTAAACCAAT TCCTGTCACCT GTTAAGAATA	960
GTTCCATAAT CTTATTCGAA CCAGTCTTTG GTAATTTTGT TTTKACATCT ACTATyTCTT	1020
TAGATTTATT AATATGATTT TCAGTTTCTC TGCCATCTCC AACTATTTTA TAGTTTACTT	1080
CTTCTGTCTT ATTATCTTGT TTATTGTCGA TCTTGTCAAT CATTGTGCTA TTATCTTTAC	1140
TTGAGTTAAA CTCTCCGTTT TTTCTGGTTAC TATCAATTAC ATTATTTGAA TTAGATTGTT	1200
TTTCCTCTT GTTTTTTCT TTTTCGTTT TATCACTTAA ATTATTTGTT ACAATTTTGT	1260
AAAGCCCAT CTCCGTTACA ATATTGAAAT TACCATCGCT ATCACGTATA ACAGGTTCTT	1320
TCCCATTGTC ATTAGATTG ATGAATGATA TATACTTACC GGATAAATTA TAAAATTGGT	1380
TATTTAAAC GGTATTTTA CCCTTTGAAT CCTCAATAAC AATTCCTTCT TTACCC	1436

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAATATCA ATCTCAAATG GTTCGTCAAT GGTTCCTGAT	60
ACGTATTTTC CGTCTTCTT CCGTTGCTTG ACACACTCTG TGAGGAGATA TTCGATTGTC	120
CCATTGACTG AACGAAAGTC GTCTTCTGCC CATGATGCGA GTGCAGCGTA TAACTTTGTT	180

1353

GAGAGTCGAA GGGGGATCTG CTTTTTTTGA GCTTCAGCCA TCTTTAGTAA AGGCTTCCTG	240
TGTTGACAAT TGGTTGTGCA TCATGATTGC CACAAAGAAC GACAAGGAGA TTTGAAACCA	300
TGGCAGCTTT TCGTCTCTCG TCAAGTTCTA CCAATTCCCC TTCATTGAGC CGTTCCTAGTG	360
CCATTTCAAC CATTCTTACA GCACCATCTA CAATCATCTT CCGTGCATCA ATAATGGCAG	420
ATGCTTGTG GCGTTGAAGC ATAACGGCAG CAATTTCTGG AGCATAAGCT AGGTAAGTGA	480
TACGTGCTTC AAGGATTTCC AAGCCAGCAT CCTCAACACG ACTTTGGATT TCTTCACGAA	540
TACGGGTAGC AACAATTTTC CTAGAGCCAC GGAGACTACC TTCATCTGCG TGCCCATCAC	600
CCGGAGTATC CACATTAGGA GACACATCGT AAGGATAGAT GCGGAC	646

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1653 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CTTGCAAGTG CAGTAGGTGT TACTTCAGAT ACATTTGAAC GTGCAGAGGC TCTTTTGTAG	60
GCAGGAGCGG ATGCGATTGT TATTGATACT GCACATGGTC ATTCTGCAGG TGTCTGCGT	120
AAAATTGCCG AGATTCTGTC TCATTTCCCA GATCGGACTT TGATTGCTGG AAATATTGCT	180
ACTGCTGAAG GTGCACGTGC CCTTTATGAA GCGGGGTAG ACGTTGTAA GGTGGTATT	240
GGACCAGGTT CTATCTGTAC TACTCGTGTG ATTGCTGGTG TTGGTGTTC GCAAGTAACA	300
GCTATCTACG ATGCTGCAGC TGTTGCGCGC GAATATGGTA AAACGATTAT TGCTGACGGT	360
GGGATCAAGT ATTCTGGAGA TATTGTAAAA GCACTTGCTG CAGGTGGAAA TGCTGTTATG	420
CTTGGATCTA TGTCTGCTGG AACTGATGAA GCTCCAGGCG AAACGAAAT CTCCAAGGA	480
CGTAAATTCA AGACTTACCG TGGTATGGGA TCAATTGCTG CTATGAAGAA AGGTTCAGC	540
GACCGTTATT TCCAAGGTTG TGTCAATGAA GCAAACAAGC TTGTTCCAGA AGGAATTGAA	600
GGTCGTGTTG CTTATAAAGG AGCGGCAGCT GATATTGTTT TCCAAATGAT TGGTGGTATT	660
CGCTCTGGTA TGGGTTACTG TGGTGCAGCT AACCTTAAAG AACTACACGA TAATGCTCAA	720
TTTATTGAAA TGTCTGGTGC TGGTTTGAAA GAAAGCCATC CTCATGATGT GCAAATTACT	780
AATGAGGCAC CAAATTATTC TATGTAAAA ACAATGAAAA GAACTCCAGT GAAACAGGA	840
GTTCTTTTAC AATGTTGTCA ATTTCCATTT ACAGCAGCTT TACCATCCTG AATAGTGAAG	900

1354

ATACTTAGAT TTTCTGGCAG ATTTTGAAGA TGGTCTAAGC TTGTTGTTGT GATAAAGGTT	960
TGGATTGATT GAGAAATCGT TTCTAATAAT TTAACTGTC TAGTGTGTC AAGTTCACCT	1020
ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCTTTCCAT TAATTCGATT	1080
TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTTGAC CTGGGCTTCC GAAACTAGCA	1140
TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCTTT	1200
TTAAATAAAT CTCTGGATCT ACTTTTCTTCT AAAGCAATTT TGAAAGATTC GGATAAGTTT	1260
TGTTTGTCAG TTATATTGAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA	1320
GAGAGTTCAA AATGTTTCTT ACGCCCAAAT GATTCTAGTT TTTTATGAA ATCTAAGCGG	1380
TGATTCATTA CACGACATCC ATAATCAACT AGCTGATCAT CTAACACAGA AAGGAATGTT	1440
TCATCTATTT TTTGAGCTGA TTTTAGGTAA GTGTTCTTTT GCTTTAGGAT GTGGTTATAA	1500
TTGGTTAAGT CAGATAAATA GATTGGCTTA ATTTGCCCAA GTTCCATATC AATGAATTTT	1560
CGTCGAATCG AAGGTGCTCC TTAAATTAGT TGTAATCTT CAGGAGCAAA TAAGACAACA	1620
TTCATGTGTC CTACATAATC TGAAAGGCGT GCC	1653

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTTCAAAGC ATTTTGTGTT AGTTTAAAT TACTCCCAT CTTCTTTTCC	60
AAACGTACAA TATATCCAAA ACCATTCAAA ATACTAGATT CTATTTTSTA TAATATCACT	120
AAATCCACCT AATTATAGGA CGTTTTCAGA TTTTGTGTC TTTAAGCTC TTTAAAGCAA AAGAACAAGT	180
TATTGTTTTA ATATAATATC TCTTTTGTG TTCTAAGCTC TTTAAAGCAA AAGAACAAGT	240
AAAGAGTCAA GACAAGGATA AAAAGTCCAT ATTAGGGCAA ATAAAAGCT TTAAGACAGA	300
TGACAAATCT AAGTCAAATA AGAAAGACCA TAGCAAAGGT GCAGAGAGAT AAATATTGGC	360
GGTCTTCGGA CTGCCTTTAT TTTTGTATCC ATTTTTCAAA TCAAATTTAT TCAGACTATA	420
TATGCACATA TACACTTAAA TTCATATAAA AACATGGCTT GTAAAAAATT ACTTTAATCA	480
CAATAATCGC ATTTAAATTT GTGATGTTTG CAAGCTAAAT TACGGACTTC ACTTGAAGT	540
TTTCCCTTGT ATCTTTTATA ATAGATAGAA AATTGTCTGG CAGATGAATA TCCAACAGAT	600
TCTGCTATCT CTTTATAGG TAGTTCAGTG TTTAAAGAA GAGTTTCAGC TACATTCACT	660

1355

CTTTTCTTT GAGTGACTC TGTAATGCTT TGACAAATATT TTTCCTTAAA TAAATTTTTT	720
AATTTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTTAC ATTCGTTGCA	780
AAATGATCAT CTAAGAATCT TGCTACATCT TCAAGTGCTT TATCATCATC AATTTCAATT	840
TTATATTTTT TTCTATTTAA GTATGTGTCA ATTACTATAC TTATCCATTC ATTTGCCTTT	900
GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC	960
ACTCTTTCTA AGGCCTTTGT AAGTATTATT TGATTCGGTT GAAGCAAGGT TGAATAAAAA	1020
GATTCTGGAT TAATGTTAAT AGATGCTAAA TGTTTTCTA TTAGCTCTTT TTAAAAACm	1080
ATGGAAACAG CAAGATAACA ACAATTCTCG TGTAATAAAA AAACAAAATT ATCTTTTATA	1140
TTATCAAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACGG ATTAACTTT	1200
TCTCCGTTTG CACTGACAAT GTAACCTGAA TAAATTGAAA CATAGTCTGA CATACTATAA	1260
GTGCTATTTT GAACTACTTC CTCTTTGATA TAAAAATCAT GTATATCGAT AATGAAGATG	1320
CCTCCTTCAT AAAACCGGTA	1340

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TATGTTCTG ATGAGTTTTT AAGTAGGAAA AACGTGCTAA CCTCTCAGAT TTTGGAACCTT	60
GTAAAAGAAA CTCTTTTTTC ACCCGTAGTA GTTGATAATG GGTTTGATCC GGCCTTATTT	120
GAAATTGAGA AAAACAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTAT	180
TTTGACATA AAGAATTGGA TAAATTGTTT TTTCATGATG AACGTCTTCA ATTGGAATAT	240
AGTGATTTAC GAAATCGTAT TTTAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA	300
GAATTTTTAG CCAATGATCG AATAGATTTT TTTTCCTAG GTGATTTTAA TGAGGTTGAA	360
ATTCAAAATG TATTAGAATC ATTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTTGAG	420
TATTGTCAAC CTATTCTAA TATCCTCAG GAAGGTATGG TTCGGAAGAA TGTGGGACAA	480
TCCATTTTGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGAGCA ACATTTACCC	540
ATGGATTGAA TGAATGGTTT ACTTGGTGGA TTTGCTCACT CTAAGCTCTT TACAAATGTC	600
CGGGAAA	607

1356

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAATACC GAATTTTGTT TTGTCCTCTA TTTCAACATT GTGAATCGCC TCAGGCAGAG	60
AACCGATACT AAAGATATAA CCAAAATAGT TGTCAATTGC TTTACCGATA TCAATCTTAT	120
TGGTTAAATC AAAATCCAGT TCGTCAATG CGCCATCGAT GTCTTGATTG ATTTCCAAAA	180
GTTTTGTAAT GAGGTTACCC GTACCGCCTG GGATAATCCC TAACTTAGGA ATGTAGTCTC	240
TCTCATCAAT ACCTGAAATG ACTTCATTGA CAGTTCCATC TCCACCAAAC ACAACCACTG	300
CATCATACTG CTCACGAGAA GCTTCTTCAG CAAAATGTGT TGCATCCAGC GCTTTTTCGG	360
TAATTTTGGT TTCAACATAT TCAAAGTATT CTTTGCTTT ATTCTCCAGC TTTTCTTTGT	420
AATCCAAAGC CTTCTCGCCA CCAGAAGTAG GGTGATAAT TACCATTGCT TTTTTCATTG	480
ATTTTATCCT TAATTTTAAA CAGAAATGTT TACATTTCTG CGTATGCAAG TAAATGTAAT	540
CCTATTATAC AATGAAAATA CAGAAAAGAG AAATCTGACG TACTGGAGAT TAATACGCTT	600
TTATTCTATT TTCCCATCGC CTAATACAT CCTTTAAGGG TTCATCCAAG TAAGAATAGG	660
CCTTATCCTT GATCCAATCA GGAATACCGT AAGCTGCCTC TGCTAWGCTA CAAGTGATTG	720
CTGCGAGAGT ATCACTGTCTG CCACCAAGTG AGATGGCATT TCTTATCGCA TCTTCGAAGT	780
CTCTACTTTC AAGAAAGGCG ATAATGGCTT GAGGGACAGT TTCCTGACAT GTTTCGTTAA	840
AACGATAGTT AGGACGGATT TCATCTAAAG TTTGAGATAG ATGTAATCG TATTCTTTTT	900

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTTCTGGC AACTGGTCT TGGAATACGG CAAACCTCT GAAATATCT ATGCTGGAAT	60
GGACGAGGAA TACCGTCGTT ATCAGCCTGC CATCATCACT TGGTACGAAA CAGCCAAACA	120
TGCTTTTGAT CGCGGACAGA TTGGCAAAAT ATGGGTGGAA TCGAAAACGA CCTCAAGGGC	180

1357

GGTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATG AGGAATTTCG TGGTGAGTTC 240
AACCTGCCAA CTAATCCTCT TTACCACCTC TCCAATCTGG CCTACACTCT CAGAAAGAAA 300
CTGCGCAGaA GcATTAAACAG AAAGGAAGCC TATGACCTTT AAAC TTCTCA GCCAAGAAGA 360
ATTCATCCAG CATACTCAG CTAGATCCCA ACGCTCTTTT ATGCAGACCG TAGAAATGGC 420
AGAGCTGCTG AGCAAGCGTG GCTTCAGTAC CCAGTATGTC GGCTACACTG ACCCACAAGG 480
GAAGGTAGTG GTGTCAGCTG TCCTCTACAG CATGCCTATG ACTGGTGGCC TTC 533

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCAGCAAACCT AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTTGAGGT TGTAGATAAG 60
ACTGACGAAG TCATGTACAA AACACTGTTT TGAGGTTGCA GATAGAACTG ACGAAGTCAC 120
TCAAAACACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAAA CACTGTTTTG 180
AGGTTGCAGA TAGAACTGAC GAAGTCanna ACCACACCTA CGGCAAAGTG AATCTGAAGT 240
GGTTTGAAGA GAGTACAACT TGTCTTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC 300
ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTTA TCTTGATGGA ATCTTAGCAG 360
TCAAGGATTC TCAAATCGTC TATGTCGGTC AAGATAAGCC AGCGTTTTTA GAGCAAGCTG 420
AGCAGATTAT AGACTATCAG GGAGCTTGGA TTATGCCTGG TTTGGTCAAT TGTACACCCC 480
ATTCTGCAAT GACAGGTCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA 540
ATGA 544

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCAGGAACTC AAATGTAAGT AGGGGTCCT TTTTGTATA TTTTCAAAT AACGCCTCTA 60

1358

CACTATTTGT AGCAAATTCA CCAACTACAG TTGTATCTTA GTTAAAATAA GTTAGAATAT	120
GTAAGTGAGT ACCAGATATA CCAAGACATC GTCACCATCT AAGGTATATT CAAAATACAA	180
AAGTTGACCA ACTAGATTTT TGAATATCCT TATATATCCA TTCTTAAAT TGGTTTAAAT	240
AGCGTAGTCT TTAAACTAG TTTTGAGAAT CCAAAAAATC TTCCTACATA TGTAAGAAGA	300
TTTTTTAGTT CAGAATGATT AGaTTTAGCT AATGGATACC TATCCTACC	349

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CTCCGATAAC CACACCAGCA ATGGAAATAA TTCCATCGTT AGCATCAAGA ACACCCGCAC	60
GCAGGATATT TAAACGACCT GCAAAATTG AATCAATTTC GTGATTGTGTT TCTGACGCTA	120
AATTTCAAGT TCAAGTTAGC CATCAAGAAG TCTTCTCTGG GTGACTTGTA GTCCAAGCAT	180
TTTTTTAGGAT AGTTGTTAAT CCACTTTTCG ATGAATGCGA CTTCTTTGGG AGTCATTTTC	240
TTGGTTCCTT TAGGTAACCA TCTACGAATG AGCCTGTTGT GATTCTCATT AGTCCCCGGG	300
ATCCTCTAGA GTCGACCTGC AGGCATGCAA GCTTGGCACT GGCCGTCGTT TTACAACGTC	360
GATGACTGGG GAAAACCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT	420
CGCCAGCTGG CGTAATAGCG AAGAGGCCCC CACCGATCGC CCTTCCCAAC AGTTGCGCAG	480
CCTGAATGGC GAATGGGGCC TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTTT	540
ACACCGCATA TGGTGCACTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC	600
CCGACACCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC	660
TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAAGTTT CACCGTCA/C	720
ACCGAAACGC GCGAAACGAA AGGGCCTCGT GATACGCCTA TTTTATAGG TTAATGTCAT	780
GATAAGGATG GTTCTTAGA CGTCAAGTGG CACTTATCGG GGAAATGTGC GCCGAGACCC	840
TATTTGTTTA TTTGTCTAAA TACATTCAAA TATGTATCCG CTCGTGAGAA AATAAACCTG	900
ATAAATGCGT CAATAATATT GAAAAATGAA GAGTATGAGT ATTCTACATT TCCGTGTCGC	960
CCTTATACCC TTTTGTGCGG CATGTTGCCT TCCTGTTTTT GCTCACCAG AAAACGCTGG	1020
TGAAAGTTTA AGATGCTGAA AAATCATTTG GGTGCACAAC TGGGGTTACA TCCAAGTGA	1080
ATCTCCAnCA GCAGTTAAGA TCCTCTGACA GTTGATACAG CCGCAAGAAC TATCCCCGAT	1140

1359

GAATGAGCAA CTTTAAAAAG TCCTGCGAAT GTTGGGGCGG TAATAATCCC CGTGTGTAG 1200
 GCCCCG 1206

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTCTGAC TTTACCAAAA GAACCATCAA AAAAGTTGCT 60
 GAAAAAGGCC ATCAGGTTAT TATTACGACA GGTGCGCCTT ACCGTATGTC AAAAGATTTT 120
 TACCGTGAAC TGGGCTTAGA CACTCCTATG ATTAACCTCA ACGGATCCCT TACTCATTTA 180
 CCAGACCAAG TTTGGGATTT TGAAAAGTGT TTGACTGTAG AAAAAAATA TCTGCTAGAT 240
 ATGGTTCAAC GTTCAGAGGA CATTCAGGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA 300
 TTCTACATTA CAAATCCCAA TGAAGAAATT GCCAATCCCA AACTATTTGG TGTAGAAGCT 360
 TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCCTAA CTGTATCCTC 420
 TTGCAGACTA GAGCCAGTGA CAAATATTCC TTGGCAAAAG AAATGAACGC CTTCTACCAG 480
 CATCAACTTT CTATCAATAC CTGGGGAGGT CCGCTCAATA TCCTTGAATG TACCCCAAAA 540
 GGTGTCAACA AGGCCTTTGC TTTGGACTAC TTGCTCAAGA TAATGAATCG TGACAAAAAA 600
 GATTTGATG CCTTTGGAGA TGAACACAAT GATACCGAAA TGCTCGCTTT TGCTGGGAAG 660
 GGTATGCCA TGAAAAATGC CAATCCAGAG CTACTCCCTT ATGCAGATGA GCAAATTTCC 720
 CTTACCAACG ACCAAGATGG GGTGCCCCAA ACCCTACAAG ACTTATTCTT ATAACCTATA 780
 CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA 813

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 683 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAAT TAAAGGAGA TTGATGATGG 60

1360

ACAAATTATT TAAACTAAAA GAGAACGGTA CAGACGTTTCG TACAGAGGTT CTCGCTGGTT	120
TAACAACCTTT CTTTGCAATG AGCTATATTC TCTTTGTAAA CCCACAAATA CTTTCACAAA	180
CAGGAATGCC TGCTCAGGGC GTCTTCCTAG CGACGATTAT TGGTGCAGTA GCGGGTACCT	240
TGATGATGGC TTTTATGCT AACCTACCTT ATGCCCAAGC GCCAGGTATG GGAATCAATG	300
CCTTCTTTAC CTTTACAGTT GTATTCGGGC TTGGTTATTC TTGGCAAGAA GCCCTAGCTA	360
TGGTCTTCAT CTGTGGGATT ATTTCAATGA TTATTACCTT GACAAATGTT CGTAAAATGA	420
TCATTGAATC GATTCCTAAT GCTCTTCGCT CAGCTATTTT AGCTGGTATC GGTGCTCTCC	480
TTGCCTATGT AGGGATTAAG AATGCTGGAC TTTTGAAATT CACGATTGAT CCAGGCAACT	540
ATACTGTGT AGGAGAAGG GCTGACAAAG CTCAAGCAAC GATTGCAGCA AACTCTTCAG	600
CAGTTCAGG ATTGGTCAGC TTTAATAATC CAGCTGTTTT AGTGGCTCTT GCAGGACTTG	660
CCATTACTAT CTTCTTTGTC ATC	683

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CTACTTTACA TGGAAGTAGT CACTGAATTC CAGTTAGAAA TTAATTTGTA ACTACGTTTT	60
GAGGAGGAGT AAAATGCTTT CCTACGTTTCG ATATTACCCA CTAGCGATAG CTAAATTAAT	120
GTGCTGTGTC TCTCCTAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT	180
ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTT CACCAGTATC GATTATTTAA	240
TTATTTTAAT TATTTTATTT GCACAGCTAT CACAGAATAA ACAGAAATGG CATATTTATG	300
CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGGCGAG TTTAGTTGCT GCTTATGTCG	360
TTAATTTTCGT GCCTGAAGAA TGGATGGTTG GATTGCTTGG TTTAATCCCT ATCTATTTAG	420
GGATTCGCTT TGCAATTGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA	480
GATTAGAACA AAGCAAGGCA AATCAACTGT TTTGGACAGT TACATTGCTG ACAATTGCGT	540
CTGGCGGAGA TAATTTAGGT ATCTATATAC CTTATTTTGC TTCGTTAGAT TGGTCACAGA	600
CCCTCGTGGC CTGCTTGTG TTTGTAATCG GCATAATTAT CTTTTCGAG ATTAGTCGGG	660
TGTTATCCTC TATTCGTTA ATATTCGAGA CAATTGAAAA ATACGAGCGA ATCATGTGTC	720
CCTTAGTATT CATTCTACTT GGACTATACA TCATGTATGA AAATGGCACG ATAGAGACTT	780

1361

TTCTGATCGT GTAGATTTTT TTGTTTCACT AGGGATTTAG CCCGAGCTCA AATCAGCTCT 840
CTGATTTTCA GA 852

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA GCGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTTAATG 60
GATAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT 120
CACCGCGCCT AGGATAACAA TTTTAGCAAT CAAGATAAAC CAAAACATCA TAACAACAAG 180
AAGAACGGAA CCTAAAATTC GGACATCCAC CAAATGATGG ACATAGTAAT TGAGATAACT 240
AGAGAACAGA GTTAGTAAAC CTAAATCAC TAAGAGAACA AAGGCACTGC CTGGTAGGGT 300
ATAGCTAATT TTCCTGTTAG ATAGATTGGG AAGAAAATAA TAAAGCATGA CCAAGATAGC 360
AAAGAGGAGG GCGTAAATCA GAGGACCTGC CAACCCTTGT AAAGCCTGAT AGATAATGCC 420
ATCTTTTGTC CAATAATGAG CAAGTAAAGC CAAATCATC TGACCAAATA AGATCAAAAA 480
CAAGGCAAAC GCAAAGAGGA GCTGCAACCA AAATGACTA GGAGACTTAG CATCTGATGG 540
GAAATAAGTC CACGACTCTT TCGACGCCA TAAGCCTTGT TAAAAGCTTT TTGCAAGAAA 600
TTCATAGATT TTGAAAACT CCATAACGCC GATAAACAG AAAAACTCAA TAAACCTGTT 660
GAAGGTTGCG TCAAGACTTC TCTGGCTATT TTTCCACAC CTTCATAGAG GCTTGGGGGG 720
CAGACGTCTT TCATAAAGCC CAAAAATTCT CCCA 754

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGGATAACT CTAGGAGTAC CGCTATTACT CGACTTAATG AGTGACAAG AAGTCAGGAT 60
TTTTATGCAG GTTGGGCGCT TCATCAGACA GGGAAGATTT ACAGCGACTA TTATGGAAGT 120

1362

CAAGGTTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTTT CTTTGCCATC	180
TTTGAGTGGT TAGCCTTGGT AGCAGGAGGA TTTTTCCTTT TTAGATCAGC GGACACCTTG	240
ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTTACATGCT AGTTACAGGT	300
CTTGCTTTTG GTGGAGGCTA TGCGACTCTT TTAGCGCTTC CTTTCTTATT CGCAGCCTTT	360
AGTTTAGTTG CGGCTTACCT AAGCAATCCA AGCCATGATA AGGGATTTGT ACGGATTGGG	420
CTAGCTTTGG CAGGCGGATT TTTCTTTGCT CCCTTATCAT CGCTCCTGTT TATTGCTGTA	480
GTGAGTTTAG GCTTGTTGGT CTTTAACCTT GGGCATAGAC GCTTTGCGCA TGGGTTTTAT	540
CAGTTTCTTG CAGTGGCTTT AGGTTTTTCA CTTGTCTTTT ATCCAAGTGC CTACTATAGT	600
GCTGCAACAG GAAGTTTGGG GGATGCGWTT AGTGGTATTC GTTATCCTAT TGACAGTATT	660
CGCTTTGATT TTACTTCTAA AATTTTAGAG AATATGTTTT TTTAAGG	707

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GGATTTTGAA AAACCATACC GATTTGACGA CGTATATTCC AAACATTTTC CTCAGTCAAA	60
CGTTGGCCAT CAATTACAAT CTCTCCGAT TCTGCTTCCA GTAAGCCATC AATTAATCGA	120
ACCGTCGTTG ATTTACCACT ACCATTATGC CCTACAATCG AAAGCCATTC TCCACGTTTC	180
ACGTGAAAgT AATATCCTTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA	240
GATTTTTTAC ATCAATTATT GATTTCAATT CGAACCAAAT GTCCCTTTAA ATACATAGGC	300
ACTACCCTTG AAATAGTCAT AGCCAGAGTA GATAGTGAAA AATAAGGCTA CATAAAGTAG	360
AAC TTGACCA AGCAAAGTCC AATGTAATAG CAAGAAAATA ATGGCAAACA TCTGACTAAA	420
AGTTTTAATT TTCCAGGCA TTGCTGCTGC TAAAATTGTT CCACCAGTTT CAACCAATAA	480
AAGCCTTAAA CCTGTACAG CTAAGTCACG ACAGATAATC ACTGCAACAA TCCAAGCCGG	540
AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAACT TATCCGCCAT	600
AGGATCTGCA AATTTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC	660
TAAATAGTCG GTAATACTGG CAACAGCAAA GATAATAGCT GCAACTATAT GACTCTCTAT	720
CGAATTTCTT ATCGTTAAAA TAAAGATAAA AATAGGTATA AA	762

(2) INFORMATION FOR SEQ ID NO: 343:

1363

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CTTTTGATAC ACTTAACTA TGAATACAAA TCTCAAGCCC AAACCTCAGC GTTTTGCTTC	60
TGCGACTGCC TTTGCCTGTC CTATCTGTCA AGAAAATCTG ACTCTGTTAG AGACTAATTT	120
CAAGTGCTGC AACCGTCATT CTTTGTACTT GCGGAAATTT GGCTATGTCA ATCTAGTCCC	180
TCAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT	240
AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA	300
AACTACCACA ACAATTTTGG ATATCGGTTG TGGTGAAGGA TTCTATTCTC GCAAACCTACA	360
AGAAAGTCAC TCTGAAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT	420
CGCGGCTAAA AGTGAACCCA ACTGGGCAGT CAATTGGTTC GTTGGCGACT TGGCACGACT	480
TC	482

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TTTATTTTAA TAAAGTCAAT ACCTGTCTTT ACTTTTCTT AAAAAAAGTT TATTATGTTC	60
TTTAAGGAGG TGTAACCAT GAAAATAAAT AATAAACTCG TTGGAGAACG TATTCAAAAT	120
ATCCGTTTAA GCCATGGCGA CTCTATGGAA AAATTTGGAG AAAAATTTAA TACTAGCAAA	180
GGTACAGTTA ACAACTGGGA AAAAGGTCGC AATTTACCAA ATAAAGAAAA CCTACTAAAA	240
ATTGCATCTA TTGGAAAAAT GAGTGTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT	300
CTACACTTAA AGATTATGGA TTTAGCTCCT GAATGTATAA AAAATTATGA TGAGTATAAC	360
TCTTTACACG ATGATATAAC AAATAAAGCG TTACAGATCG CTCAAAATAC CATTTCTAAG	420
ATTGATTATC AAATTTTCTA CGAAACGATC AAAAAATTTA TTGATTTAGC TATCGAACAA	480
TCGAGAGATT TGCAAGGAAA TTTGTTGAAA AATAACGGGT	520

1364

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```
GCATCAAATC CGCCATCAAA GAAGTTCTCT GGATTTACCA AGACCAGTCA AATAGCTTAG      60
AAGTGCTTAA TGACAAGTAC AATGTTCACT ACTGGAATGA CTGGGAAGTT GGAGACACGG      120
GAACCATTGG TGAGCGCTAT GGTGCCGTG TTAAGAAACA CGACATTATC AATAAGCTTC      180
TCAAACAGTT GGAAACCAAT CCTTGAACC GCCGCAATAT TATTTCGCTC TGGGATTACC      240
AAGCTTTCCA AGAAACAGAT GGGCTGCTCC CGTGCGCCTT TCAGACCATG TTTGATGTTT      300
GGCGTGTTGA TGGGAAATC TATCTGGATG CGACCTTGAC CCAGCGCTCC AATGATATGC      360
TGGTGGCCCA CCACATCAAC GCTATGCAGT ATGTGGCTTT GCAGATGATG ATTGCCAAAC      420
ATTTTGGCTG GAAGGTTGGG AAGTTCTTCT ACTTCATCAA CAACCTCCAT ATCTATGATA      480
ATCAATTGTA ACAAGCTCAG GAATGCTCC GTCGGGAGCC GTCAAAGTGC CAACCACGCT      540
TGGTTTAAAA TGTTCTGAT GGGACTAATT TCTTTGATAT CAAAGCAGAA GATTTTGAGT      600
TGGTGGATTA TGACCCTGTT AAGCCACAGT TGAAGTTTGA CCTAGCTATT TAAAAGAATA      660
GAAAAAAGAA GTTGAGAATA ATCCCAACTT CTTTGTGTTT TTAACGTGAT ACGCGGCGAC      720
GAGCTGCTTT TTTACGGTTT TCTTCGATGA AAGCTGCTTT TTGCTCTTCT GGTTCGATTA      780
CTTTCTTTTT AAATGCGTAT ACTGCACCTG CAACGGCAGC GACAGTTCCT GCGACACCTG      840
TTACAAGACC TTTAGCGAAT CCTTTAGCCA TGAGTCTTCC TCCTTTATAT TCTCAATCAG      900
CCAGCCTCCT CAAGAGGTCA CATTTTCTG ACTGACCTTT TTGTGTTATA ATAATAGTAA      960
CGAAAAAATG GGAATTTTTC AAGGAAAAAA GATGAGAACA AAA                      1003
```

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```
CCGCACGTAC TATTCCAGAT GCCGAGGAAG TGGACCTCAT CCTCGTTGGC GCAACTGGTC      60
```


1365

TCAACGCCTT TGAACGCCTC TTGGTCGGCT CTTTCATCTGA ATACATACTC CGCCATGCTA	120
AGGTCGATTT GCTGGTTGTG AGAGACAAG AAAAAACCTT ATAATCACAA AGAAAAGGAG	180
CCCCTAGCTC CTTTTGTTT ACGATTTATT TCTCTCTTTA TGGCGTTCGT AAGCCTTGAG	240
CTGGCGCTGC AGTTCCCTTT TAATAGCAGG TTCTGGAGCA TATTTTCTT CCCAATTATC	300
TGGTTTTAAG ATTTTATGGG TCACTGGATC AAAATGAGCC TTGCCATCTG GAAAAATTTT	360
CCCCATATTG GCCTGATGGA CAATATCAAA AATACGTTCT GGGTCCACCC CCATCAAGAC	420
AAACTGCCG TAGGTGAAGT AAAGCGTGC AATCAAGGCA TCCACTTGCC CTATCAAATC	480
TTGCTGAGCA GGTGCTTCT TGGCTACTTT ATCTGCTGCC TTATCAAGGG CCTGATGAAG	540
TTGCGATACA GCTTGACCAA AATCTTCTTC AGAAGGACTG GCTGCTCGAA CAACTCCAC	600
CAATTCTTCT ATTTTAAAC CAGCCCTATG GGTGACCCC TCTAAATCCC AAGCTCGAGG	660
TTCTTCTTGG GTTCGTTTAT CCATCATGTG GTGAAAGTC TTGACCTTAT TGAAATGATA	720
GTCACGGCTG ACAAAGACTT TTTCTGAAGA	750

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CGCAACATAC GGATAACCTC CAAAGAATAT TTTTATATTA TAGCAAAGCT TTAAATTGAA	60
TGTTAGAGTC TTGTTCAAAA CAATCATCAA AACCACGTGG ATGATGGTAT TCTACTAAGT	120
GTTGATCTTG AGGATAAGTG TACTTACCGC CAACTTCCCA GATAAATGGA TGGAAATCGT	180
ATTGCAAGCG ATCTTTTCGC ATTTTCCTAA GTTCTAGAAT CTCATTAGTA GAAGCCATGA	240
AGTTAGACCA GATATCATAG TGAAGTGGG TAATGACTTT GGTACGCAGA TTTTCTGCCA	300
TACGAAGAAG GTCGATAGAT GTCATTTGT CTTGGATACC TACCGGATTT TCACCATACT	360
TATTCAAAGC AACATCAATT TTAAAGTCTT TACCATGTTT TGCAAATAG TTTGAGAAGT	420
GAGAATCTGC ACCATGATAG ATGGTTCCAC CTGGTGTTC AAAGATATAG TTAACAGCCT	480
TTTGAGCCAT TTCTTCATCT GTAACAGCCA AGCCAGCAGT TCACCGCCTG TCTCATCAGC	540
ACCGTTCACT GGGAGAGTTA CCAAGCAAGT ACGGTCAAAT GATTCTACTG CATGAA	596

(2) INFORMATION FOR SEQ ID NO: 348:

1366

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```
CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA      60
GCTCCTCCAT CAGTTTTTTC TTTAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA      120
ATCACAATGT CAGCGCCTAC TTCTTTTGCA AGGGCAAAGT TGTCAATGTT GATATCGACT      180
GCGATAACAT GAGCATTGAA TACTTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA      240
CCAGCACCGT AAAGAACAAC CCATTGGCCT GGTTCACCTT TTGCTTCTTT GATAGCTTTA      300
TAGGTTGTTA CTCCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA      360
ACTTTGACAG CATAGTCAGC AGTTACGATA CATTGTTTCA CCATACCACC GTCTACTGAG      420
TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTGCGAA      480
GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC      540
ACATCTGGAG CAATCTCTTT AACGATACCG ATACCTTCGT GCCCAAGAAC ACGTCTCGGG      600
ACTTGACCAA AGTCACCATG AGCAACGTGG AGGTGCGTGT GGCAAACGCC CACAGTATTC      660
ACTTCTACAA GTG                                                    673
```

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

```
GTACCCTACA AATGCTTTAC AGTATGGGTT GAGGGTGGTC AATGGAAC TAAGTAGGTT      60
TGGACAGGAA CTTTGGGATA TTCTGATTAC TTACATTCTA CTCGATATCA TACAGCAACT      120
GTTAGACATG GGGGTAGAAC CTCTAAGGAT TATGCAAAAC CTGAGGCATG GGCTAGAGCT      180
TCCCTCACCA AGATTCCG                                                    198
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(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid

1367

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

```

GCTTCTTCTA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG      60
GACCAATCCA CTACTAATCC TAAGAACAAA ACACTCAAGA GAGCAGAAGA GAGAGGTTCA      120
CTGGCACTGA TAACGGCAAC CACCAAAGGA GAAACCAAGG ACACAGCCTT CATGGAAATG      180
AAAAAAGCAA AAGCCGTTC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA      240
TCAAGAGTAA AGGAAAGCTG ATAAACCGGC GAGAGGACAT TGCTAAACAA ACCTGCCAAA      300
ATCATCCCCC ACCCAACCGT AGGAACAAAA CCATAACGCT TAGCAAAAGG TTGGGGCAAG      360
ATAACATTAA ACATAACACC CATGGCACTC AGCAAACCTG TTATAAGAGC TAGCGCGCTC      420
ATGGATAACT GAGAGAGGTC TCCCTTTGTC GCCATCAAGC AAACACCCAG CATGGCAACC      480
AAAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTTGAT AAACCAAGCG ATTGTAAAAG      540
AGGATAAAGA CAGGGCTAAT AAAGTGTAAA ATAGTTGCTG TCGTAGCATT TGAGTATTCT      600
ACACAGAGAT AGAAAAAATA CTGAACTGAA AAAATCCCCA AAATAGCATA GGCTAAAAAG      660
GGCAGGTAAT TTTTCTTGTC TCGCCAAATA TCTAGCACTT GCGATTTTAA TTGTATTGCA      720
GACCAATGA GTACAAGACT CCCTGCCAGT GTCAAACGCA TAGAGGTAAT CCAGCCCGAA      780
GACACCTGAT AATGAGTAAA GAAGTACTCT CCTAAAATTC CACAGATTCC CCATATTAAG      840
CCGGATAGGA GCGAATAAAT TTTTCCGTTA ACAATCTTTT TCTGATACTG A              891

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(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

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GAAAGCGTTC AATAGAACAT TGCTTTTSTA TTTTtagagt AAGCTAAGCG CTTcagcATC      60
TGCGATGATG GTTACATCAG GGTGATTTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC      120
TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTTCGAC TCACCGTAAG CAAAAAGAAT      180
AATAGACTTG GCATCCAAAA TGTTTTTAAT CCCCATTGAA ATAGCTTGGG TTGGGACGTC      240
TTCAATCTTG GCAAAGAAGC GTGCATTGGC TTCGATAGTA GACTGGTCAA GTTCTACTAG      300

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ATGCGTTTGA CTGTCAAATG GAGTG 1368 325

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAAGAGCAGT TTGATGATTT TTGATAAGCA TGCGAATTTA AAATACAAAT ATGGCAATCG	60
CAAGTTTGG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC	120
TGAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTCC	180
AGTCAGTAGA TCCGTTTACT GGCAGAAATAA ATAAGAGGAA GTAACGThAA GTGCTTTAGC	240
ACCTGCTCGG GAAAGTGGTG CGCGAGGAAG CTATTTTCAGG ATGCTTTGGC CCTGGCCGGT	300
AGAAGCGTTA TAGCCGCAGA CTACGACACT TCACACTGGT GGTT	344

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT	60
TGGACCTGTT CCCTTCACTC TGCAAACTT TGCAATCGGC TTGATTCTAC TGTCTTTAGA	120
CCGAGAGAGG CTGTACTTTC TGCTGGACTC TATCTTCTTC TAGGTGCTAT CGGTCTTCCT	180
GTCTTTGCAG GAGGTGGAGC TGGTTTTTCAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT	240
TGGTTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGTT	300
GTTAAGATTT TTCTTGCAA CCTCTTGGGT GATGCCCTTG TCTTTGTCGG CGGGATTCTC	360
AGCTTGCATT TCCTAGCTGG AATGGCATT GAAAAAGCTC TTGCTGTGGG GGTCTTCCC	420
TTTATCATTC CAGACCTTGG CAACTTCTA GCTATTAGTT TTATTAGCCG TCCCCTACTT	480
CAACGCCTTA AAAATCAGGC TTACTTTACT AACTAAAAA GGATATCGAG TTATCATGAC	540
TCAATATCCT TTTCTTTTAT TTTGAAAACT TATACTCAAT GAAATCAAA GAGCAAATA	600
GGAAGCTAGC CGCAGGCTnG CAAACACTG TTTTGAGGTT GTGGATGAAA CTGACGAGTA	660

1369

AnATCTCATA CATACGGCAA GGCAAAGCTG AC

692

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTTCAA AACGCATCCA GAAGATTTTT TCGATAATGT CGGACCTCTT	60
GTAGCCAGTA ACTTTTTTCA TACTTACACC GAAGATTTCC ACTTGATGAA GGAAATTGGA	120
GTTAATTCTT TCCGCACTTC CATCCAATGG AGTCGACTCA TCAAGAATTT AGAGACAGGT	180
GAGCCTGATC CAAAAGGTAT TGCTTTCTAC AATGCCATCA TTGAAGAAGC TAAAAAGAAC	240
CAGATGGATC TTGTGATGAA TTTACATCAT TTTGATTTAC CAGTGGAAC TCTTCAAAAA	300
TACGGTGGTT GGGAAAGCAA ACATGTAGTG GAGTTATTCG TGAAGTTTGC CAAGACTGCT	360
TTCACATGCT TTGGAGATAA GGTTCATTAC TGGACAACCT TCAATGAGCC AATGGTCATT	420
CCAGAAGCAG GGTACTTATA TGCTTTCCAT TATCCAAATC TAAAAGGAAA GGGAAAAGAG	480
GCCGTACAAG TCATCTATAA TCTAAACCTT GCTAGTGCAA AAGTGATTCA ACTATATCGC	540
TCATTAGAAC TTGATGGAAA GATTGGGATT ATTTTAAACT TGACACCTGC TTATCCAAGA	600
AGTAATTCTC CAGAAGACTT AGAAGCAAGT CGATTTACAG ATGACTTCTT TAACAAAGTC	660
TTCTTGAATC CAGCTGTTAA AGGAACTTTC CCAGAAAGAT TGGTAAAACA GCTAGAGAGA	720
GATGGCGTGT TATGGAGTCA TACCGAAAAA GAGCTTCAAC TGATGAAATC AAATACGGTT	780
GATTTTCTTG GAGTAAACTA CTACCATCCA AAACGTGTTT AAGCACAAGC AAATCCTGAG	840
GAATATCAGA CGCCCTGGAT GCCAGACCAA TACTTCAAAG AGTATGAATG GCTGGAGCGT	900
CGCATGAATC CATATCGTGG TTGGGAAATT TTTCCGAAAG CCATTTATGA TATTGCTATG	960
ATTGTGAAGG AAGAATATGG TAATATCCCA TGGTTTATCA GTGAA	1005

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTAAAA GAGTAACTA TTAAGTAGTT AATTAACCGG TTTATTACTT	60
TATAGTGAAT CAAATATACT TAAGAAAAGA GGAAAGAATG AAAATTAATA AAAAATATCT	120
AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTTTGTTC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAG AGTCTAATCG AGTTGCTTAT ATAGATGGTG ATCAGGCTGG	240
TCAAAAGGCA GAAAACTTGA CACCAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGATTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAAGGTTT CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCAATGAA ATCAAGGGTG GTTATGTCAT	480
TAAGGTAAAC GGTAATACT ATGTTTACCT TAAGGATGCA GCTCATGCGG ATAATATTCG	540
GACAAAAGAA GAGATTAAAC GTCAGAAGCA GGAACGCAGT CATAATCATA ACTCAAGAGC	600
AGATAATGCT GTTGCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC	780
CTATTGGAAT GGGAAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAAATCC	840
AGCTCAACCA AGATTGTCAG AGAACCACAA TCTGACTGTC ACTCCAATT ATCATCAAAA	900
TCAAGGGGGA AACATTTCAA GCCTTTTACG TGAATTGTAT GCTAACCCCTT ATCAGAACGC	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGT CTGCTGCCCCG	60
TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG	120
CACCAATTCTG TCAAACATCAT TGCCACGGTC CAAACCACCT GCAATCAAGA CGACCTTGCT	180
GTTGTCAAAT CCTGACAAGC TTTTGTAGTA GCCAAGATAT TAGTTGATTT ACTGTCGTTA	240
TAGAATTTAA CACsCTTGAT GTCATCCACA AACTGGAGAC GGTGTTTGAC ACCACCGAAG	300
GCTGAAAGAG TTTCCTTGAT GGTGTTGATTG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

1371

GTCGCAAGGG CATTTTCCAC ATTGTGGCTA CCTGGAACAC CGATTTCATT CGCTGCCATG	420
ACTACTTCAC CACGGAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTTCA	480
AGTGTGTAAA ATGGTACAAC AGTGGCTTCT GTCTTGGAAG TCAAGTCTTT TGCCAAGTCT	540
TGATTAAAGT TCAAGACAAG GAAATCAGCT GCTGTCATCT TGTTCCTGGAT ATTCCACTTG	600
GCTGTACAT ATTCCGAAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA	660
ATAACCGCAA TCTCTGGATG GAATTCTTGA ACACCCATGA GTTGGAAGA AGAAAGTTCC	720
ATAACAAGCG TGTCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA	780
TTCCCTGATA AAAGACCATG TTGGCCAGCA GCAGTCAAAA CTTCCCGGGn TCCTCTAGAG	840
TCG	843

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

TTTTTTTAT ATTTTTTTA TTTATTATTT TTGGCAAAA AAGACCAATT TGCTTTGGAG	60
CATTGCTTCT GCATTAAATT GTCTATTTTT GCTCGTGCTG TTACGCTCTT TGTATCATGT	120
ATTAAGTAGC AAGTGCAACT TGCAAACTAC TAGTAAGAGG AGAAAAACAA AATGGTTATG	180
ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCGTAATG CTAACCAAGC TAAACACGAA	240
GTACTTGAAG TACCTGCATC AAACATCAAA AAAGGGATTG CTGAAATCCT TAAACGCGAA	300
GGTTTTGTAA AAAACGTTGA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT	360
CTTAAATACG GACCAAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA	420
GGACTTCGTG TCTACAAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGGAAAT	480
GCCATCCTTT CAACTTCTGA AGGTTTGCTT ACTGATAAAG AAGCACGCCA AAAGAATGTT	540
GGTGGTGAGG TTATCGCTTA CGTTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA	600
GCAAAATTAG GAAGTTGGAG AAGTTTGTTC ACAAACAGGC CAACCTATCT ATTTTGCACA	660
GTTCTTAGAG CGTGTTCAGT TCAGCTCTTG AGCTAAGTAA GTATCTGAAC CCCGTGAAAA	720
CTGGCCGTGC TGGCATGTTT GGGTAACAGG AGAATAATAA CATGTCACGT ATTGGTAATA	780
AGTTCAGCTA AGGCCTTCGT AAAAGTT	807

1372

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

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CCCAGTATTT TTGTCCAAGC ACGACCAGAA AAGGATGATA CAGATCTGGA ATTGGCTCTC      60
TTAACCATCT tTGAACAAAA TCCTCAGGCT CAGGTCAC TA TTTTCGGTGC CTTGGGTGGC      120
CGTATTGACC ATATGTTGGC CAATGTCTTT CTGCCTAGCA ATCCTAAGTT GGCACCCTAT      180
ATGCATCAAA TAGAAATTGA GGATGGGCAA AACTTGATTA CTTATTGTCC AGAAGGAATC      240
AGTCAGCTAG AACCTCGTTC AGACTACGAC TATCTAGCCT TTATGCCAGT TCGGGATAGC      300
CAAGTATGAG TTGACAGAGG AAAATTTTTT CTTTAAAAA GTGTACGCTT CTAACGAATA      360
TATAGATAGG GAAGTGTCGG TAACTTGCCC AGATGGTTAT GTGGTCGTAC TGCATAGCAA      420
GGACAGGAGG TAGGATGGAA AGTTTACTTA TTCTATTATT AATTGCCAAT CTAGCTGGTC      480
TCTTTCTGAT TTGGCAAAGG CAGGATAGGC AGGAGAAACA CTTAAGTAAG AGCTTGGAGG      540
ATCAGGCAGA TCATTGTGCA GACCAGCTGG ATTACCGCTT TGACCAAGCC AGACAAGCCA      600
GCCAGTTAGA CCAAAAAGAT TTGGAAGTGG TTGTACGCGA CCGTTTGCAA GAA              653
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(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

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CACCATGTGA TGTGACGCTG GCCACAGCTG TCAGAAATCT GGCGAGCCAT CGTGTGCAAT      60
GACTCTTCCC GATGTAATCT TGTTCATAGT CCTTTGATGA ATATGTTCAA GCTGTAGAAG      120
GTGCGCTTCC TGAACACTTA TCAACTGTTA CAGGCGAGTT GACCAGTCAG GAAACAGATG      180
GCTGGTACAC ACTTGCCAAC ACTTCTTCAT CCCGCATTTA CCTAAAACAA GCCTTCCAAG      240
AAAATAGCAA CCTCCTAGAG CAAGTGGTAG AACCTTGAC TATTATCACT GGTGGACACA      300
ACCACAAGGA CCAGTTGACC TATGCTTGGA AAACACTTTT GCAGAATGCG CCACATGATA      360
GTATCTGTGG CTGTAGCGTG GACGAAGTTC ACCGCGAGAT GGAAACGCGT TTTGCCAAGG      420
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1373

TCAACCAAGT AGGAACTTT GTTAAAAGTA ACTTGCTCAA CGAGTGGAAG GGTAATAATG	480
CTACGGATAA GGCTCAAAGT GACTATCTCT TTAAGTGCAT TAACACAGGC TTGCATGATA	540
AGGTGCGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTCAAG GAATTGCACC	600
CAACAGAAGG CTACAAAAAG ATGGCTGCTC TTATCTTGCC G	641

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1958 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTGAAGG CTCTAAAACA ATGGAAAAGT GCTACACAGA TGTGACAGAA	60
TTTGCCATTC CAGCAAGTAC TCAAAAGCTT TACTTATCAC CAGTTTGTAGA TGGCTTTAAT	120
AGCGAAATTA TTGCTTTTAA TCTTTCGACT TCACCCAACT TAGAACAAGT ACAACAATG	180
TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAATACGA TTCTCCATAG TGACCAAGGC	240
TGGCAATATC AACACGATTC TTATCATCGG TTCCTAGAGA GTAAGGGAAT TCAAGCATCT	300
ATGTCACGCA AGGGCAACAG CCAAGACAAC GGTATGATGG AATCTTTCTT TGGCATTTTA	360
AAATCCGAAA TGTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAACAA	420
GCCATTATAG ACTATATTGA TTAACAAC AAACAACGAA TTAAGGTAAA ACTAAAAGGA	480
CTTAGTCCCTG TGCACTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTGG	540
GGTCAGTACA AAACCTCTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTTCT	600
CTCAAATCGA GTTTTACTC AATTTCTTA CTTGATTGGG ATTGAAATTC CAATTAATTT	660
CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTTT	720
CAAGAAAAAT TCTTGAATGG TTTCGATTC AGGCTCACGA ATAGCACGGT GTTTGTTTGA	780
GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAAAATA ACATCTGTAT TCCCTGCAGA	840
ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCGAGTG	900
TGAGTTTGTC GTATTGATAA GCTTCATAAT ATTCCTCCG ATTTTCTAAT TCTATTATAG	960
CACTTTTGA ATAAAGTCGC TTGATTATA CTCAATGAAA ATCAAAGAGC AACTAGGAA	1020
GCTAGCCGCA GGCTATACTT GAGTACGGTA AGGCGACGCT GACGTGGTTT GAATTTTATT	1080
TTCGAAGAGT ATTAGCCAAT CTATGCTGT TTTTCCAAG ATTCAATGGC CCATTTATGG	1140

1374

CTACCACGTT TAAGGTTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG	1200
TTTTCTAGTG GCTTTTGAC TTCTTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG	1260
TAGTAGTAGG TATCACCATG ACGAGAATAG AAATATTCGT CAGCTTGTCG GTAATAGGTA	1320
CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA	1380
TTTTCACCTG CTTCATTTT TCCACATGGT AGGAACCAAG CACCATTGTTG TTCTTGAACA	1440
AGAACAATTT GTTTTGTTC AGGATTAGGG ATAACATGCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACTTTTTT TCTCCGAAAG TTGGGTTTGC CATTGCATTT TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTTCTC TCTTATTGTG AGCGAACAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTCCA AATCTCACGT AATACCATTT ATGGCTGGTT	1740
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA	1800
GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
tACACTCGAA AAAAAAAGA ACTACACCTA CTATGAAC	1958

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATAG	60
CTTAGAGAAG CTTTCAATA AATTGCGGAT AmACAATTCT AATCTTAGGT ATATGATTAA	120
ATTGATTGAT CGTTACGGAA TAGAGTTTCGT CAAAAAGGA AAAAATCGTT ACTATTCTCC	180
TGATTTAAAA CAAGAAATGA TTAATAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTTGAA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG	300
GAAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA GCGGAGAATG	360
CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGAGAAA GAAGAAAGAC	420
AGAAATTGTT TAAGAATTAA TGACTGAGTT TTCGTTAGAT CTTCTTTTAA AAGTCATTAA	480
ACTAGCTCGT TCGACCTACT ACTATCACTT GAAACAGCTA GATAAACCAG ATAAGGACCA	540
AGAGCTTAAA GCTGAAATTC AATCCATTTT TATCGAACAC AAAGGAAATT ATGCTTATCG	600

1375

TCGGATTTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG	660
CTTGATGAAA GTACTCAATt TACAAGCTAA AACGCGACAG AAACGAAAAT ATTCTTCTCA	720
TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCAA GGCCAATTTG AAGGCTCTAA	780
AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTTGCC ATTCCAGTAA GTACTTAAAA	840
GCTTTACTTA T	851

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGAATC GATATCTCCA ATGAGTTGGT tTAGCTGGTG AACTGTAAA AAGATTTGw	60
CCAATTCAG GTGAGGCAT CGCAAATAT GGACTGTTT CTCGTCAGTT CTGGAAGAA	120
AACGGGATAA GGTGGCTGT GAAGCAAGCT GCCCTCCTT CAACAATTTT GGAAAGTAGG	180
CATCAGCTGA CAATCTTTA CAAGCATAGT CCGTTCCATA ACCTGTTAAC AGTTGAAAGA	240
GGAAGTGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCGTTGG TCATTCGTTA	300
CTAAATACTT AGAAATCCGC TCTTTTAGTT TCAACTGGGA AAAAAGTTCC TGAAAAAGA	360
TAAGACCACC ATACTGGGT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT	420
TTTGGAAGTG ATGATTTGGT AACTGTTCA TGTGAGTTT CTTTCTTTT GTGTTTTTT	480
CTACACTTAT ACCATAAAGG GGAACTCTT TTTGTCTAG TAAAAACAC CCATTGGGTG	540
AAAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGGTT TTTAGATTTG	600
GGGTGAATAA TTGGGTTTT AGCTGCTTGC GGCCAATCAG GTTCAGATAC AAAAATTAC	660
TCATCAACCT TTAGTGAAA TCCAATACA TTAACTATC TATTAGACTA TTACGCTGAT	720
AATATAGTCA ATTGAAACAA GAACAAGACA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG	780
GTAATACCTT TTTGAGGTGC TTTTGTATAT GAGCCCATGT TTTCTCAATA GGATGTACT	840
CAGGTGAGTA GGGAGGAAGA GGTAAGTT TATACCCAAA CTCTTCACAC AAGAGTTCTA	900
ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTAATG	960
TTGGTAAGAG AAATTCTGA AACCAAGCTT CAAAAAGTC GCTCGTCATC GTCTCTTCGT	1020
AAGTTATTGG AGCGATTAAC TCACCATTTG TTAGACCTGC AACCAAGAA ATCCTCTGAT	1080

1376

ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC 1140

GATAAAAATA AGTATCGAAT CCTGTTC 1168

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CCGCTTCAGC	60
GTCACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC	120
GTCGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCGGC	180
TTCAGCAAGC ACAAGTGCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC	240
GAGTGCGTCT GAGTCAGCAT CAACGAGTAC GTCAGCCTCA GCAAGCACAT CAGCTTCTGA	300
ATCTGCATCA ACCAGTGCCT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC	360
CAGTGCTTCA GCCTCAGCGT CGACAAGTGC GTCGGCCTCA ACCAGTGCAT CTGAATCGGC	420
ATCAACCAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC	480
ATCGGCTTCA GCATCAACCA GTGCCTCGGC TTCAGCGTCA ACCAGTGCCT CAGCTTCAGC	540
AAGTACCAGT GCTTCAGTCT CAGCATCAAC AAGTGCTTCA GCCTCAGCAT CGACAAGTGC	600
CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCG ACAAGCGCCT CAGCTTCAGC	660
AAGTACCAGT GCGTCAGCCT CAGCGTCGAC AAGTGCGTCA GCCTCAGCAA GTACTAGTGC	720
ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCGGCGTCA ACCAGTGCAT CAGAGTCAGC	780
AAGTACCAGT GCGTCAGCTT CCGCATCAAC AAGTGCCTCG GCTTCAGCAA GCACCAGTGC	840
GTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCCTCA ACCAGTGCCT CAGCCTCAGC	900
AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCGTCC GCTTCAGCAA GTACTAGCGC	960
CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGCCT CTGAATCGGC	1020
ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC	1080
ATCGGCTTCA GCATCAACGA GTGCGTCCGC TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC	1140
GTCAACAAGT GCATCGGCTT CAGCGTCAAC GAGTGCGTCT GAGTCAGCAT CAACGAGTGC	1200
GTCAGCCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CAGCCTCAGC	1260
ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGCGTCA GcTCAGCGTC GACAAGTGCS	1320

1377

TCrGCTTCAG CAAGTACCAG TGCCTCAGCC TCAGCAAGTA CCAGTGCKTC AGCCTCAGCG	1380
TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TGCCTCAGCC	1440
TCAGCAAGTA CTAGCGCCTC AGCCTCAGCA TCAACGAGTG CGTCCGCTTC AGCAAGTACT	1500
AGTGCATCAG CTTAGCAAG TACTAGCGCC TCAGCCTCAG CGTCGACAAG CGCCTCAGCT	1560
TCAGCAAGTA CCAGTGCGTC AGCCTCAGCG TCGACAAGTG CGTCGGCTTC AGCAAGTACC	1620
TCAGCGTCTG AATCAGCATC AACAAAGTGCG TCGGCTTCAG CATCAACGAG TGCATCAGCT	1680
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	1740
AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCCG CATCAACAAG TGCCTCGGCT	1800
TCAGCAAGCA CCAGTGCTTC GGCTTCAGCG TCAACGAGTG CGTCTGAGTC AGCATCAACG	1860
AGTGCGTCAC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCACTTC	1920
CGCATCAACA AGCGCCTCGG CCTCAGCAAG TACAAGTGCT TCAGCCTCAG CATCAACCAG	1980
TGCATCAGCT TCAGCCTCAA CAAGTGCTTC AGCCTCAGCG TCAACCAGTG CCTCGGCTTC	2040
AGCAAGTACC AGTGCGTCAG cTTCAGCAAG CACAAGTGCG TCAGCTTCAG CATCAACCAG	2100
TGCTTCGGCT TCGGCATCAA CAAGTGCCTC AGCATCAGCA TCAACGAGTG CGTCA _s CTCA	2160
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGCGT CAGCCTCAGC AAGTATCTCA	2220
GCGTCTGAAT CGGCATCAAC GAGTGCGTCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA	2280
GCGTCAACCA GTGCATCAGT CTCAGCAAGC ACCAGTGCGT CGGCTTCAGC ATCAACCAGT	2340
GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT CAACGAGTGC GTCAG _c CTCA	2400
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACGAGTGCGT CGGCTTCAGC AAGTACCAGC	2460
GCCTCAGCTT CAGCAAGCAC CAGTGCGTCA GCCTCAGCAA GTACCAGCGC CTCAGCCTCA	2520
GCAAGCACCA GTGCCTCAGC TTCAGCAAGT ACCAGTGCGT CAGCCTCAGC GTCGACAAGT	2580
GCGTCGGCTT CAGCAAGTAC CTCAGCGTCT GAATCAGCAT CAACGAGTGC ATCAGCTTCA	2640
GCATCAACAA GTGCTTCAGC TTCAGCAAGT ACCAGTGCGT CGGCTTCAGC ATCAACGAGT	2700
GCTTCAGTCT CAGCGTCAAC CAGTGCCTCT GAATCAGCAT CAACAAGTGC CTCGGCTTCA	2760
GCAAGCACCA GTGCGTCGGC TTCAGCAAGT ACTAGTGCGT CGGCTTCAGC ATCGACAAGT	2820
GCGTCTGAAT CGGCATCAAC GAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCAGCCTCA	2880
GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CCGCTTCAGC GTCAACCAGT	2940
GCGTCGGCTT CAGCGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCGGCCTCA	3000
GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCCGC TTCAGCAAGC	3060

1378

ACAAGTGCCT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCCTCG	3120
GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT CAACCAGTGC GTCGGCTTCA	3180
GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT	3240
GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG	3300
GCATCAACCA GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT	3360
GCTTCAGCCT CAGCGTCGAC AAGTGCCTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA	3420
ACCAAGTGCCT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG	3480
GCTTCAGCAT CAACCAGTGC CTCGGCTTCA GCGTCAACCA GTGCGTCAGC TTCAGCAAGT	3540
ACCAAGTGCTT CAGTCTCAGC ATCAACAAGT GCTTCAGCCT CAGCATCGAC AAGTGCCTCG	3600
GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT	3660
ACCAAGTGCCT CAGCCTCAGC GTCGACAAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA	3720
GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT	3780
ACCAAGTGCCT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT CAGCAAGCAC CAGTGCCTCG	3840
GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGCGTCAGC CTCAGCAAGT	3900
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA	3960
GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA GTGCGTCTGA ATCGGCATCA	4020
ACGAGTGCCT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAAC AAGTGCATCG	4080
GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA	4140
ACAAGTGCAT CGGGTTCAGC GTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTGCCTCA	4200
CCTCAKCAAG CACATCAGCT TCTGAATCTG CATCAACCAG TCGCTCACTT CCGCATCAAC	4260
AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC	4320
TTCAGCCTCA ACAAGTGCTT CAGCCTCAGC GTCAGACCAG TGCCTCGGCT TCAGCAAGTA	4380
CCAGTGCCTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCGCG	4440
TTCGGCATCA ACAAGTGCCT CAGCATCAGC ATCAACGAGT GCG	4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

GTACCTCAGC GTCCTTCCGC CTCACCAGT GCGTCCGCTT CAGCAAGCAC AAGTGCGTCA	60
CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TCGGTCGGCC TCAGCAAGCG	120
CAAGTACCTC AGCGTCACTT CCGCCTCAAC CAGTGCGTCG GCTTCAGCAA GCACAAGTGC	180
GTCAsCTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCGTC TGAGTCAGCA	240
TCAACGAGTA CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCGGCATC AACCAGTGCG	300
TCAGCCTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG	360
TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG TCGGTCAGCC	420
TCAGCAAGTA CTAGTGATC AGCTTCAGCA TCAACGAGTG CATCGGCTTC AGCATCAACC	480
AGTGCCCTCGG CTTTCAGCGTC AACCAGTGCG TCAGCTTCAG CAAGTACCAG TGCTTCAGTC	540
TCAGCATCAA CAAGTGCTTC AGCCTCAGCA TCGACAAGTG CCTCGGCTTC AGCAAGCACA	600
TCAGCATCTG AATCAGCGTC GACAAGTGG TCGGCCTCAA CCAGTGATC TGAATCGGCA	660
TCAACCAGTG CGTCAGCCTC AGCAAGTACT AGTGATCAG CTTTCAGCATC AACGAGTGCA	720
TCGGCTTCGG CGTCAACCAG TGCATCAGAG TCAGCAAGTA CCAGTGCGTC AGCTTCCGCA	780
TCAACAAGTG CCTCGGCTTC AGCAAGCACA TCAGCATCTG AATCAGCGTC AACCAGTGCT	840
TCGGCTTCAG CAAGTACCAG TGCTTCAGCT TCAGCATCAA CCAGCGCCTC GGCTCAGCA	900
AGCACCTCAG CTTCTGAATC GGCCTCAACC AGCGCCTCGG CCTCAGCAAG CACCTCAGCT	960
TCTGAATCGG CCTCAACCAG CGCCTCAGCC TCAGCATCAA CGAGTGCTTC GGCTTCAGCA	1020
AGCACAAGCG CCTCGGGTTC AGCATCAACG AGTACGTCAG CTTTCAGCGTC AACCAGTGCT	1080
TCAGCCTCAG CATCAACAAG TCGGTCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	1140
TCAACGAGTG CGTCTGAGTC AGCATCAACG AGTACGTCAG CCTCAGCAAG CACAAGTGCT	1200
TCAGCCTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCGTC CGCTTCAGCA	1260
AGTACTAGCG CCTCAGCATC AGCGTCAACA AGTGCTTCGG CTTTCAGCGTC AACGAGTGCG	1320
TCTGAGTCAG CATCAACGAG TACGTCAGCC TCAGCAAGCA CATCAGCTTC TGAATCTGCA	1380
TCAACCAGTG CGTCAGCCTC AGCATCGACA AGCGCCTCAG CTTTCAGCAAG TACCAGTGCG	1440
TCAGCCTCAG CAAGTACCAG TGCTTCAGCC TCAGCGTCGA CAAGTGCGTC GGCTCAACC	1500
AGTGATCTG AATCGGCATC AACCAGTGCG TCAGCTCAGC AAGTACTAGT GCATCAGCTT	1560
CAGCATCAAC GAGTGATCG GCTTCGGCGT CAACCAGTGC ATCAGAGTCA GCAAGTACCA	1620
GTGCGTCACT TCCGCATCAA CAAGTGCCTC GGCTTCAGCA AGCACATCAG CATCTGAATC	1680
AGCGTCAACC AGTGCTTCGG CTTTCAGCAAG TACCAGTGCT TCAGCTTCAG CATCAACCAG	1740

1380

CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACCAGCG CCTCGGCCTC	1800
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGCGCC TCAGCCTCAG CATCAACGAG	1860
TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTTCAGCA TCAACGAGTA CGTCAGCTTC	1920
AGCGTCAACC AGTGCTTCAG CCTCAGCATC AACAAGTGCG TCAGCCTCAG CAAGTATCTC	1980
AGCGTCTGAA TCGGCATCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC	2040
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAGTGCG TCAGCCTCAG CATCGACAAG	2100
CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC	2160
AACCAAGTGCA TCTGAATCGG CATCAACCAG TGCCTCAGCC TCAGCAAGTA CTAGTGATC	2220
GGCTTCAGCA TCAACCAGTG CCTCGGCTTC AGCGTCAACC AGTGCGTCAG CTTCAGCAAG	2280
TACCAAGTCTG TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCCTC	2340
GGCTTCAGCA AGCACATCAG CATCTGAATC AGCGTCGACA AGCGCCTCAG CTTCAGCAAG	2400
TACCAAGTGG TCAGCCTCAG CGTCGACAAG TGCCTCAGCT ACAGCAAGTA CTAGTGATC	2460
AGCTTCAGCA TCAACGAGTG CATCGGCTTC GCGTCAACC AGTGATCAG AGTCAGCAAG	2520
TACCAAGTGG TCAGTTCAG CATCAACAAG	2550

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA	60
CCAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCGTCAC	120
CTCAGCAAGT ACTAGTGCAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC	180
CAGCGCCTCA GCTTCAGCAA GCACCAGTGC GTCA ₅ CTCAG CAAGTACCAG CGCCTCAGCC	240
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	300
AGTGCGTCGG CTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	360
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG	420
AGTGCGTCCG CTTCAGCAAG TACTAGCGCC TCAGCATCAG CGTCAACAAG TGCTTCGGCT	480
TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA	540
TCAGCTTCTG AATCTGCATC AACCAAGTGG TCAGCCTCAG CATCGACAAG CGCCTCAGCT	600

1381

TCAGCAAGTA CCAGTGCCTC AgCCTCAGCA AGTACCAGTG CTTCAGCCTC AGCGTCGACA	660
AGTGCCTCGG CCTCAACCAG TGCATCTGAA TCGGCATCAA CCAGTGCCTC AGCCTCAGCA	720
AGTACTAGCG CCTCAGCCTC AGCATCAACG AGTGCCTCCG CTTCAGCAAG TACTAGTGCA	780
TCAGCTTCAG CAAGTACTAG CGCCTCAGCC TCAGCGTCGA CAAGCGCCTC AGCTTCAGCA	840
AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CTTCAGCAAG TACCTCAGCG	900
TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCATCAA CGAGTGCATC AGCTTCAGCA	960
TCAACAAGTG CTTCAGCTTC AGCAAGTACC AGTGCCTCGG CTTCAGCATC AACGAGTGCT	1020
TCAGTCTCAG CGTCAACCAG TGCCTCTGAA TCCGCATCAA CAAGTGCCTC GGCTTCAGCA	1080
AGCACCAGTG CTTGGCTTC AGCGTCAACG AGTGCCTCTG AGTCAGCATC AACGAGTGCG	1140
TCAGCCTCAG CAAGCACATC AGCTTCTGAA TCTGCATCAA CCAGTGCCTC AGCTTCCGCA	1200
TCAACAAGCG CCTCGGCCTC AGCAAGTACA AGTGCTTCAG CCTCAGCATC AACGAGTGCA	1260
TCAGCTTCAG CCTCAACAAG TGCTTCAGCC TCAGCGTCAA CCAGTGCCTC GGCTTCAGCA	1320
AGTACCAGTG CGTCAGCTTC AGCAAGCACA AGTGCCTCAG CTTCAGCATC AACGAGTGCT	1380
TCGGCTTCGG CATCAACAAG TGCCTCAGCA TCAGCATCAA CGAGTGCCTC AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA CACCGTGCTG ACCAGCACCC GTTCCTGCGA TAATTTTCTT TTTACCCATG	60
CGTwTGGCAA GCCAAACTTG TCCTAAGGCA TTGTTAATCT TGTGGGCTCC TGTATGGTTA	120
AGGTCTTCCC GTTTGAGATA AATCTTGCTC CGCCAATATG CTGGGTCAAG TTTTTCGCT	180
AATAAAGAGG AGTTTCACGT CCTACGTACT GCGCAAAAAG CTGGTTTAAT TCCTCTTGGA	240
AACTTGGGTC TGCCTGACTT TCACGGTAGG CTTCTCCAA CTCCAAAAC TGTGTCATCA	300
ATGTTTCTGG GACAAAACGT CCGCCGAATT TTCCGTAAAA TCCATCTTTA TTTGGTTCCT	360
GATATGCCAT GCTTTACCCT CTCTATAAAT CTTCTAATCT TTTCATGATC TTTTGTCCA	420
TCTGTCTCCA CTCCGCTCGA TACATCTACT GCATAGGGAG TAAAGTGTG AATTGCTTTT	480
ACTACATTAT CTTCATTAAG GCCACCTGCG ATAAAGAAGG GCTGTGCTAG TCCAGTCGTA	540

1382

TCCAGTTGAC	CCCAATCAAA	GGGCTGGCCA	CTTCCTGCCA	CAGGGGCATC	AAAGAGTAGA	600
TAATCTGCCT	GAGAATTGGG	GACATGCCCA	TTTCCATCTA	CCTGCACAGC	CTGAATACTG	660
GCACAAGGCA	AATTCTCAAA	TAAATCATCT	GCCACCTGAC	CGTGAAC TTG	AACCAAGTCC	720
AAGCCGGGGA	TCCTC					735

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC	TCAGCCTCAG	CGTCAACAAG	TGCATCGGCT	TCAGCATCAA	CGAGTGCCTC	60
CGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	AGCGTCAACA	AGTGCAATCGG	CTTCAGCGTC	120
AACGAGTGCG	TCTGAGTCAG	CATCAACGAG	TGCGTCAGCC	TCAGCAAGCA	CATCAGCTTC	180
TGAATCTGCA	TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	240
TACCAGTGCG	TCAGCCTCAG	CGTCGACAAG	TGCGTCGGCT	TCAGCAAGTA	CCAGTGCCTC	300
AGCCTCAGCA	AGTACCAGTG	CGTCAGCCTC	AGCGTCGACA	AGTGCGTCGG	CCTCAACCAG	360
TGCATCTGAA	TCGGCATCAA	CCAGTGCGTC	AGCCTCAGCA	AGTACTAGTG	CATCAGCTTC	420
AGCATCAACG	AGTGCAATCGG	CTTCAGCATC	AACAGTGCA	TCAGAGTCAG	CAAGTACCAG	480
TGCGTCAGCT	TCCGCATCAA	CAAGTGCCCTC	GGCTTCAGCA	AGTACTAGCG	CCTCAGCCTC	540
AGCGTCAACA	AGTGCTTCAG	CTTCCGCGTC	AACCAGCGCC	TCGGCCTCAG	CAAGTATCTC	600
AGCGTCTGAA	TCGGCATCAA	CAAGTGCCCTC	GGCTTCAGCA	TCAACGAGTG	CATCAGTCTC	660
AGCAAGCACC	AGTGCGTCGG	CCTCAGCAAG	CACCAGCGCG	TCTGAATCCG	CATCAACCAG	720
TGCCTCAGCT	TCAGCAAGTA	CCTCAGCATC	TGAATCAGCA	TCAACAAGTG	CATCGGCTTC	780
AGCAAGCACA	AGTGCTTCAG	CCTCAGCAAG	TATCTCAGCG	TCTGAATCCG	CATCAACGAG	840
TGCGTCCGCT	TCAGCAAGTA	CTAGCGCCTC	AGCATCAGCG	TCAACAAGTG	CTTCGGCTTC	900
AGCGTCAACG	AGTGCGTCTG	AGTCAGCATC	AACGAGTACG	TCAGCCTCAG	CAAGCACATC	960
AGCTTCTGAA	TCTGCATCAA	CCAGTGCGTC	AGCCTCAGCA	TCGACAAGCG	CCTCAGCTTC	1020
AGCAAGTACC	AGTGCGTCAG	CCTCAGCAAG	TACCAGTGCT	TCAGCCTCAG	CGTCGACAAG	1080
TGCGTCGGCC	TCAACCAGTG	CATCTGAATC	GGCATCAACC	AGTGCGTCAG	CCTCAGCAAG	1140
TACTAGCGCC	TCAGCCTCAG	CATCAACGAG	TGCGTCCGCT	TCAGCAAGTA	CTAGTGCATC	1200

1383

AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTAGCAAG	1260
CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC TCAGCAAGCA CCAGTGCCTC	1320
AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CTTAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT TCAGCATCAA CAAGTGCTTC	1440
AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG AGTGCTTCAG TCTCAGCGTC	1500
AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCAAGCA CCAGTGCCTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGCCTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TCGCTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACGAGTG CG	1702

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

AACAGTGCAT CAGCTTCAGC CTCAACAAGT GCTTCAGCCT CAGCGTCAAC CAGTGCCCTCG	60
GCTTCAGCAA GTACCAGTGC GTCACCTCAG CAAGCACAAG TGCCTCACTT CAGCATCAAC	120
CAGTGCTTCG GCTTCGGCAT CAACAAGTGC CTCAGCATCA GCATCAACGA GTGCGTCACC	180
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCATCGGCT	300
TCAGCGTCAA CCAGTGCATC AGTCTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACG	360
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCCTCAGCC	420
TCAGCAAGTA CTAGTGCATC GGCTTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCCTCAGCC	540
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCCTCAG CTTAGCAAG CACCAGTGCG TCAGCCTCAG CAAGTACCAG CGCCTCAGCC	660
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGCCTCGG CTTAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	780
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAACG	840

1384

AGTGCTTCAG TCTCAGCGTC AACCAAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT 900

TCAGCAAGCA CCAAGTGCCTC GGCTTCAGCA AGTACTAGTG C 941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCAATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA 60

GTGCATCAGA GTCAGCAAGT ACCAGTGCCT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT 120

CAGCAAGCAC CAGTGCCTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA 180

GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT 240

CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA 300

GTGCGTCTGA ATCGGCATCA ACGAGTGCCT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT 360

CAGCGTCAAC AAGTGCAATG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA 420

GCGCCTCAGC CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT 480

CAGCATCAAC GAGTGCCTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA 540

GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAGT GCGTCAGCCT 600

CAGCGTCGAC AAGTGCCTCG GCTTCAGCAA GTACCAAGTGC GTCAGCCTCA GCAAGTACCA 660

GTGCGTCAGC CTCAGCGTCG ACAAGTGCCT CGGCCTCAAC CAGTGCAATCT GAATCGGCAT 720

CAACCAAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT 780

CGGCTTCAGC ATCAACCAAGT GCATCAGAGT CAGCAAGTAC CAGTGCCTCA GATTCGCGAT 840

GCAACAAGTG CCTCGGCTTC AGCAAGTAC 869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAGTG CCTCAGCATC AGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA 60

1385

TCAGCATCAG CATCAACCAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAACGAGTG CATCAGCATC AGCATCAACG AGTGCATCGG CTTCAGCGTC AACCAGTGCA	180
TCAGTCTCAG CAAGCACCAG TCGCTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	300
TCGGCTTCAG CAAGCACCAG TCGCTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAGTG CGTCAGCCTC AGCAAGTACC AGCGCCTCAG CCTCAGCAAG CACCAGTGCC	540
TCAGCTTCAG CAAGTACCAG TCGCTCAGCC TCAGCGTCGA CAAGTGCCTC GGCTTCAGCA	600
AGTACCTCAG CGTCTGAATC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAAAGTGCT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCCTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGGAAAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCCTGC	60
GGAAATGGCT AAGATGCGCG TGTTAGAACT TGATTTGATG AATGTCGTTG CAGGGACACG	120
CTTCCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAGTCATC CTCTTTATCG ATGAACTCCA CACCATCATG GGTTCCTGGTA GCGGGATTGA	240
TTCGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG GCGCGTGGA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGACTATTTT	420
ACAAGGTTTG AAGGCGACTT ATGAGAAACA TCACCGTGTA CAAATCACAG ATGAAGCGGT	480
TGAAACAGCG GTTAAGATGG CTCATCGTTA TTAAACCAGT CGTCACTTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAAT AAGGCAAAGC ATGTAAAAGC	600
AGACGATTCA GATTTGAGTC CAGCTGACAA GGCCCTGATG GATGGCAAGT GGAAACAGGC	660

1386

AGCCCAGCTA ATCGCAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC	720
TGATATTTTG ACCACCTTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGA CTCAAAC	780
GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA	840
TCAAGCTGTT TCAAGCATTG GCCGTGCCAT TCGCCGCAAC CAGTCAGGGA TTCGAGTCA	900
TAAGCGTCCG ATTGGTTCCT TTATGTTTCT AGGGCCTACA GGTGTCGGGG TATCCGA	957

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG	60
GCTTCAGCGT CAACCAGTGC GTCACATTCA GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAGTGC TTCGGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA	240
ACCAGCGCCT CGGCCTCAGC AAGCACCTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCACAAAG GCCTCGGGTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAGTGC TTCAGCCTCA GCATCAACAA GTGCGTCAGC CTCAGCAAGT	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG	600
ACAAGCGCCT CAGCTTCAGC AAGTACCAAG GCTTCAGCCT CAGCGTCGAC AAGTGCCTCG	660
GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGCGT CAGCCTCAGC AAGTACTAGT	720
GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAGTGC GTCAGCTTCA	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGCCTCCG CTTAGCAAG TACTACCGCC TCAGCCTCAG	60
CGTCAACAAG TGCATCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CACCTCAGCA	180
TCGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG ACAAGTGCCT	240
CGGCTTCAGC AAGTACCAGT GCGTCASCTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG	300
ACAAGTGCCT CGGCCTCAAC CAGTGCATCT GAATCGGCAT CAACCAAGTGC GTCACCTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACCAAGTG	420
CATCAGAGTC AGCAAGTACC AGTGCCTCAG CTTCCTGCATC AACAAGTGCC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCTTC AGCTTCCGCG TCAACCAAGCG	540
CCTCGGCCTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACAAGTGCC TCGGCTTCAG	600
CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAAGTGCCTC GGCCTCAGCA AGCAACGAGC	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CTTAGCAAG TACCTCAGCA TCTGAATCAG	720
CATCAACAAG TGCATCGGCT TCAGCAAGCA CAAGTGCTTC AGCCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAACG AGTGCCTCCG CTTAGCAAG TACTAGCGCC TCAGCATCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGCCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAAGTGC TCAGCCTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAAGTGCCTC AGCCTCAGCA AGTACCAGTG	1020
CTTCAGCCTC AGCGTCGACA AGTGCCTCGG GCTCAACCAG TGCATCTG	1068

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTTCAGCGT CAACCAAGTGC CTCTGAATCA GCTTCAACAA	60
GTGCCTCGGC TTCAGCAAGC CCCAGTGCCT CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGCCTCT GAATCGGCAT CAACGAGTGC TTCGGCTTCA GCATCAACGA	180
GTGCGTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAAGT GCGTCCGyTT	240

1388

CAGCGTCAAC CAGTGCGTCG GCTTCAGCGT CGACAAGTGC TTCGGCTTCA GCATCAACGA	300
GTGCGTCGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTCCGCCTCA ACCAGTGCCT	360
CGGCTTCAGC AAGCACAACT GCGTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA GCTTCAGCAA	540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCGGC CTCAACCAGT GCATCTGAAT	600
CGGCATCAAC CAGTGCGTCA	620

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTGGGGC GCCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGGATA	60
AACCATTTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGCCCA AGAAAGCCAA	120
TTATTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCC ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGGTGACGG TTAACGGCCA	240
AGTGGTGCGT GAACTAGCAA CCACTATCAA GTCAGGCGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGCG GTGTGATTTC	360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTGTGCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTTAC CCTGTGGGTC GTTTGGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGTGTT AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGTTTT GTAGCCTCTA CACCATAAAT	660
ATTGCTAAT AAAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTCTT	720

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTTCC CATCGTACCG CCGAAAATCC CAGCGCCTCA GCCATCAAAT ATCCTATCAA	60
CGTTCTCAAA AAAAGTGACC GCTCTCTCAT CATGTTTCCA AGTGGTAGCC GCCACTCAAA	120
CGATGTCAAG GGGGGCGCAC ACTskATTGC CAAAATGGCC AAGGTCCGTA TCATGCCGGT	180
TACCTACACC GGTCCCATGA CTTTGAAGGG CTTGATTAGC CGTGAACGTG TCGATATGAA	240
CTTTGGAAAT CCAATCGATA TCTCAGATAT CAAGAAAATG AATGATGAAG GCATTGAAAC	300
AGTCGCCAAT CGTATTCAAA CAGAATTCCA ACGTCTGGAC GAAGAAACGA AACAAATGGCA	360
CAATGATAAA AAACCAAATC CACTCTGGTG GTTTATCCGC ATCCCTGCCC TCATCCTTGC	420
TATTATCCTC GCTATCCTAA CCATCATCTT TAGCTTTATC GCAAGCTTCA TCTGGAACCC	480
AGATAAGAAA AGAGAAGAAC TTGCATAGAA GAAATGAACC TTGGCCAAAC AGCTAAGGTT	540
TTCATTTATA TAGTAGATTG GwACTAGAAT AGTACACCTC TACTTCTAAA ACATTTTATG	600
AAATCGATTT GACTGTCCTG ATCGATTTGT CCTAATCTTA TTTCAATT	648

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 690 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT TTCAGCATCG ACAAGTGCCT CTGAATCGGC ATCAACGAGT GCTTCGGCTT	60
CAGCATCAAC GAGTGCCTCA GCTTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	120
GTGCGTCCGC TTCAGCGTCA ACCAGTGCCT CGGCTTCAGC GTCGACAAGT GCTTCGGCTT	180
CAGCATCAAC GAGTGCCTCG GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCGCCTT	240
CAACCAGTGC GTCCGCTTCA GCAAGCACAA GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT	300
CTGAATCGGC ATCAACGAGT GCGTCGGCCT CAGCAAGCGC AAGTACCTCA GCGTCAGCTT	360
CCGCCTCAAC CAGTGCCTCG GCTTCAGCAA GCACAAGTGC GTCAGCCTCA GCAAGTATCT	420
CAGCGTCTGA ATCGGCATCA ACGAGTGCCT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT	480
CAGCAAGCAC ATCAGCTTCT GAATCGGCAT CAACCAGTGC GTCAGCCTCA GCATCGACAA	540
GCGCCTCAGC TTCAGCAAGT ACCAGTGCTT CAGCCTCAGC GTCGACAAGT GCGTCGGCCT	600
CAACCAGTGC ATCTGAATCG GCATCAACCA GTGCGTCAGC CTCAGCAAGT ACTAGTGCAT	660

CAGCTTCAGC ATCAACGAGT GCATCGGCTT 1390 690

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTT CAATATGTGC ACGTTGGAAT GTTAGTGCTT 60
ATATGGGGGG AACAGAATCC TCTCTTGATT GAAGACAAGC TAGTCATTAG GCTGGTTTGT 120
CTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT 180
TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTATA TACTAGTGGT GTTTTGGGG 240
CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTATACT TACAGTTGTT CTGCTCCAAA 300
GAGCTGTAG AGAAGAATTA GTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAATG 360
CACAGGATAA CCTGATGCAT TTTTTAGCG ACAATGCTTG CTACTTCCTT CTGTCGAATT 420
TAGACAATT TAAACCCCAA TTATTCACCC CAAATCTAAA AACCATCCAG AATCCTTGCC 480
TTAGCTTAGA TCCTGGATGG TTTCTTTT CACCCAATGG GTGTTTTTA CTAGACAAAA 540
AAGAGTTTCC CCTTTATGGT ATAAGTGTAG AAAAAACAC AAAAAGAAAG GAAACTCACA 600
TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGTCTTT TTACCAACTA TCTTTCGATG 660
GAGGTCATTT AACCCAGTAT GGTGCTCTTA TCTTTTCA GGAACTTTTT TCCCAGTTGA 720
AACTAAAAGA GCGGATTCTT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT 780
ATTCGGATT CAGATATCCTT GTCCAGTTCC TCTTCAACT GTTAACAGGT TATGGAACGG 840
ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTCC AAAATTATTG GAAGGAGGGC 900
AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTCCAG AACTGACGAG GAAACAGTCC 960
ATAGTTTGCG ATGCCTCAAC CTTGAATTGG TCGAATTCTT TTT 1003

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

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CCGATGATTC TGATTGGTTT GCTCTTTACT TTGCTGGGAA TTTTGAGGTA GATCTATGAT      60
TGAAATACTA ATTGTTTTAG CTATTATCCT ATCTCTTGCT TTGATTGTAT TGGTAACTAT      120
ACAACCCCGT CAAAATCAAC TATTTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG      180
CTACTGGCAG AGCAACACCT TGGTCAAGGT GCTCACTTTA TTGGTGAGTT TGGCTTTATT      240
TATTCTACTA TTAACCTTTA TGGTGATTAC TTATAAATAA AAGAAAACCT CAGATATTCA      300
CCTTTTGTGG ATTGGTCTGA AGTTTCTTTT TTTATACTCA ATGAAAATCA AAGAGCAAAC      360
TAGGAAGCTA GCCGCackGC TCAAAACACC GTTTTGAGGT TGTAGATATA ACTGACGAGc      420
GACTCAAAAC ACCGTTTTGA GGTGTAGAT ATAAGTACG AGcGACTCAA AACACCGTTT      480
TGAGGTTGTG GATAGAACTG ACGAGcGACT CAAAACACCG TTTTGAGGTT GTGGATAGAA      540
CTGACGAAGT CGcTCAAAAC ACCGTTTTGA GGTGTGGAT AGAACTGACG AatgctCAA      600
ACACCGTTTT GAGGTTGTGG ATAGAACTGA CGAAGCgaaC ATATATACAG CAAGGCGACG      660
CTGACGTGGT TTGAAGAGTA TTAAGTCTA TATTTTGGT AAAAATCAAC TTTTACTTGG      720
ATGAAGGTTT TTTTMTTT      738

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(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

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CCGTCTTATC AAAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAACG ACTTTAGCAC      60
GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAACCAGC AATAATTTCT TTGGCACGGT      120
TAATAGCATC TTGGTCACTA GAGTAGATAG ACACATTTCC TTCTTCGTCT ATATCAATCT      180
TAACACCTGT TTCAGCGATA ATCTTGTCGA TGGTTTCTCC ACCCTTACCG ATGACAACTC      240
TAATCTTGTC CACATCAATC TTGATCGTAT CAATTTTCGG AGCAGTTGGA GCCAATTCTG      300
GACGAACTTC TGGAATGGTT GCTTCAATGA CATCAAGGAT TTCAAAACGC GCTTTCTTGG      360
CTTGAGCAAG AGCCTCCGTC AAGATTCTG CAGTAATCCC TTGAATCTTG ATATCCATTT      420
GAAGGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA GTCCATATCT CCAAAGTGAT      480
CTTCCAAACC TTGGATATCT GTCAATACTG TGTAGTTATT TCCATCTGAG ATAAGCCCCA      540
TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACCACC AGCCATAAGG GCAAGAGTTC      600

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1392
CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTC CAAAACTTCT GCTACTAGAC 660
GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG 695

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 691 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT 60
TCACTCATCT TTCATCATTC CTTATACAAC TATGCAGTAT AAATAGAATA GTTTTCTCAT 120
CAGAATGAGA CTATTTTAAT ATTAGATCCC CAATTATTCA CCCCAAATCT AAAAACCATC 180
CAGAATCCTT GCCTTAGCTT AGATCCTGGA TGGTTCCTTT TTTCACCCAA TGGGTGTTTT 240
TTACTAGACA AAAAAGAGTT TCCCCTTTAT GGTATAAGTG TAGAAAAAAA CACAAAAAGA 300
AAGGAAATC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTACCAA 360
CTATCTTTTCG ATGGAGGTCA TTTAACCAG TATGGTGGTC TTATCTTTT TCAGGAACCT 420
TTTTCCTCAGT TGAAACTAAA AGAGCGGATT TCTAAGTAT TAGTAACGAA TGACCAACGC 480
CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCTCTTTCA ACTGTTAACA 540
GGTTATGGAA CGGACTATGC TTGTAAAGAA TTGTCAGCTG ATGCCTACTT TCCAAAATTG 600
TTGGAAGGAG GGCAGCTTGc TTCACAGCCA ACCTTATCCC GwTTTCTTTC CAGAACTGAC 660
GAGGAAACAG TCCATAGTTT GCGATGCCTC A 691

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC 60
CAAGTTATGC CTAAAGGGCC TTAGGAATAG GAGCTTTCAC AAGCTTATCC AGATGATTAT 120
CTTTTACTCG TTATGGACAA TGCTATATGG CATAAATCAA GTACCTTAAA GATTCCGACT 180
AATATTGGCT TTGCATTAT TCCTCCATAC ACACCAGAGA TGAACCCCAT TGAACAAGTG 240

1393

TGGAAAGAGA TTCGTAAACG TGGATTTAAG AATAAAGCCT TTCGAACTTT GGAAGATGTC	300
ATACAAGGAC TGGAGAAGGA GGTGATAAAG TCCATCGTTA ATCGGAGACG GACTAGAATG	360
CTTTTGTAAA ACAGATGAGT ATAAAAAGAA AGTCCTCATT TCAATAGAAA TCACGACTTT	420
CTGATGAATT TATAGTAAAA TGAAATAAGA ACAGGATAGT CAAATCGATT TCTAACAATG	480
TTTTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTGGGG AGTGATAGAA	540
AAGCCCTTCA TCAGCCAATC TACTTGTTCG GGTGCGAGAG CTTTGACATC CTTTCTGTGA	600
CTGGACCAAG TCAGTTTTCG GTTCTCAAAG CGTTTATATA ATATCCAAAA TCCTTGACCA	660
TCCCAGTAAA GAACTTTAAA GCGGTCTTTA CGTCCACCAC AAAAGAGAAA GACTTGATCG	720
GAGAAAGGAT CCAATTCAAA GTGGGTTTGG	750

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAAATTCCTT CGTGGTCCGC ATATCTnTCT TCGTACACGG CAGTCACTTG GTCTTTCCT	60
ACTCGAGTCG CAGCTTCACG GGCCAATTTC TCTTCTACTT GAACTGCCTT TTGGAGGTCA	120
CTGTTGTAGG CTGCAATGAT TTCAGCTTGC AATTCAGCAT CCACGTGAAG CAATTCCACT	180
TCTGCTTTT CTTTACCGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATTCTTTG	240
ACAGCTTCGT GCCCTTTAAG GAGCGCTTCC AACATGATTT CTTCTGACAA TTCTTTGGCA	300
CCAGACTCTA CCATGTTGAT AGCGTGCTTG GTTCCAGCTA CTGTCAATTC AAGAAGAGAT	360
TGCTCTGCTT GTTCTTGACT TGGGTTGATG ATGATTGGC CATCTACATA TCCCCTTGT	420
ACCCAGCAA TTGGTCCGTC AAATGGAATA TCTGAAATAG ACAGTGCCAA AGATGAACCA	480
AACATAGCAG CCATTGGTGC AGATGCATTT TCATCATAAG AAAGCACTGT ATTGATGACT	540
TGGACTTCAT TACGGAAC TCCGCAAAC ATAGGACGAA TCGGACGGTC AATCAAACGC	600
GCTGTCAAGG TCGCATCTGT TGAAGGACGT CTTTACGTT TCATAAGCC ACCAGGAAAC	660
TTCCCAGCCG CATACATTTT TTCTTCGTAG TTGACTTGGA GTGGGAAGAA ATCCTCAGTT	720
GCCATTTTCT GGGGATCC	738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

CCCCCTATTT ACCGTGGACT AAAGTTGTAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT	60
TAGGAACTAT ATATGAGTTC TCTAGTCTGG AGATTTTTC AATAGACTTCG TTATTGGGCG	120
GTTACTTTCG AAACCTTGAA AACTTCAAAA AACGGATTTT TATCGCTTTC AAATCTTTT	180
GGGGTCAAAC TCAGTAACTT ATTCGCCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC	240
AAGGTCCCAA ATAGCCAAGA ATCGTCAGCG ATATTATCTG AATCATCTCC TTCTTGTCT	300
CCTTTAGTTC GCCTGAGGAC AGCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAAAGGCT	360
TGGTCAGGTA GTCATCAGCC CCTAATTCCA AGGCCAAAAC CTTATCAAAT TCATCACTTT	420
TCGCAGAAAC CATCATAATT GGAGTTTGA CGCCTTTGGC TCTCAGCCGC TTACAAACTT	480
CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTCTGTTT	540
CTGCCAAAGC TAAGGCCTTC CGTCCATTG TCACCAATTG AGTAGAAAAG CCTTCCTTAC	600
TTAAATGGTA GTCAAGCAAT TTCAGAATGT GTTCTTCATC ATCCACTAAT AAGACTT	657

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 586 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

CCGCATCAGC ATCAACGAGT GCATCGGCTT CACGTCAACC AGTGCATCAG TCTCAGCAAG	60
CACCAGTGCG TCGGCTTCAG CATCAACGAG TGCCTCAGCC TCAGCAAGTA TCTCAGCGTC	120
TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGGC TTCAGCAAGC	180
ACCAAGTGCCT CGGCTTCAGC ATCAACCAAGT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT	240
GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGCATCAGCA TCAGCATCAA	300
CGAGTGATC GGCTTCAGCA AGTACCAGCG CCTCAGCTTC AGCAAGCACC AGTGCGTCAC	360
CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC	420
CAGTGCGTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACCTC AGCGTCTGAA	480

1395

TCAGCATCAA CGAGTGCCTC AGCTTCAGCA TCAACCACTG CCTCAGCCTC AGCAAGTATC 540
 AGTGCCTCAG CTTCAGCATC AACGAGTGCCT TCAGCTGCAG CAAGTA 586

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCATC AACAACTGCT TCAGCTTCAG 60
 CAAGTACCAG TGCCTCGGCT TCAGCATCAA CGAGTGCCTC AGTCTCAGCG TCAACCACTG 120
 CCTCTGAATC CGCATCAACA AGTGCCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG 180
 CGTCAACGAG TGCCTCTGAG TCAGCATCAA CGAGTGCCTC ACCTCAGCAA GCACATCAGC 240
 TTCTGAATCT GCATCAACCA GTGCGTCAGC TTCCGCATCA ACAAGCGCCT CGGCCTCAGC 300
 AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC 360
 TTCAGCCTCA GCGTCAACCA GTGCCTCGGC TTCAGCAAGT ACCAGTGCCT CAGTTcAGCA 420
 AGCACAAGTG CGTCAATTTA GCATCAACCA G 451

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATTGCG TCGGCTTCAT CAAGCACCAG CGCGTTTGAA TCCGCATCAA 60
 CCAGTGCTTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC 120
 GGCTTCAGCA AGCACAAGTG CTTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA 180
 ACGAGTGCCT CCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCTTCG 240
 GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTGAGC CTCAGCAAGC 300
 ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA 360
 GCTTCAGCAA GTACCAAGTG GTCAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTGC 420

ACAAG

1396

425

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

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AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTTT ATCATGTAgt      60
AGACAAATC TTCATACTCC AACACTTGCC CATTtTATGC GAATCTCATC TATTTTtTCT      120
TTTTTTTGCA ATTTAGCTGA TTTTtCTTTT TTACCATTtA CAGTCACGCG CCCAGCCTTG      180
AGCAAGTTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT      240
CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCTTTTTCG      300
TTTCATACTC TTCAAAAATC TCTTCAAACC GCGTCAACGT CGCCTTGCCG TATATATGTT      360
ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTTCGTCAGT      420
TCTATCTGCA ACCTCAAAGC AGTGCTTTGA GCATCCTGCG GCTAGTTTCC kAGTkTGCTC      480
TTTGATTTwC ATTGAGTATC AGATTtAGGA AATTAACTTC CTCGkCTCCA AAAAAKAGCT      540
AAAACAATCA AGGCTCCTAA AATCGCTGGG AT                                          572

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(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

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CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT      60
CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT      120
CAAcAwGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT      180
CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGCGTCA GCCTCAGCAT      240
CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT      300
CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAAGTGC ATCTGAATCG GCATCAACCA      360
GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT      420

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1397

CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA 480
GCGCCTCAGC TTCAGCAAGC ACCGG 505

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA CCTCATTAGG GGCATAGGCT GCTAAAAATAA CTGCAGCTGT GGTTAATGAC 60
AATACTGTAC TTTTTCAT TTTAATTCCT TACATATTTA TATAACTTCC AATAGATAAT 120
AAACTTTAAC TTTGCTAGCC TTTGTTATAA AAAGTTTAC TAAGTATTAT CTAGGAAATA 180
GAGTAGTACA TTTATATATA ATTGTATCT CTCTATAAAA ACAGTATATC ATTTAAAAA 240
ATTTAAGTCA AAAAAATTAA CATTAGTTAA TTTATTTTTC AGCACACATT AAAAAATAAG 300
ATTAGTACTC AATGAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGAT TGCTCAAAAC 360
AGTGTTTTGA GGTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT 420
GGATAGAACT GACGAAGTCG GTACCGA 447

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 572 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACTTGTC GTTGAATTCT ACAACAAAAT GTTGAATAT TTTATTGAAT AAGATAGGCC 60
TTGATATTAA GCACTTTGGG ACGTTCTCCC TTAGTGCTTT TTTGATTTCT CTTAGTATCC 120
AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGATATA GTAAATGAA 180
CCAAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTCAATAG ATTTTCGTAA 240
AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTCCCA 300
AATCTCACGT AATACCATTT ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA 360
CCACCAAGTA TAGTGTATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT 420

1398

AAATTAATTT GACTTTCCTG ATAGAGATGT TCACATCTTA TTTCAAATA CTATATAAGT	480
TCTATAATCT CTTTATAAGA TTTGCCCATC AGACAAAATA GAACGATTG AAGGCGTTTA	540
TGATATTAG CTGTACGAGA GTCTTTTAAA AG	572

MISSING UPON TIME OF PUBLICATION

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegians Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

What Is Claimed Is:

- 25 1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.
- 30 2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.
- 35 3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 40 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:
- 45 a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;
- b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
- c) retrieval means for obtaining said homologous sequence(s) of step (b).
- 50 6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a
- 55 nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

60 7. A method for identifying an expression modulating fragment of *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

70 8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a degenerate variant thereof.

75 9. A vector comprising any one of the fragments of the *Streptococcus pneumoniae* genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.

80 10. An isolated fragment of the *Streptococcus pneumoniae* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a degenerate variant thereof.

85 11. A vector comprising any one of the fragments of the *Streptococcus pneumoniae* genome of claim 8.

12. An organism which has been altered to contain any one of the fragments of the *Streptococcus pneumoniae* genome of claim 8.

90 13. An organism which has been altered to contain any one of the fragments of the *Streptococcus pneumoniae* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;

b) identifying members of said library which contain sequences that hybridize to said target sequence; and

c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

a) isolating mRNA, DNA, or cDNA produced from an organism;

b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;

c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

130

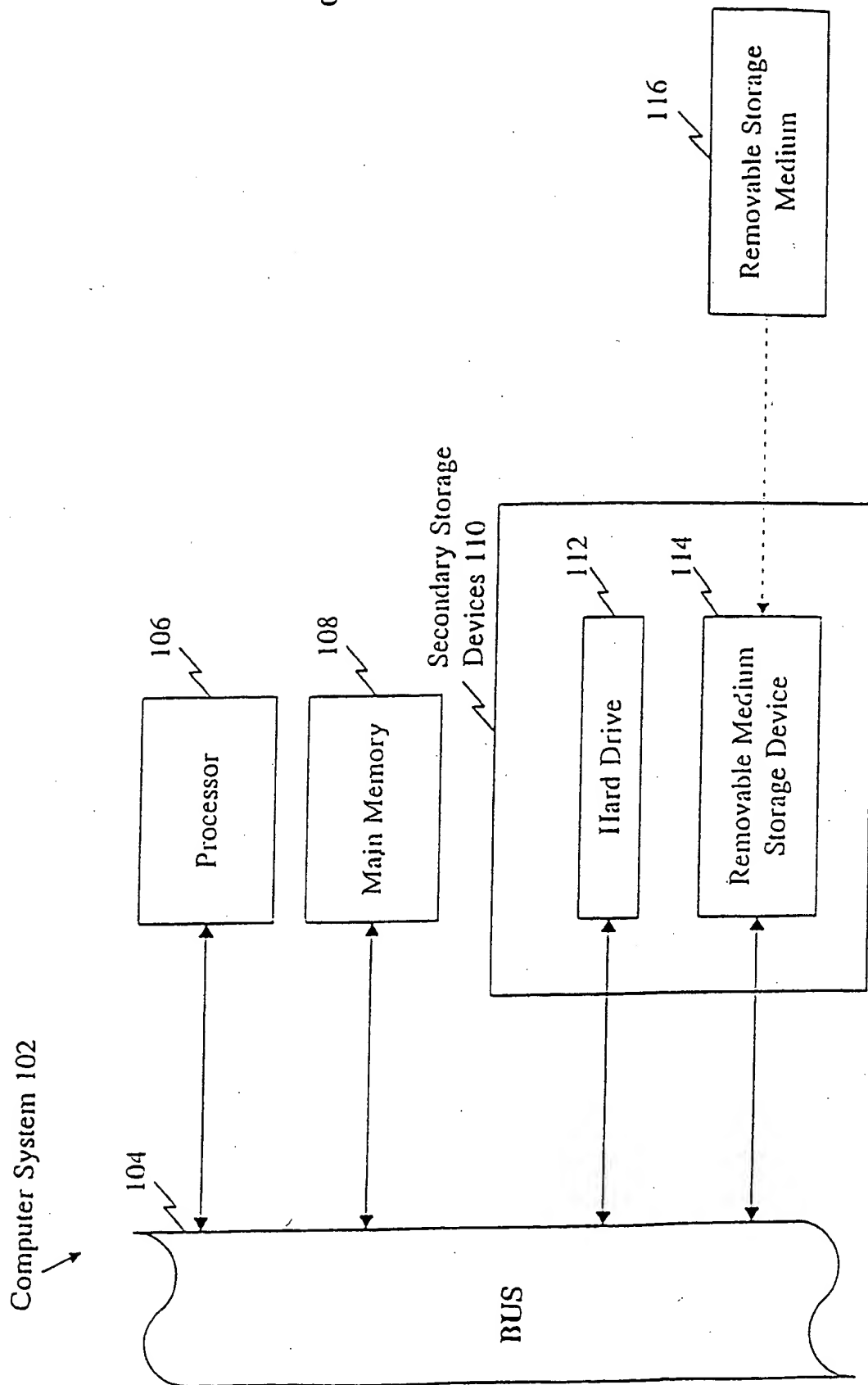
20. A method for producing a polypeptide in a host cell comprising the steps of:

135

a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.

Figure 1



2/2

Figure 2

